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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 20.3612 Seconds

(without alignments)  
2678.292 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVCLRENFAVYV.....ESEVAISEELVQKYSNALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	680.5	96.5	522 3	AAy71312 Rat neuro
2	510	72.3	199 5	Abb81077 Rat neuro
3	503	71.3	118 5	Abb8192 Human pol
4	503	71.3	199 2	AAW53947 Human NSP
5	503	71.3	199 2	AAW78313 Fragment
6	503	71.3	199 2	AAy35903 Extended
7	503	71.3	199 3	AAy35903 Human NSP
8	503	71.3	199 4	AAy35903 Human NSP
9	503	71.3	199 5	AAy35903 Human NSP
10	503	71.3	199 5	AAy35903 Human NSP
11	503	71.3	199 8	ADP19211 Human sec
12	503	71.3	199 8	ADP67236 Human sec
13	499.5	70.9	199 3	AAy71559 Rat Nogo
14	496	70.4	199 7	ADK67504 Human RTN
15	448	63.5	1178 3	AAy71311 Human neu
16	447	63.4	403 3	AAy71563 Rat Nogo
17	447	63.4	893 3	AAy95012 Human sec
18	447	63.4	983 6	ABU11573 Human MDD
19	447	63.4	1162 3	AAy71557 Rat Nogo
20	447	63.4	1162 8	ADT89537 Mus muscu
21	447	63.4	1163 3	AAy71310 Rat neuro
22	447	63.4	1163 3	AAy71384 Alternati
23	447	63.4	1163 5	Abb81074 Rat neuro
24	447	63.4	1163 8	ADO26399 Rat trunc
25	447	63.4	1163 8	ADP45572 Rat NogoA

26	447	63.4	1192 3	AAy56967 Human MAG
27	447	63.4	1192 4	AAy82349 Human NOG
28	447	63.4	1192 4	AAU04591 Human NOG
29	447	63.4	1192 5	ABG30938 Human NOG
30	447	63.4	1192 5	ABP68600 Human pan
31	447	63.4	1192 5	ABB81078 Human neu
32	447	63.4	1192 6	ABr59667 Human NOG
33	447	63.4	1192 8	ADO08103 Human pol
34	447	63.4	1192 8	ADO26400 Human tru
35	447	63.4	1192 8	ADP45551 Human NOG
36	447	63.4	1192 8	ADP67234 Human NOG
37	447	63.4	1192 8	ADP13966 Human NOG
38	443	62.8	103 4	AAE03980 Human gen
39	443	62.8	200 4	AAy64514 Human sec
40	443	62.8	359 3	AAy71558 Rat Nogo
41	443	62.8	360 3	AAy71383 Rat neuro
42	443	62.8	360 4	AAE03987 Human gen
43	443	62.8	360 5	ABB81076 Rat neuro
44	443	62.8	361 3	AAy71385 Alternati
45	443	62.8	373 3	AAy53624 A bone ma

## ALIGNMENTS

RESULT 1

AAy71312  
ID: AAy71312 standard; protein; 522 AA.

XX AC AAy71312;

DT 02-NOV-2000 (first entry)

DE Rat neurite growth inhibitor Nogo C.

XX Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.

XX Rattus sp.

XX Key Location/Qualifiers

FT Region 1..39 /note= "Sequence upstream to the N-terminus of Nogo C protein"

FT Misc-difference 3 /note= "Encoded by TAG"

FT Region 11..191 /note= "Region specifically described in claim 16"

FT Misc-difference 29 /note= "Encoded by TAA"

FT Protein 40..238 /label= Nogo\_C\_protein

FT Region 51..238 /note= "C-terminal common region found in Nogo A, B and C isoforms"

FT Region 239..522 /note= "Sequence downstream to the C-terminus of Nogo C protein"

FT Misc-difference 239 /note= "Encoded by TGA"

FT Misc-difference 263 /note= "Encoded by TGA"

FT Misc-difference 276 /note= "Encoded by TAG"

FT Misc-difference 281 /note= "Encoded by TGA"

FT Misc-difference 295 /note= "Encoded by TAA"

FT Misc-difference 298 /note= "Encoded by TAA"  
 FT Misc-difference 314 /note= "Encoded by TGA"  
 FT Misc-difference 318 /note= "Encoded by TGA"  
 FT Misc-difference 335 /note= "Encoded by TGA"  
 FT Misc-difference 371 /note= "Encoded by TAG"  
 FT Misc-difference 374 /note= "Encoded by TGA"  
 FT Misc-difference 380 /note= "Encoded by TAG"  
 FT Misc-difference 406 /note= "Encoded by TAA"  
 FT Misc-difference 408 /note= "Encoded by TAA"  
 FT Misc-difference 410 /note= "Encoded by TAG"  
 FT Misc-difference 422 /note= "Encoded by TAA"  
 FT Misc-difference 433 /note= "Encoded by TGA"  
 FT Misc-difference 440 /note= "Encoded by TAG"  
 FT Misc-difference 453 /note= "Encoded by TAG"  
 FT Misc-difference 465 /note= "Encoded by TAG"  
 FT Misc-difference 482 /note= "Encoded by TAG"  
 FT Misc-difference 513 /note= "Encoded by TAA"  
 FT FT  
 XX WO200031235-A2.  
 XX PN  
 XX PD 02-JUN-2000.  
 XX PF 05-NOV-1999; 98WO-US026160.  
 XX PR 06-NOV-1998; 98US-0107446P.  
 XX PA (SCHW/) SCHWAB M E.  
 XX PA (CHEN/) CHEN M S.  
 XX PI Schwab ME, Chen MS;  
 XX XX  
 XX WPI; 2000-400052/34.  
 XX DR N-PSDB; AAD01175.  
 XX XX  
 XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 XX of the central nervous system and inducing regeneration of neurons.  
 XX  
 XX Claim 7; Fig 14; 122pp; English.  
 XX  
 XX The present sequence is a rat Nogo C protein which is a potent neural  
 XX cell growth inhibitor and is free of all central nervous system (CNS)  
 XX myelin material with which it is natively associated. Nogo proteins and  
 XX fragments displaying neurite growth inhibitory activity are used in the  
 XX treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
 XX medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
 XX haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,  
 XX neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
 XX Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
 XX activity can be used to treat or prevent hyperproliferative or benign  
 XX dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
 XX Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
 XX production of Nogo protein to induce regeneration of neurons or to  
 XX promote structural plasticity of the CNS in disorders where neurite  
 XX growth, regeneration or maintenance are deficient or desired. The animal  
 XX models can be used in diagnostic and screening methods for predisposition  
 XX to disorders and to screen for or test molecules which can treat or

CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers  
 XX  
 SQ Sequence 522 AA;  
 Query Match 96.5%; Score 680.5; DB 3; Length 522;  
 Best Local Similarity 98.6%; Pred. No. 3.8e-71;  
 Matches 138; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 Qy 3 SGEAGVCLRENFAVYSVGMHNL-LLEGRSQEMDGGQKKHWKDKVVDLLYWRDIKKT 61  
 Db 4 SGEAGVCLRENFAVYSVGMHNL-LLEGRSQEMDGGQKKHWKDKVVDLLYWRDIKKT 63  
 Qy 62 GVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIAIAKSDGHPFRAYL 121  
 Db 64 GVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIAIAKSDGHPFRAYL 123  
 Qy 122 ESEVAISEELVQKYSNSALG 141  
 Db 124 ESEVAISEELVQKYSNSALG 143  
 RESULT 2  
 ABB81077  
 ID ABB81077 standard; protein; 199 AA.  
 XX AC ABB81077;  
 XX DT 05-NOV-2002 (first entry)  
 XX DE Rat neurotransmitter receptor protein Nogo-C.  
 XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnery; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.  
 XX OS Rattus norvegicus.  
 XX PN US2002072493-A1.  
 XX PD 13-JUN-2002.  
 XX PF 28-JUN-2001; 2001US-00893348.  
 XX PR 19-MAY-1998; 98IL-00124500.  
 XX PR 21-JUL-1998; 98WO-US014715.  
 XX PR 22-DEC-1998; 98US-00318277.  
 XX PR 19-MAY-1999; 99US-00314161.  
 XX PA (VEDA ) VEDA RES & DEV CO LTD.  
 XX PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Béserman P, Mosonogo A;  
 PI Mosalem G;  
 XX WPI; 2002-607255/65.  
 XX DR N-PSDB; ABN86600.  
 XX  
 XX Promoting nerve regeneration and preventing neuronal degeneration in the  
 XX central/peripheral nervous system from injury/disease, comprises  
 XX administering nervous system-specific activated T cells/antigen, or  
 XX analogs/peptides.  
 XX  
 XX Example 5; Page 48-49; 93pp; English.  
 XX  
 XX The invention relates to promoting nerve regeneration or conferring  
 XX neuroprotection and preventing or inhibiting neuronal degeneration in the  
 XX central/peripheral nervous system (NS). The method involves administering  
 XX NS-specific activated T cells, NS-specific antigen, its analogue or its



peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, Glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, amyloid polynuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-C, an example of NS-specific antigen

XX SQ Sequence 199 AA;

Query Match 72.3%; Score 510; DB 5; Length 199;  
Best Local Similarity 99.0%; Pred. No. 1.4e-51;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 97  
DB 1 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVIOIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 141  
DB 61 PRIYKGVIOIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 3  
ID ABB89192 standard; protein; 118 AA.

XX AC ABB89192;

XX DT 24-MAY-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 1568.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
XX KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;  
XX KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX KW neurological disease; infection; human; secreted protein.

XX OS Homo sapiens.

XX XX WO200190304-A2.

XX XX 29-NOV-2001.

XX XX 18-MAY-2001; 2001WO-US016450.

XX XX 19-MAY-2000; 2000US-0205515P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Birse CE, Rosen CA;

XX XX WPI; 2002-122018/16.

DR N-PSDB; ABL89601.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.

XX Claim 11; SEQ ID NO 1568; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 118 AA;

Query Match 71.3%; Score 503; DB 5; Length 118;  
Best Local Similarity 98.1%; Pred. No. 4.7e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 97  
DB 1 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVIOIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 141  
DB 61 PRIYKGVIOIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 4

AAW53947

ID AAW53947 standard; protein; 199 AA.

XX AC AAW53947;

XX DT 24-JUL-1998 (first entry)

XX DE Human NSPLP protein A.

XX KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;  
XX KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer.

XX OS Homo sapiens.

XX PN WO9806841-A2.

XX PD 19-FEB-1998.

XX PF 24-JUL-1997; 97WO-US013469.

XX PR 12-AUG-1996; 96US-00700607.

XX XX (INCY-) INCYTE PHARM INC.

XX XX Bandman O, Au-Young J, Goli SK, Hillman J;

XX XX WPI; 1998-159533/14.

XX XX N-PSDB; AAV23695.

XX Human neuro-endocrine-specific protein-like proteins - useful for diagnosis, monitoring and treatment of cancer and neuro-degenerative

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PT disease.
XX Claim 1; Page 38; 73pp; English.
XX
CC This sequence is a human neuroendocrine-specific protein-like protein
CC (NSPLP) of the invention. Recombinant cells transformed with the DNA are
CC used to express the NSPLP proteins, which are used to treat cancer and
CC neurodegenerative diseases such as amyotrophic lateral sclerosis. Also
CC antisense nucleic acids and antagonists of NSPLP can be used to inhibit
CC activity of the NSPLP proteins. Antibodies specific for NSPLP are used
CC for diagnosis and monitoring treatment of diseases associated with NSPLP
CC expression, in usual immunoassays, and to isolate NSPLP from natural
CC sources. The NSPLP proteins, or their fragments can also be used in drug
CC screening to identify NSPLP antagonists. The nucleic acid can be used
CC diagnostically and for monitoring treatment (in hybridisation or
CC amplification assays); to isolate closely related sequences; in gene
CC therapy for both sense and antisense applications (including use of
CC ribozymes) and for mapping the natural genomic sequence
XX
SQ Sequence 199 AA;
Query Match 71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 9.4e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 38 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
DB 1 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
QY 98 PRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
DB 61 PRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALG 104
RESULT 5
AAW78313
ID AAW78313 standard; protein; 199 AA.
XX
AC AAW78313;
XX
DT 13-APR-1999 (first entry)
DE Fragment of human secreted protein encoded by gene 69.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
XX WO9856804-A1.
XX
PD 17-DEC-1998.
XX
XX 11-JUN-1998; 98WO-US012125.
XX
PR 13-JUN-1997; 97US-0049547P.
PR 13-JUN-1997; 97US-0049548P.
PR 13-JUN-1997; 97US-0049549P.
PR 13-JUN-1997; 97US-0049550P.
PR 13-JUN-1997; 97US-0049556P.
PR 13-JUN-1997; 97US-0049606P.
PR 13-JUN-1997; 97US-0049607P.
PR 13-JUN-1997; 97US-0049608P.
PR 13-JUN-1997; 97US-0049609P.
PR 13-JUN-1997; 97US-0049610P.
PR 13-JUN-1997; 97US-0049611P.
PR 13-JUN-1997; 97US-0050901P.

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PR 13-JUN-1997; 97US-0052989P.
PR 08-JUL-1997; 97US-0051919P.
PR 18-AUG-1997; 97US-0055984P.
PR 12-SEP-1997; 97US-0058665P.
PR 12-SEP-1997; 97US-0058666P.
PR 12-SEP-1997; 97US-0058667P.
PR 12-SEP-1997; 97US-0058668P.
PR 12-SEP-1997; 97US-0058669P.
PR 12-SEP-1997; 97US-0058670P.
PR 12-SEP-1997; 97US-0058671P.
PR 12-SEP-1997; 97US-0058672P.
PR 12-SEP-1997; 97US-0058675P.
PR 02-OCT-1997; 97US-0060834P.
PR 02-OCT-1997; 97US-0060835P.
PR 02-OCT-1997; 97US-0060841P.
PR 02-OCT-1997; 97US-0060844P.
PR 02-OCT-1997; 97US-0060865P.
PR 02-OCT-1997; 97US-0061059P.
PR 02-OCT-1997; 97US-0061060P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;
PI Feng P;
XX
XX WPI; 1999-080881/07.
XX N-PSDB; AAX04379.
DR
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Disclosure; Page 62; 380pp; English.
XX
CC This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 86 novel genes and their fragments (nucleic acid sequences:
CC AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 86 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAX04311 for
CC described uses)
XX
SQ Sequence 199 AA;
Query Match 71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 9.4e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 38 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
DB 1 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
QY 98 PRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
DB 61 PRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALG 104
RESULT 6
AAW35903
ID AAW35903 standard; protein; 199 AA.
XX
XX AAW35903;
AC AAW35903;
XX
DT 13-SEP-1999 (first entry)
DE Extended human secreted protein sequence, SEQ ID NO. 152.
XX
XX Secreted protein; human; cytokine; cellular proliferation; cell movement;

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KW cellular differentiation; immune system regulator; anti-inflammatory;  
 KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
 KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
 KW genetic disease.  
 XX Homo sapiens.  
 XX WO9931236-A2.  
 XX 24-JUN-1999.  
 XX 17-DEC-1998; 98WO-IB002122.  
 XX 17-DEC-1997; 97US-0069957P.  
 PR 09-FEB-1998; 98US-0074121P.  
 PR 13-APR-1998; 98US-0081563P.  
 PR 10-AUG-1998; 98US-0096116P.  
 XX (GEST ) GENSET.  
 XX Bougueleret L, Duclert A, Dumas Milne Edwards J;  
 XX WPI; 1999-385906/32.  
 DR N-PSDB; AAX97587.  
 XX New isolated human secreted proteins.  
 XX Claim 9; Page 185-186; 516pp; English.

XX This sequence is encoded by an extended human secreted protein coding  
 sequence of the invention. The secreted proteins can be used in treating  
 or controlling a variety of human conditions. The secreted proteins may  
 act as cytokines or may affect cellular proliferation or differentiation  
 or may act as immune system regulators, haematopoiesis regulators, tissue  
 growth regulators, regulators of reproductive hormones or cell movement  
 or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or  
 tumour inhibition activity. The DNAs can be used in forensic procedures  
 to identify individuals or in diagnostic procedures to identify  
 individuals having genetic diseases resulting from abnormal expression of  
 the genes corresponding to the extended cDNAs. They are also useful for  
 constructing a high resolution map of the human chromosomes. They can  
 also be used for gene therapy to control or treat genetic diseases  
 XX Sequence 199 AA;  
 SQ

Query Match 71.3%; Score 503; DB 2; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
 DB 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
 QY 98 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 141  
 DB 61 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 104

RESULT 7  
 AAB12805  
 ID AAB12805 standard; protein; 199 AA.  
 XX AAB12805;  
 XX 24-NOV-2000 (first entry)  
 DT Human NSPH protein sequence SEQ ID NO:4.  
 DE Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC.  
 KW Homo sapiens.  
 XX CN1253180-A.

XX 17-MAY-2000.  
 PD 30-OCT-1998; 98CN-00121473.  
 PF 30-OCT-1998; 98CN-00121473.  
 XX 30-OCT-1998; 98CN-00121473.  
 PR (UYFU-) UNIV FUDAN.  
 XX Yu L, Zhao Y, Zhang H;  
 PI WPI; 2000-466537/41.  
 XX DR N-PSDB; AAA72981.  
 XX Specific protein of human neuroendocrine, coding sequence and its  
 PT preparing process and application.  
 XX Claim 4; Page 14-15; 21pp; Chinese.  
 PS The present invention relates to a new member of the human neuroendocrine  
 CC specific protein family, designated NSPH. The present sequence represents  
 CC the human NSPH protein  
 XX Sequence 199 AA;  
 SQ

Query Match 71.3%; Score 503; DB 3; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
 DB 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
 QY 98 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 141  
 DB 61 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 104

RESULT 8  
 AAB82348  
 ID AAB82348 standard; protein; 199 AA.  
 XX AAB82348;  
 XX 23-JUL-2001 (first entry)  
 DT Human NSPH protein.

XX NSPH; 2001-343822/36.  
 DR N-PSDB; AAF90323.  
 XX New polypeptide designated NSPH-C is a splice variant of the human NSPH  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; neurotropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy.  
 XX Homo sapiens.  
 OS WO200136631-A1.  
 XX 25-MAY-2001.  
 PD 14-NOV-2000; 2000WO-GB004345.  
 PF 15-NOV-1999; 99GB-00026995.  
 PR 24-JAN-2000; 2000GB-00001550.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Michalovich D, Prinjha R;  
 PI WPI; 2001-343822/36.  
 DR N-PSDB; AAF90323.  
 XX New polypeptide designated NSPH-C is a splice variant of the human NSPH

PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.  
 XX  
 XX Claim 3; Page 25; 25pp; English.  
 XX  
 CC The present sequence is that of human Nogo-C, encoded by a novel splice  
 CC variant of the human Nogo gene on chromosome 2p21. 2 Other splice  
 CC variants, Nogo-A and Nogo-B, have previously been identified. The  
 CC invention provides Nogo-C polypeptides and polynucleotides, and methods  
 CC for producing such polypeptides by recombinant techniques. Also disclosed  
 CC are methods for utilizing Nogo-C polypeptides and polynucleotides in the  
 CC treatment of diseases including neuropathies, spinal injury, brain  
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease  
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders  
 CC and developmental disorders. Also provided are methods for identifying  
 CC agonists and agonists for use in treating conditions associated with Nogo  
 CC -C imbalance, and diagnostic assays for detecting diseases associated  
 CC with inappropriate Nogo-C activity or levels  
 XX  
 XX Sequence 199 AA;  
 SQ  
 Query Match 71.3%; Score 503; DB 4; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 38 MDGQKKHWKDVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 97  
 DB 1 MDGQKKHWKDVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 60  
 QY 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNLSALG 141  
 DB 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNLSALG 104  
 RESULT 9  
 ABG30939  
 ID ABG30939 standard; protein; 199 AA.  
 XX  
 XX AC ABG30939;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human NogoC protein.  
 XX  
 KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoC;  
 KW Nogo-associated disease; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200257483-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 PF 18-JAN-2002; 2002WO-GB000228.  
 XX  
 XX 18-JAN-2001; 2001GB-00001312.  
 XX  
 XX (GLAXO) GLAXO GROUP LTD.  
 XX (SMK) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
 XX  
 XX WPI; 2002-599722/64.  
 DR N-P8DB; ABK90135.  
 XX  
 XX Identifying modulators of Nogo or BACE activity for treating acute  
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
 PT providing and monitoring interaction between Nogo and BACE polypeptides.  
 XX

PS Disclosure; Page 64; 68pp; English.  
 XX  
 CC The present invention relates to a new method of identifying modulators  
 CC of Nogo function or BACE activity. The method involves providing Nogo and  
 CC BACE polypeptides capable of binding with each other, monitoring the  
 CC interaction between these polypeptides, and determining if the test agent  
 CC is a modulator of Nogo or BACE activity. The method is useful in treating  
 CC acute neuronal injuries, such as spinal or head injury, stroke,  
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
 CC hypertrophy) of the central nervous system. The BACE polypeptide is  
 CC useful in screening methods to identify agents that may act as modulators  
 CC of BACE activity and in particular agents that may be useful in treating  
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
 CC and the polynucleotide encoding the BACE polypeptide are useful in  
 CC manufacturing a medicament for the treatment or prevention of disorders  
 CC responsive to the modulation of Nogo activity, in alleviating the  
 CC symptoms or improving the condition of a patient suffering from this  
 CC disorder, in axon regeneration, or in preventing metastasis or spreading  
 CC of a cancer. The polynucleotide may also be an essential component in  
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
 CC techniques. The present amino acid sequence represents the human NogoC  
 CC protein of the invention  
 XX  
 XX Sequence 199 AA;  
 SQ  
 Query Match 71.3%; Score 503; DB 5; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 38 MDGQKKHWKDVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 97  
 DB 1 MDGQKKHWKDVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 60  
 QY 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNLSALG 141  
 DB 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNLSALG 104  
 RESULT 10  
 ABB81080  
 ID ABB81080 standard; protein; 199 AA.  
 XX  
 XX AC ABB81080;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human neurotransmitter receptor protein Nogo-C.  
 XX  
 KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnery; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW neurotic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; human; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002072493-A1.  
 XX  
 XX 13-JUN-2002.  
 XX  
 XX 28-JUN-2001; 2001US-00893348.  
 XX  
 XX 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX  
 XX (YEDA) YEDA RES & DEV CO LTD.  
 PA  
 XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI

PI Moalem G;  
XX WPI: 2002-607255/65.  
DR N-PSDB; ABN86601.  
XX  
XX Promoting nerve regeneration and preventing neuronal degeneration in the  
PT central/peripheral nervous system from injury/disease, comprises  
PT administering nervous system-specific activated T cells/antigen, or  
PT analogs/peptides.  
XX  
XX Example; Page 57-58; 93pp; English.  
PS  
XX The invention relates to promoting nerve regeneration or conferring  
XX neuroprotection and preventing or inhibiting neuronal degeneration in the  
CC central/peripheral nervous system (NS). The method involves administering  
CC central/peripheral nervous system (NS). The method involves administering  
CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
CC combinations. The method is useful for promoting nerve regeneration and  
CC preventing neuronal degeneration in central/peripheral nervous system  
CC from injury/disease, where the injury is spinal cord injury, blunt  
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
CC damages caused by surgery such as tumour excision. The disease is not an  
CC autoimmune disease or neoplasm. The disease results in a degenerative  
CC process occurring in either gray or white matter or both. The disease is  
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
CC neuropathies associated with various diseases, including but not limited  
CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
CC syndromes, polycythemia vera, immunoglobulin (IgA- and IgG gamma-  
CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
CC disease, or lipoproteinemia. The present sequence represents the human  
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific  
XX antigen  
XX  
SQ Sequence 199 AA;  
Query Match 71.3%; Score 503; DB 5; Length 199;  
Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 38 MDGQKXHWKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKNWKKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
QY 98 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNALS 141  
Db 61 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNALS 104  
RESULT 12  
ADP67236  
ID ADP67236 standard; protein; 199 AA.  
XX  
XX ADP67236;  
AC  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human Nogo-C protein.  
XX human; Nogo-C; neurite outgrowth inhibitor; Nogo;  
KW contactin-associated protein-1; Caspr; neuroprotective; gene therapy;  
KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.  
XX  
OS Homo sapiens.  
XX  
XX US2004110939-A1.  
XX

PD 10-JUN-2004.  
XX  
XX 15-OCT-2001; 2001US-00978360.  
XX  
XX 17-DEC-1998; 98WO-IB002122.  
PR 09-FEB-1999; 99WO-IB000282.  
PR 21-JUN-2000; 2000WO-IB000951.  
PR 15-SEP-2000; 2000US-00663600.  
XX  
XX (GEST ) GENSET SA.  
XX  
XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;  
PI Duclert A;  
XX  
XX WPI: 2004-440404/41.  
DR N-PSDB; ADP18806.  
XX  
XX New isolated polynucleotide encoding secreted polypeptide, useful for  
PT gene therapy, or in diagnostic procedures to identify individuals having  
PT genetic diseases resulting from abnormal expression of the genes.  
XX  
XX Claim 2; SEQ ID NO 467; 113pp; English.  
PS  
XX The invention relates to human cDNA sequences that encode human secreted  
CC proteins. The invention also relates to an antibody that specifically  
CC binds to a polypeptide of the invention and a method of binding the  
CC polypeptide to an antibody. The polynucleotides are useful for expressing  
CC the entire secreted proteins which they encode and for distinguishing  
CC human tissues and cells from non-human tissues and cells, and for  
CC distinguishing between human tissues and cells that do or do not express  
CC the polynucleotides comprising the cDNAs. The polynucleotides and  
CC polypeptides are useful in forensic procedures or diagnostic procedures  
CC to identify individuals with genetic diseases resulting from abnormal  
CC expression of the genes corresponding to the cDNAs. The sequences are  
CC also useful in gene therapy to control or treat genetic diseases. This  
CC sequence represents a human secreted polypeptide of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
XX Sequence 199 AA;  
Query Match 71.3%; Score 503; DB 8; Length 199;  
Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 38 MDGQKXHWKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKNWKKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
QY 98 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNALS 141  
Db 61 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNALS 104  
RESULT 12  
ADP67236  
ID ADP67236 standard; protein; 199 AA.  
XX  
XX ADP67236;  
AC  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human Nogo-C protein.  
XX human; Nogo-C; neurite outgrowth inhibitor; Nogo;  
KW contactin-associated protein-1; Caspr; neuroprotective; gene therapy;  
KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.  
XX  
OS Homo sapiens.  
XX  
XX WO2004052389-A2.  
XX



```

XX Human RTN-4C protein.
DE
XX
XX neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis;
KW Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX WO2003088926-A2.
XX
XX 30-OCT-2003.
XX
XX 08-APR-2003; 2003WO-US008829.
XX
XX 17-APR-2002; 2002US-0373284P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Yan R, Lu Y;
XX
XX WPI; 2003-854033/79.
XX
XX New polypeptide having BACE1 activity, useful in preparing a composition
PT for treating amyloidosis or Alzheimer's disease.
XX
XX Claim 52; SEQ ID NO 9; 42pp; English.
XX
XX The invention relates to an isolated polypeptide having BACE1 activity.
CC The protein is RTN4 or RTN3 protein. The polypeptide is useful in
CC preparing a composition for treating amyloidosis or Alzheimer's disease.
CC This sequence corresponds to the RTN-4C protein.
XX
XX Sequence 199 AA;
SQ

Query Match 70.4%; Score 496; DB 7; Length 199;
Best Local Similarity 97.4%; Pred. No. 6.3e-50;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLSLTVFVSIVSTAYIALALLSVTIS 97
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLSLTVFVSIVSTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 141
Db 61 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 104

RESULT 15
AA71311
ID AA71311 standard; protein; 1178 AA.
XX
XX AA71311;
AC
XX
XX 02-NOV-2000 (first entry)
DT
XX
XX Human neurite growth inhibitor Nogo.
DE
XX
XX Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH
XX Misc-difference 187 /label= Unknown
FT
XX Misc-difference 188 /label= Unknown
FT
XX Misc-difference 189
FT

Human RTN-4C protein.
Misc-difference 190 /label= Unknown
FT
XX
XX Misc-difference 221 /label= Unknown
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XX
XX Misc-difference 328 /label= Unknown
FT
XX
XX Misc-difference 477 /label= Unknown
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XX /note= "Region specifically described in claim 16"
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XX Region 994..1174 /label= Unknown
FT
XX /note= "Region specifically described in claim 16"
FT
XX Region 1079..1114 /label= Unknown
FT
XX /note= "Region specifically described in claim 16"
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX
XX Schwab ME, Chen MS;
XX
XX WPI; 2000-400052/34.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 11; Fig 13; 122pp; English.
XX
XX The present sequence is a human Nogo protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The human Nogo
CC sequence was derived by aligning human expressed sequence tags (ESTs)
CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092585, AA081525
CC displaying neurite growth inhibitory activity are used in the treatment
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
XX these SEQ ID numbers
XX
XX Sequence 1178 AA;
SQ

Query Match 63.5%; Score 448; DB 3; Length 1178;
Best Local Similarity 74.6%; Pred. No. 3.2e-43;
Matches 97; Conservative 3; Mismatches 8; Indels 22; Gaps 1;

Qy 12 RENFAVYSVGVGMHLLLEGRSQWMDGQKHKDKVVDLLYWRDIKKTGVVFGASLFL 71
Db 976 RSPSAIFSDLG-----KTSVDLLYWRDIKKTGVVFGASLFL 1013
Qy 72 LLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAIKSDGHPFRAYLESEVAISEEL 131

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Db 1014 LSLTVFSIVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEEL 1073

Qy 132 VQKYSNSALG 141

Db 1074 VQKYSNSALG 1083

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Job time : 21.3612 secs



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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 5.32448 Seconds  
(without alignments)  
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Title: US-09-830-972-32

Perfect score: 705

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCFUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	72.8	201	4	US-09-949-016-9124
2	503	71.3	199	2	US-08-700-607-1
3	349	49.5	208	2	US-08-700-607-7
4	348	49.4	267	2	US-08-700-607-8
5	337	47.8	356	2	US-08-700-607-6
6	337	47.8	439	4	US-09-949-016-9180
7	337	47.8	776	2	US-08-700-607-5
8	337	47.8	776	4	US-09-949-016-6998
9	309	43.8	192	4	US-09-949-016-8859
10	305	43.3	241	2	US-08-700-607-3
11	262	37.2	114	4	US-09-513-999C-7861
12	250	35.5	219	4	US-09-270-767-45132
13	227	32.2	168	4	US-09-149-476-563
14	214	30.4	588	4	US-09-949-016-7290
15	99	14.0	80	3	US-08-905-223-411
16	75	10.6	593	4	US-09-328-352-4866
17	73	10.4	374	4	US-09-248-796A-16008
18	73	10.4	597	4	US-09-949-016-7719
19	72.5	10.3	208	4	US-09-248-796A-14596
20	72.5	10.3	598	2	US-08-853-659A-53
21	71.5	10.1	154	1	US-08-366-783-5
22	71	10.1	408	4	US-09-710-279-2286
23	70	9.9	518	3	US-09-134-001C-4744
24	70	9.9	563	4	US-09-422-936-79
25	70	9.9	619	3	US-08-262-220-6
26	70	9.9	619	3	US-08-471-733-6
27	70	9.9	619	3	US-08-468-878-6

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28 70 9.9 619 3 US-08-750-494-6 Sequence 6, Appli
29 70 9.9 619 4 US-08-470-638-6 Sequence 6, Appli
30 70 9.9 844 4 US-09-422-936-47 Sequence 47, Appli
31 70 9.9 844 4 US-09-422-936-51 Sequence 51, Appli
32 70 9.9 886 4 US-09-422-936-77 Sequence 77, Appli
33 70 9.9 892 4 US-09-422-936-75 Sequence 75, Appli
34 70 9.9 899 4 US-09-422-936-71 Sequence 71, Appli
35 70 9.9 960 4 US-09-422-936-45 Sequence 45, Appli
36 70 9.9 961 4 US-09-422-936-49 Sequence 45, Appli
37 70 9.9 961 4 US-09-914-259-14 Sequence 14, Appli
38 69 9.8 621 3 US-08-262-220-8 Sequence 8, Appli
39 69 9.8 621 3 US-08-471-733-8 Sequence 8, Appli
40 69 9.8 621 3 US-08-468-878-8 Sequence 8, Appli
41 69 9.8 621 3 US-08-750-494-8 Sequence 8, Appli
42 69 9.8 621 4 US-08-470-638-8 Sequence 8, Appli
43 69 9.8 1621 4 US-09-949-016-8450 Sequence 8450, Ap
44 68.5 9.7 383 4 US-09-248-796A-14833 Sequence 14833, A
45 68 9.6 232 4 US-09-897-425-46 Sequence 46, Appli

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#### ALIGNMENTS

##### RESULT 1

```

US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9124

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Query Match 72.8%; Score 513; DB 4; Length 201;
Best Local Similarity 98.1%; Pred. No. 2.5e-53;
Matches 104; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 36 QEMDGGKHKWKVLDLLYWRDINKTGVFGASFLLLSLTVFSIVSVTAYIALLSVT 95
Db 1 QEMDGGKHKWKVLDLLYWRDINKTGVFGASFLLLSLTVFSIVSVTAYIALLSVT 60

```

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Qy 96 ISFRIYKGVIOATKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 61 ISFRIYKGVIOATKSDGHPFRAYLESEVAISEELVQKYSNSALG 106

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##### RESULT 2

```

US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:

```

```
;
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
;
US-08-700-607-1
;
Query Match 71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 3.8e-52;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
Qy 38 MDGQKHWDKVVLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTYIALALLSVTIS 97
Db 1 MDGQKHWDKVVLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTYIALALLSVTIS 60
;
Qy 98 FRIYGVQIAKSDGHPFRAYLSEVAISEELVQKYSNLSALG 141
Db 61 FRIYGVQIAKSDGHPFRAYLSEVAISEELVQKYSNLSALG 104
;
RESULT 3
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
;
US-08-700-607-7
;
Query Match 49.5%; Score 349; DB 2; Length 208;
Best Local Similarity 63.4%; Pred. No. 1.2e-33;
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
;
Qy 37 EMDGQKHWDKVVLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTYIALALLSVTI 96
Db 9 KMDCVSNWKSQAIDLLYWRDIKKTGVVFGSFLLLFSLTQFSVSVVYALALALSATI 68
;
Qy 97 SFRIYGVQIAKSDGHPFRAYLSEVAISEELVQKYSN 137
Db 69 SFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 109
;
RESULT 4
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
;
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; CLONE: 281046
US-08-700-607-8
Query Match          49.4%; Score 348; DB 2; Length 267;
Best Local Similarity 64.0%; Pred. No. 2.2e-33;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDCWSNWKSQADLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALSAIS 60

Qy 98 FRIYKGVQIAKSDGHPFRAYLSEVAISELVQKYSN 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FRIYKSVLQAVQKTDGHPFRAYLEILTLSQEIQKYTD 100

RESULT 5
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
; US-08-700-607-6

Query Match          47.8%; Score 337; DB 2; Length 356;
Best Local Similarity 67.4%; Pred. No. 6.7e-32;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVLDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 KQAKDLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALSAISFRIYKSVL 225

Qy 106 QATAKSDGHPFRAYLSEVAISELVQKYSN 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 226 QAVQKTDGHPFRAYLEILTLSQEIQKYTD 257

; CLONE: 281046
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9180

Query Match          47.8%; Score 337; DB 4; Length 439;
Best Local Similarity 67.4%; Pred. No. 8.9e-32;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVLDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 KQAKDLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALSAISFRIYKSVL 308

Qy 106 QATAKSDGHPFRAYLSEVAISELVQKYSN 137
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Db 309 QAVQKTDGHPFRAYLEILTLSQEIQKYTD 340

RESULT 7
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
; US-08-700-607-6

Query Match          47.8%; Score 337; DB 2; Length 356;
Best Local Similarity 67.4%; Pred. No. 6.7e-32;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVLDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 KQAKDLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALSAISFRIYKSVL 225

Qy 106 QATAKSDGHPFRAYLSEVAISELVQKYSN 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 226 QAVQKTDGHPFRAYLEILTLSQEIQKYTD 257
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

Query Match          47.8%; Score 337; DB 2; Length 776;
Best Local Similarity 67.4%; Pred. No. 2e-31;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 46 KDKVDDLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
Db 586 KQKAIIDLLYWRDIKKTGVVFGSFLLLSLTFQFSVVSVVAYIALAALSATISFRIYKSVL 645
QY 106 QAIKSDGHPFRAYLESEVAISEELVQKYSN 137
Db 646 QAVQKTDEGHPFKAYLEILTSQEQIQKYTD 677

RESULT 8
US-09-949-016-6998
; Sequence 6998, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6998
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6998

Query Match          47.8%; Score 337; DB 4; Length 776;
Best Local Similarity 67.4%; Pred. No. 2e-31;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 46 KDKVDDLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
Db 586 KQKAIIDLLYWRDIKKTGVVFGSFLLLSLTFQFSVVSVVAYIALAALSATISFRIYKSVL 645
QY 106 QAIKSDGHPFRAYLESEVAISEELVQKYSN 137
Db 646 QAVQKTDEGHPFKAYLEILTSQEQIQKYTD 677

RESULT 9
US-09-949-016-8859
; Sequence 8859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match          43.8%; Score 309; DB 4; Length 192;
Best Local Similarity 60.9%; Pred. No. 6.4e-29;
Matches 56; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 108
Db 4 VHDLFWRDVKKTGVVFGTLLMLLSLAAFSVISVSYLLALLSVTISFRIYKSV 63
QY 109 AKSDGHPFRAYLESEVAISEELVQKYSN 140
Db 64 QKSEGHPPFKAYLDVDTLSSEAFHNYN 95

RESULT 10
US-08-700-607-3
; Sequence 3, Application US/08700607
; Patent No. 5859708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: THPNOB01
; CLONE: 31870
US-08-700-607-3

Query Match          43.3%; Score 305; DB 2; Length 241;
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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      32.2%; Score 227; DB 4; Length 168;
Best Local Similarity 60.0%; Pred. No. 3.6e-19;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 71 LLASLVFVSIVTAYIALLSVTISFRIYKGVIOAKSDGHPFRAYLESEVAISEE 130
Db 1 MLLSLAASFVISVSYLLALLSVTISFRIYKSVIOAQKSEGHPPKAYLDVDITLSE 60

Qy 131 LVQKYSNSAL 140
Db 61 AFHNYNNAAM 70

RESULT 14
US-09-949-016-7290
; Sequence 7290, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7290
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290

Query Match      30.4%; Score 214; DB 4; Length 588;
Best Local Similarity 46.7%; Pred. No. 7.4e-17;
Matches 42; Conservative 21; Mismatches 27; Indels 0; Gaps 0;

Qy 48 KVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSTAYIALLSVTISFRIYKGVIOA 107
Db 387 KVADLLYWKDTRTSGVVTGLMVSLLCLLHFSIVSVAHLALLLGLCGTISLRVYRKVLOA 446

Qy 108 IAKSDGHPFRAYLESEVAISEELVQKYSN 137
Db 447 VHRGDGANPFQAYLDVLDLTITREQTERLSH 476

RESULT 15
US-08-905-223-411
; Sequence 411, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 411:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: -78..-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV
US-08-905-223-411

Query Match      14.0%; Score 99; DB 3; Length 80;
Best Local Similarity 58.8%; Pred. No. 0.00028;
Matches 20; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLS--LTVFSI 80
Db 47 VHDLIWRDVKTGFVGTTLIMLLSWQLSVSV 80

Search completed: June 16, 2005, 12:33:41
Job time : 6.32448 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:29:05 ; Search time 18.2906 Seconds  
(without alignments)  
2960.058 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVCLRENFAYISV.....ESEVAISEIVQKYSNALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*

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16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*

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18: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*

19: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*

20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*

21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510	72.3	199	9	US-09-893-348-21
2	510	72.3	199	16	US-10-810-653-21
3	503	71.3	118	15	US-10-264-237-1568
4	503	71.3	199	9	US-09-893-348-25
5	503	71.3	199	11	US-09-978-360A-467
6	503	71.3	199	15	US-10-660-946-1
7	503	71.3	199	16	US-10-466-258-11
8	503	71.3	199	16	US-10-810-653-25
9	496	70.4	199	15	US-10-408-967-9
10	447	63.4	1162	16	US-10-633-423-10
11	447	63.4	1162	16	US-10-427-741-10
					Sequence 21, Appl
					Sequence 21, Appl
					Sequence 1568, Ap
					Sequence 25, Appl
					Sequence 467, App
					Sequence 1, Appli
					Sequence 11, Appl
					Sequence 25, Appl
					Sequence 9, Appli
					Sequence 10, Appl

Query Match 72.3%; Score 510; DB 9; Length 199;  
Best Local Similarity 99.0%; Pred. No. 2.4e-49;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12	447	63.4	1163	9	US-09-893-348-18	Sequence 18, Appl
13	447	63.4	1163	16	US-10-810-653-18	Sequence 18, Appl
14	447	63.4	1192	9	US-09-789-386-2	Sequence 2, Appli
15	447	63.4	1192	9	US-09-758-140-6	Sequence 6, Appli
16	447	63.4	1192	9	US-09-893-348-23	Sequence 23, Appli
17	447	63.4	1192	9	US-09-972-599A-6	Sequence 6, Appli
18	447	63.4	1192	14	US-10-060-036-71	Sequence 71, Appl
19	447	63.4	1192	15	US-10-267-502-429	Sequence 429, App
20	447	63.4	1192	16	US-10-327-213-9	Sequence 9, Appli
21	447	63.4	1192	16	US-10-466-258-9	Sequence 9, Appli
22	447	63.4	1192	16	US-10-810-653-23	Sequence 23, Appli
23	443	62.8	360	9	US-09-893-348-20	Sequence 20, Appl
24	443	62.8	360	16	US-10-810-653-20	Sequence 20, Appl
25	443	62.8	373	9	US-09-789-386-6	Sequence 6, Appli
26	443	62.8	373	9	US-09-765-205-6	Sequence 6, Appli
27	443	62.8	373	9	US-09-893-348-24	Sequence 24, Appl
28	443	62.8	373	14	US-10-060-036-72	Sequence 72, Appl
29	443	62.8	373	15	US-10-408-967-8	Sequence 8, Appli
30	443	62.8	373	16	US-10-466-258-4	Sequence 4, Appli
31	443	62.8	373	16	US-10-810-653-24	Sequence 24, Appl
32	443	62.8	373	17	US-10-347-669-6	Sequence 6, Appli
33	443	62.8	379	14	US-10-205-194-164	Sequence 164, App
34	440	62.4	1192	15	US-10-408-967-7	Sequence 7, Appli
35	436.5	61.9	1163	15	US-10-267-502-431	Sequence 431, App
36	349	49.5	208	15	US-10-660-946-7	Sequence 7, Appli
37	348	49.4	267	14	US-10-205-194-127	Sequence 127, App
38	348	49.4	267	15	US-10-660-946-8	Sequence 8, Appli
39	337	47.8	356	15	US-10-660-946-6	Sequence 6, Appli
40	337	47.8	776	15	US-10-660-946-5	Sequence 5, Appli
41	337	47.8	776	15	US-10-267-502-430	Sequence 430, App
42	337	47.8	776	16	US-10-723-860-1481	Sequence 1481, Ap
43	337	47.8	777	14	US-10-205-219-93	Sequence 93, Appl
44	337	47.8	780	15	US-10-267-502-432	Sequence 432, App
45	309	43.8	236	9	US-09-729-674-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-893-348-21

Sequence 21, Application US/09893348

Patent No. US20020072493A1

GENERAL INFORMATION:

APPLICANT: EISENBACH-SCHWARTZ, Michal

APPLICANT: COHEN, Irun R.

APPLICANT: BESERMAN, Pierre

APPLICANT: MOSONEGO, Alon

APPLICANT: MOALEM, Gila

TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE:

FILE REFERENCE: EIS-SCHWARTZ=2A

CURRENT APPLICATION NUMBER: US/09/893,348

CURRENT FILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: US 09/314,161

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: US 09/218,377

PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: PCT/US98/14715

PRIOR FILING DATE: 1998-07-21

PRIOR APPLICATION NUMBER: IL 124500

PRIOR FILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 199

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-893-348-21

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Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
Db 1 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 2
US-10-810-653-21
; Sequence 21, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Itun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-810-653-21

Query Match 72.3%; Score 510; DB 16; Length 199;
Best Local Similarity 99.0%; Pred. No. 2,4e-49;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
Db 1 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 3
US-10-264-237-1568
; Sequence 1568, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1568
; LENGTH: 118
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (118)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1568

Query Match 71.3%; Score 503; DB 15; Length 118;
Best Local Similarity 98.1%; Pred. No. 7.5e-49;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
Db 1 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 4
US-09-893-348-25
; Sequence 25, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Itun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-25

Query Match 71.3%; Score 503; DB 9; Length 199;
Best Local Similarity 98.1%; Pred. No. 1.5e-48;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
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Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 5
US-09-978-360A-467
; Sequence 467, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
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;; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
;; FILE REFERENCE: 56.USA.CIP  
;; CURRENT APPLICATION NUMBER: US/09/978,360A  
;; PRIOR FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: US 60/066,677  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: US 60/069,957  
;; PRIOR FILING DATE: 1997-12-17  
;; PRIOR APPLICATION NUMBER: US 60/074,121  
;; PRIOR FILING DATE: 1998-02-09  
;; PRIOR APPLICATION NUMBER: US 60/081,563  
;; PRIOR FILING DATE: 1998-04-13  
;; PRIOR APPLICATION NUMBER: US 60/096,116  
;; PRIOR FILING DATE: 1998-08-10  
;; PRIOR APPLICATION NUMBER: US 60/099,273  
;; PRIOR FILING DATE: -09-04  
;; PRIOR APPLICATION NUMBER: US 09/191,997  
;; PRIOR FILING DATE: 1998-11-13  
;; PRIOR APPLICATION NUMBER: US 09/215,435  
;; PRIOR FILING DATE: 1998-12-17  
;; PRIOR APPLICATION NUMBER: PCT/IB98/02122  
;; PRIOR FILING DATE: 1998-12-17  
;; PRIOR APPLICATION NUMBER: US 09/247,155  
;; PRIOR FILING DATE: 1999-02-09  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 810  
;; SOFTWARE: Patent.pm  
;; SEQ ID NO 467  
;; LENGTH: 199  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SIGNAL  
;; LOCATION: -42...-1  
US-09-978-360A-467

Query Match 71.3%; Score 503; DB 11; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.5e-48;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 FRIYKGVIOAIKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 6  
US-10-660-946-1  
; Sequence 1, Application US/10660946  
; Publication No. US20040063131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/660,946  
;; FILING DATE: 12-Sep-2003  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/228,213A  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: 08/700,607  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0114 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-855-0555  
;; TELEFAX: 415-845-4166  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 199 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; IMMEDIATE SOURCE:  
;; LIBRARY: <Unknown>  
;; CLONE: Consensus  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-660-946-1

Query Match 71.3%; Score 503; DB 15; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.5e-48;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 FRIYKGVIOAIKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 7  
US-10-466-258-11  
; Sequence 11, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-466-258-11

Query Match 71.3%; Score 503; DB 16; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.5e-48;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 FRIYKGVIOAIKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 8  
US-10-810-653-25

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; Sequence 25, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MORLEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-810-653-25

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Query Match	71.3%;	Score 503;	DB 16;	Length 199;
Best Local Similarity	98.1%;	Pred. No. 1.5e-48;		
Matches 102;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;

  

Qy	38	MDGQKHKKVVDLLIWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYTALALLSVTIS	97
Db	1	MDGQKKNKKVVDLLIWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYTALALLSVTIS	60
Qy	98	FRIYKGVIOAIKSDGCHPPRAYLESEVAISEELVQKYSNALS	141
Db	61	FRIYKGVIOAIKSDGCHPPRAYLESEVAISEELVQKYSNALS	104

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RESULT 9
US-10-408-967-9
; Sequence 9, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-9

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Query Match	70.4%	Score 496;	DB 15;	Length 199;
Best Local Similarity	97.1%;	Pred. No. 9.2e-48;		
Matches 101;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	38	MDCGKHKWKDVLLIYWRDIKKTGGVFGASFLILLSTVFSIVSVTAYTALALLSVTIS	97	
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	1	MDCGKNWKDVLLIYWRDIKKTGGVFGASFLILLSTVFSIVSVTAYTALALLSVTIS	60	
QY	98	FRIYKGVIAKSDGCHPPRAYLESEVAISELVQKYSNSALG	141	

Db 61 PRIYGVIOAIQSDGHPHPAYLESEVAISELVBQKYSNALG 104

RESULT 10  
US-10-633-423-10  
; Sequence 10, Application US/10633423  
; Publication No. US20040191240A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; APPLICANT: Yamashita, Toshihide  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023.US00  
; CURRENT APPLICATION NUMBER: US/10/633,423  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: US 10/427,741  
; PRIOR FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 1162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-633-423-10

Query Match 63.4%; Score 447; DB 16; Length 1162;  
Best Local Similarity .96.9%; Pred. No. 3.3e-41;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 11
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; APPLICANT: Yamashita, Toshihide
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023
; CURRENT APPLICATION NUMBER: US/10/427,741
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: prt
; ORGANISM: Mus musculus
US-10-427-741-10

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	Query Match	63.4%	Score 447;	DB 16;	Length 1162;
	Best Local Similarity	96.9%;	Pred. No. 3.3e-41;		
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Qy	46	KDKVDLLYWRDIKKTCGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPIRYKGI	105		
Db	972	KTSDVLLYWRDIKKTCGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPIRYKGI			
Qy	106	QAATKDEGHPPRAYLESEVAISEELVQKYSNALG	141		
Db	1032	QAATKDEGHPPRAYLESEVAISEELVQKYSNALG	1067		

```
RESULT 12
US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SWARTZ-2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match      63.4%; Score 447; DB 9; Length 1163;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
Db 973 KTSVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1032

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1033 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 13
US-10-810-653-18
; Sequence 18, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match      63.4%; Score 447; DB 9; Length 1163;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
Db 973 KTSVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1032

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1033 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 14
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: PRINJHA, RABINDER KUMAR
; APPLICANT: MICHALOVICH, DAVID
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

Query Match      63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 3.4e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
Db 1002 KTSVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1061

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1062 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 15
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
```

```
US-10-810-653-18

Query Match      63.4%; Score 447; DB 16; Length 1163;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
Db 973 KTSVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1032

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1033 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 14
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: PRINJHA, RABINDER KUMAR
; APPLICANT: MICHALOVICH, DAVID
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

Query Match      63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 3.4e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
Db 1002 KTSVDDLWYRDIKKTGVWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1061

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1062 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 15
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

Query Match      63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 3.4e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
Db      1002 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1061

QY      106 QAIKSDGHPPEAYLSEVAISELVOKYNSALG 141
Db      1062 QAIKSDGHPPEAYLSEVAISELVOKYNSALG 1097
```

Search completed: June 16, 2005, 13:04:05  
Job time : 19.2906 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 4.23986 seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	49.5	208	2 I60904	neuroendocrine-spe
2	348	49.4	267	2 A60021	tropomyosin-relate
3	337	47.8	776	2 A46583	neuroendocrine-spe
4	162	23.0	2484	2 T26216	hypothetical prote
5	159	22.6	2607	2 T26215	hypothetical prote
6	158	22.4	222	2 T26213	hypothetical prote
7	83.5	11.8	295	2 S59439	probable membrane
8	81.5	11.6	464	2 C88198	protein Cl8H9.5 [i
9	79	11.2	618	2 T24228	hypothetical prote
10	78.5	11.1	458	2 A72258	hypothetical prote
11	77.5	11.0	261	2 F64924	probable thiosulfa
12	77.5	11.0	583	2 T49359	hypothetical prote
13	76.5	10.9	481	2 C95920	hypothetical membr
14	75.5	10.7	545	2 F64655	glucose-6-phosphat
15	74.5	10.6	545	2 E71851	glucose-6-phosphat
16	74	10.5	268	2 F64034	hypothetical prote
17	73	10.4	393	2 S67763	probable membrane
18	73	10.4	888	2 T01081	hypothetical prote
19	72.5	10.3	278	2 AD0147	probable ABC trans
20	72.5	10.3	302	2 AE2863	conserved hypothet
21	72.5	10.3	302	2 D97640	hypothetical prote
22	72.5	10.3	417	2 B96977	probable Mn transp
23	72.5	10.3	598	2 T14886	leukotoxin express
24	72	10.2	271	2 T13013	hypothetical prote
25	72	10.2	299	2 B69155	hypothetical prote
26	72	10.2	1783	2 T42386	unconventional myo
27	72	10.2	3511	2 A59295	hypothetical prote
28	71.5	10.1	255	2 E84899	conserved hypothet
29	71.5	10.1	537	2 G82873	

```

30 71 10.1 346 1 WMV21W 3beta-hydroxy-Delt
31 71 10.1 346 1 WMV22W 3beta-hydroxy-Delt
32 71 10.1 346 2 T37430 hydroxysteroid deh
33 71 10.1 476 2 B97096 2-oxoglutarate/mal
34 71 10.1 1065 2 T25068 hypothetrical prote
35 70.5 10.0 153 2 AB3226 conserved hypothet
36 70.5 10.0 261 2 A90926 conserved hypothet
37 70.5 10.0 261 2 E85774 hypothetrical prote
38 70.5 10.0 291 2 B69098 phosphate transpor
39 70 9.9 271 2 AC1320 hypothetrical prote
40 70 9.9 619 2 S55502 membrane-associate
41 70 9.9 737 2 AE1678 heavy metal-transp
42 69.5 9.9 188 2 T04714 hypothetrical prote
43 69.5 9.9 403 2 T04821 hypothetrical prote
44 69.5 9.9 415 2 D95248 conserved hypothet
45 69.5 9.9 504 2 E83898 spore germination

```

#### ALIGNMENTS

##### RESULT 1

I60904

neuroendocrine-specific protein C - human

C/Species: Homo sapiens (man)

C/Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C/Accession: I60904

R/Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V

J. Biol. Chem. 268, 13439-13447, 1993

A/Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A/Reference number: A46583; MUID:93293865; PMID:7685762

A/Accession: I60904

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-208 <RES>

A/Cross-references: UNIPROT:Q16799; GB:L10335; NID:G307310; PIDN:AAA59952.1; PID:G307311

C/Genetics:

A/Gene: GDB:RTN1; NSP

A/Cross-references: GDB:203968; OMIM:600865

A/Map position: 14q21-14q22

Query Match 49.5%; Score 349; DB 2; Length 208;  
Best Local Similarity 63.4%; Pred. No. 6.7e-28;  
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

```

Qy 37 EMDGQKHWDKVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVYATIALALLSVTI 96
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 9 KMDCVWSNWKSQAIIDLILYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATI 68
   ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

```

```

Qy 97 SFRIYKGVIOAIKSDGHPFRAYLSEVAISELVLQKYSN 137
   ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 69 SFRIYKSVLQAVQKTDGHPFKAYLEILTSQEIQIKYTD 109
   ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

```

##### RESULT 2

A60021

tropomyosin-related protein, neuronal - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 05-Nov-1999

C/Accession: A60021

R/Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A/Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A/Reference number: A60021; MUID:91278684; PMID:1647480

A/Accession: A60021

A/Molecule type: mRNA

A/Residues: 1-267 <MIE>

A/Cross-references: EMBL:X52817; NID:G456549; PIDN:CAA37001.1; PID:G456550

C/Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Query Match 49.4%; Score 348; DB 2; Length 267;  
Best Local Similarity 64.0%; Pred. No. 1.1e-27;  
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;





Db 156 GTISEWSWPINEIGTFVAFLLSSAFQIS 182

RESULT 9

T24228

hypothetical protein R166.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T24228

R;Matthews, P.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z19859

A;Accession: T24228

A;Molecule type: DNA

A;Residues: 1-618 <WIL>

A;Cross-references: UNIPROT:Q22003; EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:R166

A;Experimental source: clone R166

C;Genetics:

A;Gene: CRSP:R166.2

A;Map position: 2

A;Introns: 41/3; 86/3; 118/3; 164/3; 207/3; 554/3

Query Match 11.2%; Score 79; DB 2; Length 618;

Best Local Similarity 29.1%; Pred. No. 4.8;

Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;

Qy 51 DLLYWRDIKK-TGVVFGASLFL-LLSLTVF-----SIVSVTAIALAL----- 91

Db 353 DIQFWNNRKDLVGLSVRSVLFNIPQSLIVELYICDNETMTMVKVTGIGLLIECKWIKPV 412

Qy 92 LSVTISFR-IYKGVIOAIKASDEGHPFRAYLESEVAISELVOKYSNAL 140

Db 413 MNVSIDWQNKWFGVIRLVISDKG----SVSEETKIYDQMAPKYLQWAL 458

RESULT 10

A72258

hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: A72258

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: A72258

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-458 <ARN>

A;Cross-references: UNIPROT:Q9X1C8; GB:AE001793; GB:AE000512; NID:G4981963; PIDN:AAD3647

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1408

Query Match 11.1%; Score 78.5; DB 2; Length 458;

Best Local Similarity 26.6%; Pred. No. 3.9;

Matches 42; Conservative 17; Mismatches 34; Indels 65; Gaps 9;

Qy 14 NEAVY-----SVSGVMHNLLEGRSQWQMDGKKH-----WKD 47

Db 196 NFILSLRSSIRIGDFDLLLL-----TRKIPQLLFGFYFYLSTWIDNFIAWKV 244

Qy 48 KVVDDL-----YWRDIKKTGVFGASLFLSLTVFSIVSVTAIALALSLVTSIFR 99

Db 245 KGIEIAPGPFMSPEY--DIPK----FMASLFFPISLVFEN-----LSMETVQR 287

Qy 100 IYKGVIOAIKASDEGHPFRAYLESEVAISELVOKYSN 137

Db 288 NYKGLMQSIV-SDK--PMRVIENKKLSLSLRHAFSN 322

Db 106 QAIKAS-----DEGHPFRAYLESEVAIS 128

RESULT 7

S59439

probable membrane protein YDR233c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YD934.17c

C;Species: Saccharomyces cerevisiae

C;Date: 30-Nov-1995 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004

C;Accession: S59439

R;Murphy, L.; Harris, D.

submitted to the EMBL Data Library, March 1995

A;Reference number: S59423

A;Accession: S59439

A;Molecule type: DNA

A;Residues: 1-295 <MUR>

A;Cross-references: UNIPROT:Q04947; EMBL:Z48612; NID:G728671; PID:G728688; GSPDB:GN00004

A;Experimental source: strain AB972

C;Genetics:

A;Gene: MIPS:YDR233c

A;Cross-references: SGD:S0002641

A;Map position: 4R

C;Keywords: transmembrane protein

F;40-56/Domain: transmembrane #status predicted <TM1>

F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 11.8%; Score 83.5; DB 2; Length 295;

Best Local Similarity 26.3%; Pred. No. 0.76;

Matches 25; Conservative 17; Mismatches 32; Indels 21; Gaps 2;

Qy 41 QKHKKDKVVDLLYWRDIKKTGVVFGASLFLSLTVFSIVSVTAIALALSLVTSIFRI 100

Db 12 QQQQKSCNCDLLWRNPVQTKYFGGSLALLILKKNLITFLKVAITLFT----- 66

Qy 101 YKGVIOAIKASDEGHPFRAYLESEVAISELVOKY 135

Db 67 --GSIEFVSK-----LFLGQGLITKY 85

RESULT 8

C88188

protein C18H9.5 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C;Accession: C88188

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: C88188

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-464 <STO>

A;Cross-references: UNIPROT:Q09484; GB:chr\_II; PID:G722384; GSPDB:GN00020; CESP:C18H9.5

A;Gene: C18H9.5

A;Map position: 2

Query Match 11.6%; Score 81.5; DB 2; Length 464;

Best Local Similarity 25.9%; Pred. No. 2;

Matches 38; Conservative 28; Mismatches 50; Indels 31; Gaps 8;

Qy 8 VSLRENFAVSVSGVMHNLLEGRSQWQMDGKKHKKVVDLLYWRDIKKTGVVFG- 66

Db 41 ITCTNANMLNFTVICNDVITBQKSF-----SNQTHLEKSSDISLTFSAAAAGAIFFT 96

Qy 67 ASLPLLLS-----LTVFSIVSV--TAYIALA-----LLSVTISFRYIKGV-----I 105

Db 97 VPATLISKYIKRVLTIVGLLSAGGTLLPLAVNYGLIPLVLA-RLFQGVGASILYSSI 155

Qy 106 QAIKAS-----DEGHPFRAYLESEVAIS 128

Db 156 GTISEWSWPINEIGTFVAFLLSSAFQIS 182

RESULT 9

T24228

hypothetical protein R166.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T24228

R;Matthews, P.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z19859

A;Accession: T24228

A;Molecule type: DNA

A;Residues: 1-618 <WIL>

A;Cross-references: UNIPROT:Q22003; EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:R166

A;Experimental source: clone R166

C;Genetics:

A;Gene: CRSP:R166.2

A;Map position: 2

A;Introns: 41/3; 86/3; 118/3; 164/3; 207/3; 554/3

Query Match 11.2%; Score 79; DB 2; Length 618;

Best Local Similarity 29.1%; Pred. No. 4.8;

Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;

Qy 51 DLLYWRDIKK-TGVVFGASLFL-LLSLTVF-----SIVSVTAIALAL----- 91

Db 353 DIQFWNNRKDLVGLSVRSVLFNIPQSLIVELYICDNETMTMVKVTGIGLLIECKWIKPV 412

Qy 92 LSVTISFR-IYKGVIOAIKASDEGHPFRAYLESEVAISELVOKYSNAL 140

Db 413 MNVSIDWQNKWFGVIRLVISDKG----SVSEETKIYDQMAPKYLQWAL 458

RESULT 10

A72258

hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: A72258

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: A72258

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-458 <ARN>

A;Cross-references: UNIPROT:Q9X1C8; GB:AE001793; GB:AE000512; NID:G4981963; PIDN:AAD3647

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1408

Query Match 11.1%; Score 78.5; DB 2; Length 458;

Best Local Similarity 26.6%; Pred. No. 3.9;

Matches 42; Conservative 17; Mismatches 34; Indels 65; Gaps 9;

Qy 14 NEAVY-----SVSGVMHNLLEGRSQWQMDGKKH-----WKD 47

Db 196 NFILSLRSSIRIGDFDLLLL-----TRKIPQLLFGFYFYLSTWIDNFIAWKV 244

Qy 48 KVVDDL-----YWRDIKKTGVFGASLFLSLTVFSIVSVTAIALALSLVTSIFR 99

Db 245 KGIEIAPGPFMSPEY--DIPK----FMASLFFPISLVFEN-----LSMETVQR 287

Qy 100 IYKGVIOAIKASDEGHPFRAYLESEVAISELVOKYSN 137

Db 288 NYKGLMQSIV-SDK--PMRVIENKKLSLSLRHAFSN 322

```
RESULT 11
F64924
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: F64924
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64924
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <BLAT>
A:Cross-references: UNIPROT:P77409; GB:AE000262; GB:U00096; NID:gi787955; PIDN:AAC74740.
A:Experimental source: strain K-12, substrain MG1655
A:Superfamily: hycA protein
C:Keywords: sulfotransferase; transmembrane protein
F:30-46/Domain: transmembrane #status predicted <TM01>
F:83-99/Domain: transmembrane #status predicted <TM02>
F:112-128/Domain: transmembrane #status predicted <TM03>
F:187-203/Domain: transmembrane #status predicted <TM04>
F:224-240/Domain: transmembrane #status predicted <TM05>

Query Match 11.0%; Score 77.5; DB 2; Length 261;
Best Local Similarity 27.6%; Pred. No. 2.7;
Matches 29; Conservative 16; Mismatches 43; Indels 17; Gaps 4;

QY 22 VGMHNLLEGRSQWQEMD-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL---SLT 76
Db :||:|||||
QY 44 LGLHALLRARGVKKSATDGHGKIYLYSKAVRLHWSN-----ALLFVLLLASGLIN 94
Db :||:|||||
QY 77 VFSIVSVTAYIALALLSVTIGFRI---YKGVQIAIAKSDGHPFR 118
Db :||:|||||
QY 95 HFAMVGATVKSIVAVHEVCGFLLCWLGFLVINA VGDNGHHYR 139
Db :||:|||||

RESULT 12
T49359
hypothetical protein BId1.130 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49359
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-583 <SCH>
A:Cross-references: UNIPROT:Q9P6A7; EMBL:AL355927; GSPDB:GN00116; NCSP:BId1.130
A:Experimental source: BAC clone BId1, strain OR74A
C:Genetics:
A:Gene: NCSP:BId1.130
A:Map position: 6
A:Introns: 44/1

Query Match 11.0%; Score 77.5; DB 2; Length 583;
Best Local Similarity 27.5%; Pred. No. 6.4;
Matches 28; Conservative 13; Mismatches 28; Indels 33; Gaps 4;

QY 52 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAIAKS 111
Db :||:|||||
QY 67 LCYV-PLERRLLVLHALLLLLSLEHYS-----AVTRVLLHLITSLNL----- 109
Db :||:|||||
QY 112 DECHPFRAYLSEVAIS-----BELVKYKSNALG 141
Db :||:|||||
QY 110 ----PLRVLVDDEVKAKIAWMAKDINPELIQRIEBCAG 147
Db :||:|||||

RESULT 13
```

```
C95920
hypothetical membrane protein [imported] - Sinorhizobium meliloti (strain 1021) magaplas
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95920
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95920
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <KUR>
A:Cross-references: UNIPROT:Q92VS2; GB:AL591985; PIDN:CAC49027.1; PID:gi5140512; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wellis, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB21048
A:Genome: plasmid

Query Match 10.9%; Score 76.5; DB 2; Length 481;
Best Local Similarity 37.7%; Pred. No. 6.6;
Matches 23; Conservative 8; Mismatches 27; Indels 3; Gaps 2;

QY 53 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAIAKSD 112
Db :||:|||||
QY 238 VYWRKTSR--VAQALAFLLVLLLTSSV-AYVGLAVLSIPVALSISWSFLSGRMDKD 294
Db :||:|||||
QY 113 E 113
Db 295 E 295

RESULT 14
F64665
glucose-6-phosphate isomerase (EC 5.3.1.9) - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: F64665
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64665
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-545 <TOM>
A:Cross-references: UNIPROT:Q25781; GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD0821
A:Superfamily: glucose-6-phosphate isomerase
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 10.7%; Score 75.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 9.5;
Matches 37; Conservative 20; Mismatches 44; Indels 45; Gaps 6;

QY 23 GMMHNL-----LLEGRSQWQEMDQO---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
Db 411 GHHEILFSNVLAQAQAFMKGSYEALGELLFKGLDKDKDLAHR-----VFFGNRP 464
QY 70 FLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAIAKSD----- 112
Db :||:|||||
QY 465 SNILLEKISPSNIGALVALVEHKVFFV-----QGVINDINSFDQGWVGLKELAVPIIQE 519
Db :||:|||||
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```

Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137
Db 520 LEGHKSNAFYDSS---TKHLIELYKN 542

RESULT 15
E71851
glucose-6-phosphate isomerase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71851
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: E71851
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <ARN>
A:Cross-references: UNIPROT:Q9ZK49; GB:AE001536; GB:AE001439; NID:94155675; PIDN:AAD0666
A:Experimental source: strain J99
C:Genetics:
A:Gene: pgi
C:Superfamily: glucose-6-phosphate isomerase

Query Match 10.6%; Score 74.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 12;
Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

Qy 23 GHNLL-----LLEGRSNQEMDQ---KKHKDKVDLLYWRDIKKTGVVFGASL 69
Db 411 GHHEILFSNVLAQAQAFMKGKGYEEALGELLSKGLDKDEAKDLAHHR-----VFFGNRP 464

Qy 70 FLILSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD----- 112
Db 465 SNILLLEKISPSNIGALVALYEHKVFV-----QGVINDINSFDQMGVELGKELAVPILOE 519

Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137
Db 520 LEGHKSNAFYDSS---TKHLIELYKN 542

Search completed: June 16, 2005, 13:32:02
Job time : 5.23986 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 19.1287 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVCLRENFAYVSV.....ESEVAISELVQKYSNLSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	503	71.3	199	2 Q6IM70	Q6im70 sus scrofa
2	503	71.3	199	2 Q7YRW9	Q7yrw9 bos taurus
3	497	70.5	199	2 Q7PCJ7	Q7pcj7 macaca fasc
4	495	70.2	199	1 RTN4_MOUSE	Q99p72 mus musculus
5	490	69.5	170	2 Q6IG20	Q6ig20 canis famill
6	460	65.2	199	2 Q7T224	Q7t224 gallus gall
7	447	63.4	578	2 Q8OW95	Q8ow95 mus musculus
8	447	63.4	639	2 Q8K230	Q8k230 mus musculus
9	447	63.4	986	2 Q8IU44	Q8iu44 homo sapien
10	447	63.4	1046	2 Q8BGK7	Q8bgk7 mus musculus
11	447	63.4	1162	2 Q8BGW9	Q8bgw9 mus musculus
12	447	63.4	1163	1 RTN4_RAT	Q9jkl1 rattus norv
13	447	63.4	1192	1 RTN4_HUMAN	Q9nqc3 homo sapien
14	443	62.8	343	2 Q6IPN0	Q6ipn0 homo sapien
15	443	62.8	356	2 Q8BH78	Q8bh78 mus musculus
16	443	62.8	375	2 Q8BH75	Q8bh75 mus musculus
17	443	62.8	392	2 Q8BH16	Q8bh16 homo sapien
18	439	62.3	187	2 Q6IG15	Q6ig15 sus scrofa
19	436.5	61.9	1163	2 Q8K3G8	Q8k3g8 mus musculus
20	432.5	61.3	357	2 Q8K3G7	Q8k3g7 mus musculus
21	423	60.0	658	2 Q6RSS8	Q6rss8 gallus gall
22	389	55.2	199	2 Q6PB23	Q6pb23 xenopus lae
23	386	54.8	179	2 Q9GMJ3	Q9gmj3 macaca fasc
24	384	54.5	214	2 Q7T222	Q7t222 carassius a
25	381	54.0	199	2 Q6JRW3	Q6jrw3 xenopus lae
26	369.5	52.4	1024	2 Q6JRV2	Q6jrv2 xenopus lae
27	369.5	52.4	1043	2 Q6JRV0	Q6jrv0 xenopus lae
28	369.5	52.4	1055	2 Q6JRV1	Q6jrv1 xenopus lae
29	368	52.2	193	2 Q6IFV5	Q6ifv5 xenopus tro
30	368	52.2	315	2 Q6IFV4	Q6ifv4 xenopus tro
31	366	51.9	193	2 Q6JRV6	Q6jrv6 xenopus lae

32 366 51.9 311 2 Q6JRV3 Q6jrv3 xenopus lae  
33 366 51.9 330 2 Q6JRV4 Q6jrv4 xenopus lae  
34 363 51.5 197 2 Q6H23 Q6h23 brachydanio  
35 362 51.3 1013 2 Q6JRV9 Q6jrv9 xenopus lae  
36 362 51.3 1032 2 Q6JRV7 Q6jrv7 xenopus lae  
37 362 51.3 1044 2 Q6JRV8 Q6jrv8 xenopus lae  
38 360.5 51.1 209 2 Q6IEJ1 Q6iej1 oncorhynchus  
39 360 51.1 316 2 Q6JRW2 Q6jrw2 xenopus lae  
40 358 50.8 193 2 Q6JRW4 Q6jrw4 xenopus lae  
41 358 50.8 304 2 Q6JRW0 Q6jrw0 xenopus lae  
42 358 50.8 323 2 Q6JRW1 Q6jrw1 xenopus lae  
43 354 50.2 196 2 Q6IEI6 Q6iei6 cyprinus ca  
44 349 49.5 172 2 Q6IG14 Q6ig14 bos taurus  
45 349 49.5 208 2 Q6IAX4 Q6iax4 homo sapien

#### ALIGNMENTS

RESULT 1

Q6IM70 PRELIMINARY; PRT; 199 AA.  
AC Q6IM70; 2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE RTN4-C.  
GN Name=RTN4;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22715887; PubMed=12832288;  
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;  
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the  
RTN/Nogo gene family.";  
RL FASEB J. 17:1238-1247(2003).  
CC -I- MISCELLANEOUS: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
DR EMBL; BK001795; DAA01967.1; -  
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS0845; RETICULON; 1.  
SQ SEQUENCE 199 AA; 22425 MW; C61D11DF3FB34D80 CRC64;

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 5.8e-41;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYTALALLSVTIS 97  
Db 1 MDGQKKHKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYTALALLSVTIS 60  
Qy 98 FRIYKGVIOIAKSDGHPFRAYLSEVAISELVQKYSNLSALG 141  
Db 61 FRIYKGVIOIAKSDGHPFRAYLSEVAISELVQKYSNLSALG 104

RESULT 2

Q7YRW9 PRELIMINARY; PRT; 199 AA.  
AC Q7YRW9; 2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 26, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE RTN4-C.  
GN Name=RTN4;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

```
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715987; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164744; A047319.2; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003398; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;

Query Match 71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 5.8e-41;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKKHKKVVDLLYRDIKKTGVFGASFLLLSLTVFVSIVTAYIALALLSVTIS 97
Db 1 MDGQKKHKKVVDLLYRDIKKTGVFGASFLLLSLTVFVSIVTAYIALALLSVTIS 60

QY 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISELKVQYSNSALG 141
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISELKVQYSNSALG 104

RESULT 3
Q7PCJ7 PRELIMINARY; PRT; 199 AA.
ID Q7PCJ7
AC Q7PCJ7
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RTN4-C.
GN Name=RTN4;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715987; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDJB third party annotation (TPA) entry.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003398; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22469 MW; 761A5FDB6C1DEC3C CRC64;

Query Match 70.5%; Score 497; DB 2; Length 199;
Best Local Similarity 96.2%; Pred. No. 2.3e-40;
Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKKHKKVVDLLYRDIKKTGVFGASFLLLSLTVFVSIVTAYIALALLSVTIS 97
Db 1 MDGQKKHKKVVDLLYRDIKKTGVFGASFLLLSLTVFVSIVTAYIALALLSVTIS 60

QY 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISELKVQYSNSALG 141
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISELKVQYSNSALG 104

RESULT 4
```

```
RTN4_MOUSE
ID RTN4_MOUSE STANDARD; PRT; 199 AA.
AC Q99F72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN Name=Rtn4; Synonyms=Nogo;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C., Craggs P.D., Morris N.J.;
RL "Mouse vp20/RTN4C cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDJB databases.
RN [2]
RP SEQUENCE OF 170-199 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Havaehizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults (By
CC similarity).
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC membrane of the endoplasmic reticulum through 2 putative
CC transmembrane domains (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms may be produced;
CC Name=1;
CC IsoId=Q99F72-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC -----AF326337; AAK08076.1; -
DR EMBL; AK003859; -; NOT ANNOTATED_CDS.
DR MGD; MGI-1915835; Rtn4
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR GO; GO:0005635; C:nuclear membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
KW Alternative splicing; Endoplasmic reticulum; Transmembrane.
FT DOMAIN 1 25 Cytoplasmic (Potential).
FT TRANSMEM 26 50 Potential.
FT DOMAIN 51 137 Lumenal (Potential).
FT TRANSMEM 138 162 Potential.
FT DOMAIN 163 199 Cytoplasmic (Potential).
FT DOMAIN 12 199 Reticulon.
FT SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

Query Match 70.2%; Score 495; DB 1; Length 199;
Best Local Similarity 97.1%; Pred. No. 3.5e-40;
Matches 101; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97
Db 1 MDDQKQKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 141
Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 104

RESULT 5
Q6IG20 PRELIMINARY; PRT; 170 AA.
AC Q6IG20; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RTN4-Cw (Fragment).
GN Name=RTN4;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klingner M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN4-Cw gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164737; AAP47312.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
DR NON_TER 170 170
SQ SEQUENCE 170 AA; 19154 MW; F73670210DE959AC CRC64;

Query Match 69.5%; Score 490; DB 2; Length 170;
Best Local Similarity 96.2%; Pred. No. 9.2e-40;
Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97
Db 1 MDCQKQKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

RESULT 6
Q7T224 PRELIMINARY; PRT; 199 AA.
AC Q7T224; 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4-C.
GN Name=RTN4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klingner M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN4-C gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164737; AAP47312.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
DR NON_TER 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

Query Match 65.2%; Score 460; DB 2; Length 199;
Best Local Similarity 88.5%; Pred. No. 9.2e-37;
Matches 92; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97
Db 1 MDSQPSGKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 141
Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 104

RESULT 7
Q8OW95 PRELIMINARY; PRT; 578 AA.
AC Q8OW95; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
DR NON_TER 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 63.4%; Score 447; DB 2; Length 578;
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Qy 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 141
Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 104

RESULT 6
Q7T224 PRELIMINARY; PRT; 199 AA.
AC Q7T224; 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4-C.
GN Name=RTN4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klingner M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN4-C gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164737; AAP47312.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
DR NON_TER 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

Query Match 65.2%; Score 460; DB 2; Length 199;
Best Local Similarity 88.5%; Pred. No. 9.2e-37;
Matches 92; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97
Db 1 MDSQPSGKWKDVLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 141
Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNLSALG 104

RESULT 7
Q8OW95 PRELIMINARY; PRT; 578 AA.
AC Q8OW95; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
DR NON_TER 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 63.4%; Score 447; DB 2; Length 578;
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Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY102284; AAM73506.1; -;  
DR EMBL; AY102286; AAM73511.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003386; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1162 AA; 126612 MW; 855697FBBE11781F CRC64;

Query Match 63.4%; Score 447; DB 2; Length 1162;  
Best Local Similarity 96.9%; Pred. No. 1e-34;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWRDIKKTGVWFGASFLFLLSLTVFSIVSTAYIALLSVTISPRIYKGI 105  
DB KTSVVDLLYWRDIKKTGVWFGASFLFLLSLTVFSIVSTAYIALLSVTISPRIYKGI 1031

QY 106 QATAKSDGHPFRAYLSEVAISEELVQKYSNALG 141  
DB QATQKSDGHPFRAYLSEVAISEELVQKYSNALG 1067

RESULT 12

RTN4\_RAT STANDARD; PRT; 1163 AA.  
AC Q9UKI1; Q9UK10; Q9ROD9; Q9WUE9; Q9WUF0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)  
DE (Glut4 vesicle 20 kDa protein).  
GN Name=Rtn4; Synonyms=Nogo;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
RX MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;  
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:  
a new member of the reticulon family.";  
RL Biochim. Biophys. Acta 1450:68-76(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;  
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
RA Spillmann A.A., Christ F., Schwab M.E.;  
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
RT antigen for monoclonal antibody IN-1.";  
RL Nature 403:434-439(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in rat: one of two  
RT minor splice variants.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP FUNCTION.  
RX MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;  
RA GrandPre T., Li S., Strittmatter S.M.;  
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
RL Nature 417:547-551(2002).  
CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (by  
CC similarity).  
CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By

CC CC similarity).

CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the

CC CC membrane of the endoplasmic reticulum through 2 putative

CC CC transmembrane domains (By similarity).

CC CC -!- ALTERNATIVE PRODUCTS:

CC CC Event-Alternative splicing; Named isoforms=4;

CC CC Name=1; Synonyms=Nogo-A, NI-220-250;

CC CC IsoId=Q9UK11-1; Sequence-Displayed;

CC CC Name=2; Synonyms=Nogo-B, Foccen-M1;

CC CC IsoId=Q9UK11-2; Sequence=VSP\_005658;

CC CC Name=3; Synonyms=Nogo-C, VP20;

CC CC IsoId=Q9UK11-3; Sequence=VSP\_005656, VSP\_005657;

CC CC Name=4; Synonyms=Foccen-M2;

CC CC IsoId=Q9UK11-4; Sequence=VSP\_005659;

CC CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic

CC CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are

CC CC present in dorsal root ganglion, sciatic nerve and PC12 cells

CC CC after longer exposure. Isoforms 2 and 3 are detected in kidney,

CC CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high

CC CC level in skeletal muscle. In adult animals isoform 1 is expressed

CC CC mainly in the nervous system.

CC CC -!- SIMILARITY: Contains 1 reticulin domain.

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CC CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC CC -----

DR EMBL; AF051335; AAF01564.1; -

DR EMBL; AJ242961; CAB71027.1; -

DR EMBL; AJ242962; CAB71028.1; -

DR EMBL; AJ242963; CAB71029.1; -

DR EMBL; AF132045; AAD31019.1; -

DR EMBL; AF132046; AAD31020.1; -

DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.

DR GO; GO:0005635; C:nuclear membrane; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.

DR GO; GO:0030517; P:negative regulation of axon extension; ISS.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS00845; RETICULON; 1.

KW Alternative splicing; Direct protein sequencing;

KW Endoplasmic reticulum; Transmembrane.

FT DOMAIN 1 989 Cytoplasmic (Potential).

FT TRANSMEM 990 1010 Potential.

FT DOMAIN 1011 1104 Luminal (Potential).

FT TRANSMEM 1105 1125 Potential.

FT DOMAIN 1126 1163 Cytoplasmic (Potential).

FT DOMAIN 976 1163 Reticulon.

FT DOMAIN 33 46 Poly-Glu.

FT DOMAIN 73 76 Poly-Ala.

FT DOMAIN 140 145 Poly-Pro.

FT VARSPPLIC 1 964 Missing (in isoform 3).

FT VARSPPLIC 965 975 /FTId=VSP\_005656.

FT VARSPPLIC 975 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3).

FT VARSPPLIC 975 975 /FTId=VSP\_005657.

FT VARSPPLIC 173 975 Missing (in isoform 2).

FT VARSPPLIC 192 975 /FTId=VSP\_005658.

FT VARSPPLIC 975 975 Missing (in isoform 4).

FT CONFLICT 1130 1131 /FTId=VSP\_005659.

FT CONFLICT 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 63.4%; Score 447; DB 1; Length 1163;

Best Local Similarity 96.9%; Pred. No. 1e-34;

Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAVIALALLSVTISFRIYKGV 105

Db 973 KTSVVDLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAVIALALLSVTISFRIYKGV 1032

QY 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNALS 141

Db 1033 QAIKSDGHPFRAYLESEVAISEELVQKYSNALS 1068

RESULT 13

RTN4 HUMAN

ID RTN4 HUMAN STANDARD; PRT; 1192 AA.

AC Q9NQC3; Q9A962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;

AC Q9Y5U6;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)

DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific

DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).

GN Name=RTN4; Synonyms=ASY; KIAA0886; NOGO;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_taxID=9606;

[1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;

RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,

RA Michalovich D., Simmons D.L., Walsh F.S.;

RT "Inhibitor of neurite outgrowth in humans.";

RL Nature 403:383-384(2000).

[2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Brain;

RX MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;

RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;

RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on

RT endoplasmic reticulum and reduces their anti-apoptotic activity.";

RL Oncogene 19:5736-5746(2000).

[3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=2037542; PubMed=10773680;

RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;

RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome

RT 2p14-->2p13 by radiation hybrid mapping.";

RL Cytogenet. Cell Genet. 88:101-102(2000).

[4]

RP SEQUENCE FROM N.A. (ISOFORM 4).

RA Jin W.-L., Ju G.;

RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

[5]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).

RC TISSUE=Placenta, and Skeletal muscle;

RA Ito T., Schwartz S.M.;

RT "Cloning of a member of the reticulon gene family in human.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

[6]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Fibroblast;

RA Yutsudo M.;

RT "Isolation of a cell death-inducing gene.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

[7]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RC TISSUE=Pituitary;

RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,

RA Luo B., Hu R., Chen J.;

RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

[8]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,

RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel human cDNA clones with function of inhibiting cancer cell  
 RT growth.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=99156230; PubMed=10048485;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,  
 RA Miyajima N., Tanaka A., Kohani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 5:355-364(1998).  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Umbilical cord blood;  
 RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 RN [12]  
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
 RC TISSUE=Brain;  
 RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;  
 RA Grandpre T., Nakamura F., Varcantian T., Strittmatter S.M.;  
 RT "Identification of the Nogo inhibitor of axon regeneration as a  
 RT Reticulon protein.";  
 RL Nature 403:439-444(2000).  
 RN [15]  
 RP FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;  
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;

RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
 RT regeneration.";  
 RL Nature 409:341-346(2001).  
 RN [16]  
 RP REVIEW.  
 RX MEDLINE=21889956; PubMed=11891768; DOI=10.1002/jnr.10134;  
 RA Ng C.E.L., Tang B.L.;  
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron  
 RT regeneration.";  
 RL J. Neurosci. Res. 67:559-565(2002).  
 CC -|- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults.  
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-x1 and Bcl-2.  
 CC This is likely consecutive to their change in subcellular  
 CC location, from the mitochondria to the endoplasmic reticulum,  
 CC after binding and sequestration.  
 CC -|- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
 CC through 2 putative transmembrane domains.  
 CC -|- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;  
 CC IsoId=Q9NQC3-1; Sequence=Displayed;  
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;  
 CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;  
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;  
 CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;  
 CC Name=4;  
 CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;  
 CC -|- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
 CC widely expressed excepted for the liver. Isoform 3 is expressed in  
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
 CC specific.  
 CC -|- SIMILARITY: Contains 1 reticulon domain.  
 CC -|- CAUTION: Ref.11 sequence differs from that shown due to  
 CC frameshifts in positions 1149 and 1156.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AJ251383; CAB99248.1; -  
 DR EMBL; AJ251384; CAB99249.1; -  
 DR EMBL; AJ251385; CAB99250.1; -  
 DR EMBL; AB040462; BAB18927.1; -  
 DR EMBL; AB040463; BAB18928.1; -  
 DR EMBL; AF148537; AAG12176.1; -  
 DR EMBL; AF148538; AAG12177.1; -  
 DR EMBL; AF087901; AAG12205.1; -  
 DR EMBL; AF320999; AAG40878.1; -  
 DR EMBL; AF132047; AAD31021.1; -  
 DR EMBL; AF132048; AAD31022.1; -  
 DR EMBL; AB015639; BAA83712.1; -  
 DR EMBL; AF077050; AAD27783.1; -  
 DR EMBL; AF177332; AAG17976.1; -  
 DR EMBL; AB020693; BAA74909.2; ALT\_INIT.  
 DR EMBL; BC001035; AAH01035.1; -  
 DR EMBL; BC007109; AAH07109.1; -

Query Match 63.4%; Score 447; DB 1; Length 1192;  
 Best Local Similarity 96.9%; Pred. No. 1.1e-34;  
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLLYWRDINKTGVFGASFLILLSTVFSVSTAYIALALLSVTISPRIYKGV 105  
 Db 1002 KTSVVDLLYWRDINKTGVFGASFLILLSTVFSVSTAYIALALLSVTISPRIYKGV 1061

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QY 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1062 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 14
Q6IPNO PRELIMINARY; PRT; 343 AA.
ID Q6IPNO
AC Q6IPNO
QY 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4 protein.
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshynki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grigunov J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071848; AAH71848.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;

Query Match 62.8%; Score 443; DB 2; Length 343;
Best Local Similarity 98.9%; Pred. No. 7.3e-35;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 108
Db 156 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 215

QY 109 AKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 216 QKSDGHPFRAYLESEVAISEELVQKYSNSALG 248

RESULT 15
Q8BH78 PRELIMINARY; PRT; 356 AA.
ID Q8BH78
AC Q8BH78;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4.
GN Name=RTN4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7; and 129SVCJ7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102281; AAM73503.1; -.
DR EMBL; AY102286; AAM73508.1; -.
DR MGD; MGI:1915835; RTN4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 62.8%; Score 443; DB 2; Length 356;
Best Local Similarity 98.9%; Pred. No. 7.6e-35;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 108
Db 169 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 228

QY 109 AKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 229 QKSDGHPFRAYLESEVAISEELVQKYSNSALG 261

Search completed: June 16, 2005, 13:17:44
Job time : 20.1287 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run On: June 16, 2005, 12:31:51 ; Search time 167.944 Seconds  
(without alignments)

2678.292 Million cell updates/sec

Title: us-09-830-972-2

Perfect score: 5848

Sequence: 1 MEDIDQSLVSSSTDSPPR.....VKDAMAKIQKIPGLKRRAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A. Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1980s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5848	100.0	1163	5	ABB81074
2	5848	100.0	1163	8	ADO26399
3	5848	100.0	1163	8	ADP45572
4	5846	100.0	1163	3	AAV71310
5	5840	99.9	1162	3	AAV71557
6	5823	99.6	1163	3	AAV71384
7	5312.5	90.8	1162	8	ADT89537
8	5307	90.7	1163	8	ADO08105
9	4921	84.1	974	3	AAV71560
10	4403.5	75.3	1192	4	AAU04591
11	4403.5	75.3	1192	5	APF68600
12	4403.5	75.3	1192	6	ABR59667
13	4403.5	75.3	1192	8	ADP45551
14	4398.5	75.2	1192	3	AAV56967
15	4398.5	75.2	1192	4	AAV82349
16	4398.5	75.2	1192	5	ABG30938
17	4398.5	75.2	1192	5	ABH1078
18	4398.5	75.2	1192	8	ADO08103
19	4398.5	75.2	1192	8	ADP67234
20	4398.5	75.2	1192	8	ADR13966
21	4389.5	75.1	1192	7	ADK67502
22	4358.5	74.5	1192	8	ADO26400
23	4276.5	73.1	1178	3	AAV71311
24	4116	70.4	1246	4	AAU33228
25	4023	68.8	803	3	AAV71562

## ALIGNMENTS

## RESULT 1

ABB81074  
ID ABB81074 standard; protein; 1163 AA.

XX AC ABB81074;

DT 05-NOV-2002 (first entry)

DE Rat neurotransmitter receptor protein Nogo-A.

XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
KW vulnery; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
KW nocotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
KW neurotransmitter receptor; rat; receptor.

OS Rattus norvegicus.

XX XX XX

PN US2002072493-A1.

XX 13-JUN-2002.

PD 28-JUN-2001; 2001US-008933348.

XX 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98MO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

PI Moalem G;

XX WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX Promoting nerve regeneration and preventing neuronal degeneration in the

PT central/peripheral nervous system from injury/disease, comprises  
PT administering nervous system-specific activated T cells/antigen, or  
XX analogs/peptides.  
PS Example 5; Page 44-47; 93pp; English.  
XX The invention relates to promoting nerve regeneration or conferring  
CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
CC central/peripheral nervous system (NS). The method involves administering

26	3834	65.6	798	8	ADO26414	Ado26414	Rat trunc
27	3714	63.5	737	3	AAV71386	Aay71386	Rat Nogo
28	3699.5	63.3	746	3	AAV71391	Aay71391	Rat Nogo
29	3651.5	62.4	736	3	AAV71398	Aay71398	Rat Nogo
30	3630.5	62.1	732	3	AAV71399	Aay71399	Rat Nogo
31	3584	61.3	739	8	ADO26415	Ado26415	Rat trunc
32	3494	59.7	695	3	AAV71387	Aay71387	Rat Nogo
33	3436	58.8	684	3	AAV71394	Aay71394	Rat Nogo
34	3385.5	57.9	983	6	ABU11573	Abu11573	Human MDD
35	3280.5	56.1	893	3	AAV95012	Aay95012	Human sec
36	2801	47.9	819	8	ADP45553	Adp45553	Human NIG
37	2779	47.5	552	3	AAV71388	Aay71388	Rat Nogo
38	2500.5	42.8	642	2	AAW58383	Aaw58383	Human sec
39	2500.5	42.8	642	4	AAB90682	Aab90682	Human BGI
40	2432	41.6	502	3	AAV71396	Aay71396	Rat Nogo
41	2388	40.8	475	3	AAV71389	Aay71389	Rat Nogo
42	2291	39.2	457	3	AAV71392	Aay71392	Rat Nogo
43	1987	34.0	403	3	AAV71563	Aay71563	Rat Nogo
44	1868	31.9	417	3	AAV71393	Aay71393	Rat Nogo
45	1801	30.8	356	3	AAV71390	Aay71390	Rat Nogo

CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC relangectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen  
 CC  
 XX  
 SQ Sequence 1163 AA;

Query Match 100.0%; Score 5848; DB 5; Length 1163;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-298; Indels 0; Gaps 0;  
 Matches 1163; Conservative 0; Mismatches 0;

QY 1 MEDIDQSLVSSSTDSPRPAPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60  
 Db 1 MEDIDQSLVSSSTDSPRPAPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60

QY 61 PAAGLSAAVPPAAAPLDFSSDVSPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120  
 Db 61 PAAGLSAAVPPAAAPLDFSSDVSPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

QY 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEPAPSTPAAPKRGSGVDLTFALP 180  
 Db 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEPAPSTPAAPKRGSGVDLTFALP 180

QY 181 AASEPVPSSAEKIMDLMEQGNVTSSGQEDFPVSLLETAASLPSLSTVSFKHEGYL 240  
 Db 181 AASEPVPSSAEKIMDLMEQGNVTSSGQEDFPVSLLETAASLPSLSTVSFKHEGYL 240

QY 241 GNLAVSSSEGTIEETLNEASKELPERATNPVFNRLAEPSELEYSEMGSFKGSPKGS 300  
 Db 241 GNLAVSSSEGTIEETLNEASKELPERATNPVFNRLAEPSELEYSEMGSFKGSPKGS 300

QY 301 ALLVENTKEVIVRSKDKEDLVCSAALHSPQSPVCKEDRVVSPKTMDFNEMQMSVVA 360  
 Db 301 ALLVENTKEVIVRSKDKEDLVCSAALHSPQSPVCKEDRVVSPKTMDFNEMQMSVVA 360

QY 361 PVREEYADFPKPEQAEVVKDTVEGSRDVLAAANVESKVDKCLEDSLEQSLGKDEGR 420  
 Db 361 PVREEYADFPKPEQAEVVKDTVEGSRDVLAAANVESKVDKCLEDSLEQSLGKDEGR 420

QY 421 NEDASFPSTPEPVKDSRAYITCASFTSATSTTANTFPLEDHSTENKTDKKEERKA 480  
 Db 421 NEDASFPSTPEPVKDSRAYITCASFTSATSTTANTFPLEDHSTENKTDKKEERKA 480

QY 481 QIITEKTSPTKSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTDLVQACESEL 540  
 Db 481 QIITEKTSPTKSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTDLVQACESEL 540

QY 541 NEATGKTIAYETKVDLVQTSIAQESLYPTAQCPSEFEAEATPSPVLPIVMEAPLNSL 600  
 Db 541 NEATGKTIAYETKVDLVQTSIAQESLYPTAQCPSEFEAEATPSPVLPIVMEAPLNSL 600

QY 601 LPSAGASVQSVSPLEAPPVSVYSIKLEPENPPPYEAMNVALKALGTKEGKPEPSF 660  
 Db 601 LPSAGASVQSVSPLEAPPVSVYSIKLEPENPPPYEAMNVALKALGTKEGKPEPSF 660

QY 661 NAAVQETAPYISIAACDLIKETKLTSTSPSPFSNVSEIAKPEKSVPEHAELVEDSSPSE 720  
 Db 661 NAAVQETAPYISIAACDLIKETKLTSTSPSPFSNVSEIAKPEKSVPEHAELVEDSSPSE 720

QY 721 PVDLFSDDSIPEVPQTOEAEAVMLKESLTVSETVAQHKERLSASPOELGKPYLESFOP 780  
 Db 721 PVDLFSDDSIPEVPQTOEAEAVMLKESLTVSETVAQHKERLSASPOELGKPYLESFOP 780

QY 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSDNDLLSKEDKIKESLTVSDSSPIE 840  
 Db 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSDNDLLSKEDKIKESLTVSDSSPIE 840

QY 841 IIDEFTTFSVSAKDDSPKLAKEYTDLVSDKSEIANIQSGADSLPCLLPCDLSPFNIVPK 900  
 Db 841 IIDEFTTFSVSAKDDSPKLAKEYTDLVSDKSEIANIQSGADSLPCLLPCDLSPFNIVPK 900

QY 901 DEVHVSDFSENRRSSVSKASISPSNVSALEPQTEMGSIKSLTKEAKKLPSTDEKED 960  
 Db 901 DEVHVSDFSENRRSSVSKASISPSNVSALEPQTEMGSIKSLTKEAKKLPSTDEKED 960

QY 961 RSLSAVLSAELSKTSVVDLLYWRDIIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020  
 Db 961 RSLSAVLSAELSKTSVVDLLYWRDIIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020

QY 1021 VTISFRIYKGVIOAIQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRL 1080  
 Db 1021 VTISFRIYKGVIOAIQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRL 1080

QY 1081 FLVDDLVSLKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA 1140  
 Db 1081 FLVDDLVSLKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA 1140

QY 1141 NKSVDAMAKTOAKTIPGLKRXAD 1163  
 Db 1141 NKSVDAMAKTOAKTIPGLKRXAD 1163

RESULT 2  
 ADO26399  
 ID ADO26399 standard; protein; 1163 AA.  
 XX  
 AC ADO26399;  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Rat truncated Nogo-A protein.  
 XX  
 KW rat; human; Nogo-A; truncated; affinity; membrane-bound protein.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO2004039836-A1.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 31-OCT-2002; 2002WO-EP012210.  
 XX  
 PR 31-OCT-2002; 2002WO-EP012210.  
 XX  
 PA (PIER-) PIERIS PROTEOLAB AG.  
 XX  
 PI Skerra A, Fiedler M;  
 XX  
 DR WPI; 2004-376159/35.  
 XX  
 PT New isolated truncated Nogo-A polypeptide that corresponds to a truncated  
 PT form of the Nogo-A protein, useful for identifying a compound having  
 PT detectable affinity to a Nogo-A protein.  
 XX

Claim 1; Fig 6A; 80pp; English.

The present invention relates to an isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein from the rat and from the human. The truncated polypeptide is useful for identifying a compound having detectable affinity to a Nogo-A protein. The present sequence is a Nogo-A polypeptide of the invention.

Sequence 1163 AA;

```
Query Match      100.0%; Score 5848; DB 8; Length 1163;
Best Local Similarity 100.0%; Pred. No. 3.7e-298;
Matches 1163; Conservative 0; Mismatches 0; Indels 0;
```

[illegible]

Qy	901	DEVIVSDEPFENRSSVSKASISPSNVSALEPQTEMGSI VKSKSLTKEAEKKLPDSTEKED	960
Db	901	DEVHVSDEPFENRSSVSKASISPSNVSALEPQTEMGSI VKSKSLTKEAEKKLPDSTEKED	960
Qy	961	RSLSAVLSAELSKTSSVVDLLYWRDIIKKTGVVFGASLFLLLSLTWFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSSVVDLLYWRDIIKKTGVVFGASLFLLLSLTWFSIVSVTAYIALALLS	1020
Qy	1021	VTISFRIYKGVIIQAIQKSDSGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021	VTISFRIYKGVIIQAIQKSDSGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081	FLVDDLLVDSLKFAVLMMVFTVVGALFNGLTLLILALISLFSIPVIYERHQQVQIDHYLGLA	1140
Db	1081	FLVDDLLVDSLKFAVLMMVFTVVGALFNGLTLLILALISLFSIPVIYERHQQVQIDHYLGLA	1140
Qy	1141	NKSVKDAMAKIQAKIPGLKERAD	1163
Db	1141	NKSVKDAMAKIQAKIPGLKERAD	1163
RESULT 3			
ADP45572	ID	ADP45572 standard; protein; 1163 AA.	
XX	AC	ADP45572;	
XX	DT	09-SEP-2004 (first entry)	
XX	DE	Rat NogoA protein SEQ ID NO:26.	
XX	KW	binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;	
XX	KW	nerve repair; neuroprotective; gene therapy;	
XX	KW	central nervous system injury; CNS injury; neurodegenerative disorder;	
XX	OS	Rattus norvegicus.	
XX	FN	WO2004052932-A2.	
XX	PD	24-JUN-2004.	
XX	PF	09-DEC-2003; 2003WO-EP013960.	
XX	PR	10-DEC-2002; 2002GB-00028832.	
XX	PA	(NOVS ) NOVARTIS AG.	
XX	PA	(NOVS ) NOVARTIS PHARMA GMBH.	
XX	PA	(UYZU-) UNIV ZUERICH.	
XX	FI	Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;	
XX	FI	Zurini M;	
XX	DR	WPI; 2004-468818/44.	
XX	DR	N-PSDB; ADP45571.	
XX	FT	New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.	
XX	PS	Example 1; SEQ ID NO 26; 121pp; English.	
XX	CC	The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) disorders.	

Example 1: SEQ ID NO 26; 121pp; English.

The present invention describes a binding molecule which binds to human NogoA polypeptide, human NIG, human NIG-D20 or human NogoA<sub>623-640</sub> with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS)







FT		/note= "used as immunogen to generate antibody AS 472"
FT	Modified-site	626
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	694. .696
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Peptide	762. .1163
FT		/note= "used as immunogen to generate antibody AS Bruna"
FT	Modified-site	794
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	863
FT		/note= "Casein kinase II site"
FT	Modified-site	868
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	893
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	912. .914
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	925. .927
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	954
FT		/note= "PKC and casein kinase II sites"
FT	Modified-site	956
FT		/note= "PKC and casein kinase II sites"
FT	Region	975. .1162
FT		/note= "This region is not essential for inhibitory activity"
FT	Region	976. .1163
FT		/note= "C-terminal common region found in Nogo A, B and C isoforms"
FT	Domain	988. .1023
FT		/label= Transmembrane domain
FT		/note= "C-terminal hydrophobic region specifically described in claim 16"
FT	Modified-site	1024
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	1071. .1073
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	1073
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	1089
FT		/note= "Protein kinase C (PKC) site"
FT	Domain	1090. .1125
FT		/label= Transmembrane domain
FT		/note= "C-terminal hydrophobic region specifically described in claim 16"
FT	Modified-site	1141. .1143
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	1143
FT		/note= "Protein kinase C (PKC) site"
XX		
PN	WO200031235-A2.	
XX		
XX	02-JUN-2000.	
XX		
XX	05-NOV-1999;	99WO-US026160.
XX		
XX	06-NOV-1998;	98US-0107446P.
PR		
XX		
PA	(SCHW/) SCHWAB M E.	
PA	(CHEN/) CHEN M S.	
XX		
XX	Schwab ME, Chen MS;	
XX		
DR	WPI; 2000-400052/34.	
DR	N-PSDB: AAD01173.	

```

Db 481 QIITEKTSKTNPFVLAVQDSEADIVTTDTLSKVTEAAVSNMPEGLTDLVQECESL 540
QY 541 NEATGTKIAIYETKVDLVQTSIAQESLYPTAQCPSEFEAEATPPSVLPDIYMEAPLNSL 600
Db 541 NEATGTKIAIYETKVDLVQTSIAQESLYPTAQCPSEFEAEATPPSVLPDIYMEAPLNSL 600
QY 601 LPSAGASVVQPSVPLEAPPVSYDSIKLEPNPPPYEAMNVALKALGTGKIGIKEPESF 660
Db 601 LPSAGASVVQPSVPLEAPPVSYDSIKLEPNPPPYEAMNVALKALGTGKIGIKEPESF 660
QY 661 NAAVQTEAPYISACDLTKETKLSPEPSPDPSNTSEIAKFKSVPEHAELVEDSSPESE 720
Db 661 NAAVQTEAPYISACDLTKETKLSPEPSPDPSNTSEIAKFKSVPEHAELVEDSSPESE 720
QY 721 PVDLFSDDSIPEVPQTEBAVLMKESLTVSETVAQHKERLSASPBQLGKPYLESFOP 780
Db 721 PVDLFSDDSIPEVPQTEBAVLMKESLTVSETVAQHKERLSASPBQLGKPYLESFOP 780
QY 781 NLHSTKDAASNDIPTLTKEKISLQMEERTAIYSNDDLLSKEDKIKESETFSDSSPIE 840
Db 781 NLHSTKDAASNDIPTLTKEKISLQMEERTAIYSNDDLLSKEDKIKESETFSDSSPIE 840
QY 841 IIDEPTTFVSADKSPKLAKEYTDLEVSQKSEIANIQSGADSLPCLLPCDLSPKNIYPK 900
Db 841 IIDEPTTFVSADKSPKLAKEYTDLEVSQKSEIANIQSGADSLPCLLPCDLSPKNIYPK 900
QY 901 DEVHVSDEFSENRSVSKASISPSNVSALEPQTEMGSIYKSKSLTKEAKKLPSDTEKED 960
Db 901 DEVHVSDEFSENRSVSKASISPSNVSALEPQTEMGSIYKSKSLTKEAKKLPSDTEKED 960
QY 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVGASLFLLLSLTVSIVSVTAYIALALS 1020
Db 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVGASLFLLLSLTVSIVSVTAYIALALS 1020
QY 1021 VTISFRIYKGVLOAIQKSDGHPFRAYLESEVAISEELVQKYSNAGLHVNSTIKELRRL 1080
Db 1021 VTISFRIYKGVLOAIQKSDGHPFRAYLESEVAISEELVQKYSNAGLHVNSTIKELRRL 1080
QY 1081 FLVDDLVDLSLKFVAVLMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA 1140
Db 1081 FLVDDLVDLSLKFVAVLMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA 1140
QY 1141 NKSVDAMAKIOAKTIGLKKAD 1163
Db 1141 NKSVDAMAKIOAKTIGLKKAD 1163

```

## RESULT 5

AA71557  
ID AAY71557 standard; protein; 1162 AA.

XX AAY71557;

XX 02-NOV-2000 (first entry)

DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.

XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutin.

OS Rattus sp.

XX WO200031235-A2.

XX 02-JUN-2000.

XX 05-NOV-1999; 99WO-US026160.

XX 06-NOV-1999; 98US-0107446P.  
XX (SCHW/) SCHWAB M E.  
XX (CHEN/) CHEN M S.  
XX Schwab ME, Chen MS;  
XX WPI; 2000-400052/34.

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
of the central nervous system and inducing regeneration of neurons.

PS Example; Page; 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of all  
central nervous system (CNS) myelin material with which it is natively  
associated. Nogo proteins and fragments displaying neurite growth  
inhibitory activity are used in the treatment of neoplastic disease of  
the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
Therapeutics which promote Nogo activity can be used to treat or prevent  
hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
used to inhibit production of Nogo protein to induce regeneration of  
neurons or to promote structural plasticity of the CNS in disorders where  
neurite growth, regeneration or maintenance are deficient or desired. The  
animal models can be used in diagnostic and screening methods for  
predisposition to disorders and to screen for or test molecules which can  
treat or prevent disorders or diseases of the CNS. The present sequence  
is a truncated form of rat Nogo A protein shown in AAY71310, which is  
tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo-A is composed of His-  
used for mapping the inhibitory sites of Nogo protein. Major inhibitory  
region was identified in the Nogo A sequence from amino acids 172-974,  
particularly amino acids 542-722. In addition, N-terminal region 1-171  
was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: the  
present sequence is not given in the specification but is derived from  
rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred  
in claim 32 and SEQ ID NO: 29 in disclosure of the specification.  
CC However, the specification does not include sequences for these SEQ ID  
CC numbers

XX Sequence 1162 AA;

Query Match 99.9%; Score 5840; DB 3; Length 1162;  
Best Local Similarity 99.9%; Pred. No. 9.8e-298;  
Matches 1161; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDIDQSSLSVSSSTDSPPRPPPAFKYQVTFPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60  
Db 1 MEDIDQSSLSVSSSTDSPPRPPPAFKYQVTFPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60  
QY 61 PAAGLSAAVPPAAAPLLDFSSDVPPAPRGPLPAAPPAAPRQPSWERSPAAAPSLP 120  
Db 61 PAAGLSAAVPPAAAPLLDFSSDVPPAPRGPLPAAPPAAPRQPSWERSPAAAPSLP 120  
QY 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVDETLFALP 180  
Db 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVDETLFALP 180  
QY 181 AASEPVIIPSSAEKIMDLMEQGNVTSSQGEPPSVLLETAASLPSLSPLSTVSPKHEGYL 240  
Db 181 AASEPVIIPSSAEKIMDLMEQGNVTSSQGEPPSVLLETAASLPSLSPLSTVSPKHEGYL 240  
QY 241 GNLSAVSSSEGTIETLNEASKELPERATNPVNRDLAEFSELEYSEMGSSFKGSPKGS 300  
Db 241 GNLSAVSSSEGTIETLNEASKELPERATNPVNRDLAEFSELEYSEMGSSFKGSPKGS 300  
QY 301 AILVENTKEEVIVRSKOKEDLVCSAALHSPOESPVGKEDRVVSPKTMDFINEMQMSVVA 360

Db 301 AILVENTKEEIVIRSKOKEDLVCSAALHSPOESPVKGEDRVVSPKTMDFINQMOMVVA 360  
Qy 361 PVREYADFPKEQAWKVDYVEGRDVLAAANVESKVDKCLDSEQKSLGKDSGR 420  
Db 361 PVREYADFPKEQAWKVDYVEGRDVLAAANVESKVDKCLDSEQKSLGKDSGR 420  
Qy 421 NEDASFPTSPVKDSSRAYITCASFTSATESSTTANTFPLEDDHTSENKTKIEERKA 480  
Db 421 NEDASFPTSPVKDSSRAYITCASFTSATESSTTANTFPLEDDHTSENKTKIEERKA 480  
Qy 481 QIITEKTSKTSNPLVAVQSEADYVTTDLTKVTEAAVSNMPEGLTPDLVQACSESEL 540  
Db 481 QIITEKTSKTSNPLVAVQSEADYVTTDLTKVTEAAVSNMPEGLTPDLVQACSESEL 540  
Qy 541 NEATGKTIAYTKVDLVOTSAIQESLYPTAQLCPSFEAEATSPVLPDVMAPLNSL 600  
Db 541 NEATGKTIAYTKVDLVOTSAIQESLYPTAQLCPSFEAEATSPVLPDVMAPLNSL 600  
Qy 601 LPSAGASVQPSVSPLAPPVVSYSIKLEPENPPPYEEAMNVALKGTKEGKEPESP 660  
Db 601 LPSAGASVQPSVSPLAPPVVSYSIKLEPENPPPYEEAMNVALKGTKEGKEPESP 660  
Qy 661 NAAVOETEAPYISACDLIKETKLTSTSPSPFSNYSEIAKPEKSVPEHAELVEDSSPESE 720  
Db 661 NAAVOETEAPYISACDLIKETKLTSTSPSPFSNYSEIAKPEKSVPEHAELVEDSSPESE 720  
Qy 721 PVDLFSDDSIPEVPOTQEEAVLMKESLTVSETVAQKHEERLSASPOELGKPYLESFQP 780  
Db 721 PVDLFSDDSIPEVPOTQEEAVLMKESLTVSETVAQKHEERLSASPOELGKPYLESFQP 780  
Qy 781 NLHSTKOAASNDIPTLTKEKISIQMEEFNTAIYSNDDLLSSKEDKIKESFTFSDSSPIE 840  
Db 781 NLHSTKOAASNDIPTLTKEKISIQMEEFNTAIYSNDDLLSSKEDKIKESFTFSDSSPIE 840  
Qy 841 IIDFPPTVSAKDSPLAKAYTDLVSDKSEIANIQSAGDLPCLLPCDLSPKNYYPK 900  
Db 841 IIDFPPTVSAKDSPLAKAYTDLVSDKSEIANIQSAGDLPCLLPCDLSPKNYYPK 900  
Qy 901 DEVHVSDFSNRSVSKASISPSNVSALEPQTEMGSIKVSLSITKEAKKLPSDTKEED 960  
Db 901 DEVHVSDFSNRSVSKASISPSNVSALEPQTEMGSIKVSLSITKEAKKLPSDTKEED 960  
Qy 961 RSLSAVLSAELSKTSSVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS 1020  
Db 961 RSLSAVLSAELSKTSSVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS 1020  
Qy 1021 VTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRL 1080  
Db 1021 VTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRL 1080  
Qy 1081 FLVDDLVDLSKAPVLMVFTVVGALFNLGLTLLILALISLFSIPVIYERHVOIDHYLGLA 1140  
Db 1081 FLVDDLVDLSKAPVLMVFTVVGALFNLGLTLLILALISLFSIPVIYERHVOIDHYLGLA 1140  
Qy 1141 NKSVKDAWAKIQAIPGLKRA 1162  
Db 1141 NKSVKDAWAKIQAIPGLKRA 1162

## RESULT 6

AAV71384

ID AAV71384 standard; protein; 1163 AA.

XX AC AAV71384;

XX DT 02-NOV-2000 (first entry)

XX DE Alternative version of rat neurite growth inhibitor Nogo A.

XX KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

XX KW central nervous system; neoplastic disease; antiproliferative; glioma;

XX KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

XX KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
XX structural plasticity; screening.

OS Rattus sp.

XX Key Location/Qualifiers

FT Inhibitory-site 1..171  
/note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30  
/note= "Casein kinase II site"

FT Region 31..58  
/note= "Acidic region"

FT Region 172..259  
/note= "This region is not essential for inhibitory activity"

FT Misc-difference 223  
/label= Unknown

FT /note= "There is Leu at this position in the sequence shown in AAY71310"

FT Modified-site 233  
/note= "Protein kinase C (PKC) site"

FT Modified-site 242..244  
/note= "Asn is N-glycosylated"

FT Modified-site 291  
/note= "Protein kinase C (PKC) site"

FT Modified-site 295  
/note= "Protein kinase C (PKC) site"

FT Misc-difference 404  
/note= "There is Ile at this position in the sequence shown in AAY71310"

FT Modified-site 436  
/note= "Protein kinase C (PKC) site"

FT Modified-site 468..470  
/note= "Asn is N-glycosylated"

FT Misc-difference 469  
/label= Unknown

FT /note= "There is Lys at this position in the sequence shown in AAY71310"

FT Modified-site 484  
/note= "Protein kinase C (PKC) site"

FT Modified-site 488  
/note= "Protein kinase C (PKC) site"

FT Modified-site 502  
/note= "Casein kinase II site"

FT Inhibitory-site 542..722

FT Modified-site 576  
/note= "Casein kinase II site"

FT Peptide 623..640  
/note= "used as immunogen to generate antibody AS 472"

FT Modified-site 626  
/note= "Protein kinase C (PKC) site"

FT Misc-difference 661  
/note= "There is Asn at this position in the sequence shown in AAY71310"

FT Modified-site 694..696  
/note= "Asn is N-glycosylated"

FT Modified-site 715  
/note= "Casein kinase II site"

FT Peptide 762..1163  
/note= "used as immunogen to generate antibody AS Bruna"

FT Modified-site 784  
/note= "Protein kinase C (PKC) site"

FT Misc-difference 820  
/note= "There is Leu at this position in the sequence shown in AAY71310"

FT Modified-site 821  
/note= "Protein kinase C (PKC) site"

FT Modified-site 850  
/note= "Protein kinase C (PKC) site"

FT Modified-site 855  
/note= "Protein kinase C (PKC) site"

FT Modified-site 863  
/note= "Protein kinase C (PKC) site"

FT Modified-site /note= "Casein kinase II site"

FT 868 /note= "Protein kinase C (PKC) site"

FT 893 /note= "Protein kinase C (PKC) site"

FT 912..914 /note= "Asn is N-glycosylated"

FT 925..927 /note= "Asn is N-glycosylated"

FT 954 /note= "PKC and casein kinase II sites"

FT 956 /note= "PKC and casein kinase II sites"

FT 975..1162 /note= "This region is not essential for inhibitory activity"

FT 976..1163 /note= "C-terminal common region found in Nogo A, B and C isoforms"

FT 988..1023 /label= "Transmembrane domain"

FT /note= "C-terminal hydrophobic region"

FT 1024 /note= "Protein kinase C (PKC) site"

FT 1071..1073 /note= "Asn is N-glycosylated"

FT 1073 /note= "Protein kinase C (PKC) site"

FT 1089 /note= "Protein kinase C (PKC) site"

FT 1090..1125 /label= "Transmembrane domain"

FT /note= "C-terminal hydrophobic region"

FT 1141..1143 /note= "Asn is N-glycosylated"

FT 1143 /note= "Protein kinase C (PKC) site"

XX WO200031235-A2.

XX 02-JUN-2000.

XX 05-NOV-1999; 99WO-US026160.

XX 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.

XX (CHEN/) CHEN M S.

XX Schwab ME, Chen MS;

XX WPI; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.

XX Claim 3; Fig 13; 122pp; English.

XX The present sequence is an alternative version of rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The

CC animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is an alternative version of the Nogo A sequence shown in Fig. 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers

XX Sequence 1163 AA;

Query Match 99.6%; Score 5823; DB 3; Length 1163;  
Best Local Similarity 99.7%; Pred. No. 7.6e-297;  
Matches 1159; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEDIDQSSLVSSSTDSPPRPAPFKYQVTEPDEDEDEDEDEDEDEDEDEDEDELEVLERK 60

DB 1 MEDIDQSSLVSSSTDSPPRPAPFKYQVTEPDEDEDEDEDEDEDEDEDEDELEVLERK 60

QY 61 PAAGLSAAAVPAAAPLLDFSSDVPPAPRGPLPAAAPAPROPSPWERSPAAAPSLP 120

DB 61 PAAGLSAAAVPAAAPLLDFSSDVPPAPRGPLPAAAPAPROPSPWERSPAAAPSLP 120

QY 121 PAAAVLPKLPEDDEPPARPPPPAGASPLAEPAPPTDPAAPKRGSGSVDETLFALP 180

DB 121 PAAAVLPKLPEDDEPPARPPPPAGASPLAEPAPPTDPAAPKRGSGSVDETLFALP 180

QY 181 AASEVPFPSSAEKIMDLMEQPGNTVSSQEDFPFVLLLETAASXPSLSPLSTVSPKHEGYL 240

DB 181 AASEVPFPSSAEKIMDLMEQPGNTVSSQEDFPFVLLLETAASXPSLSPLSTVSPKHEGYL 240

QY 241 GNLSAVSSSEGTIEETLNEASKELPERATNPVNDLAEFSELEYSEMGSSFGKPGKES 300

DB 241 GNLSAVSSSEGTIEETLNEASKELPERATNPVNDLAEFSELEYSEMGSSFGKPGKES 300

QY 301 ALLVENTKEEIVTRSKDKEDLVCSAALHSPQESPVGKEDRVVSPKKTMDIFNEMQMSVVA 360

DB 301 ALLVENTKEEIVTRSKDKEDLVCSAALHSPQESPVGKEDRVVSPKKTMDIFNEMQMSVVA 360

QY 361 PVREYADFKPFEQAWVEKDYEGSRDVLAAANVESKDRKCLDSLEQSLGKDSGR 420

DB 361 PVREYADFKPFEQAWVEKDYEGSRDVLAAANVESKDRKCLDSLEQSLGKDSGR 420

QY 421 NEDASFPSTPVPKDSRAYITCASFTSATSTTANTPFLLEDHTSENKTDKKTEERKA 480

DB 421 NEDASFPSTPVPKDSRAYITCASFTSATSTTANTPFLLEDHTSENKTDKKTEERKA 480

QY 481 QIITEKTSPTKTSNPFVAVQDSEADYVTTDLTKVTEAAVSNMPEGLTPDLVQEAACESL 540

DB 481 QIITEKTSPTKTSNPFVAVQDSEADYVTTDLTKVTEAAVSNMPEGLTPDLVQEAACESL 540

QY 541 NEATGKIAYETKVQDLVOTSEAIQESLYPTAQLCPSPFEAEATPSPVLPDIWMEAPLNSL 600

DB 541 NEATGKIAYETKVQDLVOTSEAIQESLYPTAQLCPSPFEAEATPSPVLPDIWMEAPLNSL 600

QY 601 LPSAGASVVQSVSPLEAPPVSVSDIKLEPENPPPYEAMNVALGCTKEGKEPERSF 660

DB 601 LPSAGASVVQSVSPLEAPPVSVSDIKLEPENPPPYEAMNVALGCTKEGKEPERSF 660

QY 661 NAAVQTEAPYISIACDLIKETKLTSTEPSDFSNYSIEIAKFEKSVPEHAELVEDSSPSE 720

DB 661 NAAVQTEAPYISIACDLIKETKLTSTEPSDFSNYSIEIAKFEKSVPEHAELVEDSSPSE 720

QY 721 PVDLFSDSDSIPEVPQTEAEVWLMKESLTVSETVAQHKERLSASPOELGKPYLESQP 780

DB 721 PVDLFSDSDSIPEVPQTEAEVWLMKESLTVSETVAQHKERLSASPOELGKPYLESQP 780

QY 781 NLHSTKDAASNDIPTLTKEKISIQMEEFNTAIVSNDLLSSKEDIKESFSDSSPTE 840

DB 781 NLHSTKDAASNDIPTLTKEKISIQMEEFNTAIVSNDLLSSKEDIKESFSDSSPTE 840

QY 841 IIDEFPTFVSAKDSPKIAKYTDLEVSKSEIANIQSGADSLPCLLEPDLSPFKNIYPK 900

DB 841 IIDEFPTFVSAKDSPKIAKYTDLEVSKSEIANIQSGADSLPCLLEPDLSPFKNIYPK 900















634 PPPEAMNVALKAL-GTKEGKIPESFNAVQETAPYISACDLIKETKLTSPSPDF 692  
 656 PPPYEAMSVLKKVSGIKKEIKPENINAALQETAPYISACDLIKETKLSAEPAPDF 715  
 693 SNYSEAKPEKSVPHAEALVESSPSESEVDLFSDDSIPEVQTOQEEAVMLAKESLTVS 752  
 716 SYSEMAKVEQVPVPHSELVESSPSESEVDLFSDDSIPEVQTOQEEAVMLAKESLTVS 775  
 753 -ETVAQHK-EERLSASPQELGKPYLESFQNLHSTKDA-ASNDIPTLTKEKISIQMEEF 809  
 776 FPMIEYENKEKLSALPPGKPYLESFKLSLNTKOTLLPDEVSTLSKEKIPLOMEEL 835  
 810 NTAIYNSNDLLSKEDKIKESITFSDSPIIEIDEPPTFVSAKODS-PKLAKEYTDLEVS 868  
 836 STAVYSNDLFIKSKAQIRETETFSDDSPIIEIDEPPTLISKTDSFKLAREYTDLEVS 895  
 869 DKSETANIOSGADSLPCLELPCDLSFKNIYPK--DEVHVYDFSENSRSVSKASISPSNV 926  
 896 HKSEIANAPDGAGSLPCTELPHDLNKNIOPKVVEKISFSDDFSRNGSATSKVLLLPDV 955  
 927 SALEPOTEMGSIYVSKSLTKAEKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986  
 956 SALATQAEIESIVKPKVLYKEAEKLPSTDEKEDRSLSAELSKTSVVDLLYWRDIK 1015  
 987 KTGWFEGASLFLLLSVTSVSVTAIYIALLSVTISPRIYKGVIOAIQKSDGHPFRA 1046  
 1016 KTGWFEGASLFLLLSVTSVSVTAIYIALLSVTISPRIYKGVIOAIQKSDGHPFRA 1075  
 1047 YLESEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKFVILMWFTYVGALF 1106  
 1076 YLESEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKFVILMWFTYVGALF 1135  
 1107 NGTLTLLILALISFSPVYIYERHQVQIDHYLGANKSVKDMAKIOAKIPGLKRRKAD 1163  
 1136 NGTLTLLILALISFSPVYIYERHQVQIDHYLGANKSVKDMAKIOAKIPGLKRRKAE 1192  
 RESULT 12  
 ABR59667  
 ID ABR59667 standard; protein; 1192 AA.  
 AC ABR59667;  
 XX  
 XX  
 22-JUL-2003 (first entry)  
 DE Human NogoA protein.  
 XX  
 XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003031462-A2.  
 PN  
 PD 17-APR-2003.  
 XX  
 XX 04-OCT-2002; 2002WO-US032007.  
 PF  
 XX 06-OCT-2001; 2001US-00972599.  
 PR  
 XX (UYUA ) UNIV YALE.  
 PA  
 XX Strittmatter SM;  
 PI  
 XX WPI; 2003-393433/37.  
 DR N-PSDB; ACC81048.  
 XX  
 XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system

neuron, or in treating central nervous system disease, disorder or  
 injury, e.g. spinal cord injury.  
 PT  
 XX  
 PS Disclosure; Page 131-135; 148pp; English.  
 XX  
 CC The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 CC human Nogo receptor (Ngr) NTLRRCT domain), or residues 27-309 of P1 with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 CC axonal growth by a central nervous system (CNS) neuron. The Ngr  
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an Ngr protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention  
 XX  
 SQ Sequence 1192 AA;  
 Query Match 75.3%; Score 4403.5; DB 6; Length 1192;  
 Best Local Similarity 75.9%; Pred. No. 2.3e-222;  
 Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;  
 QY 1 MEDIDSSIVSSSTDPSPRPAPFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDELEVELEK 60  
 DB 1 MEDDQSPVLSSS-DSPRPAPFKYQVREPEDEE-BEEEEDEDEDEDEDELEVELEK 58  
 QY 61 PAAGLSAAAVP--PAAAPLPLFSDSVPPAPGRPLPAAPPAAPRQPSWERSPAA--P 115  
 DB 59 PAAGLSAAVPTAPAGAPLMDFGNDFVPPAPGRPLPAAPPVAPRQPSWDSFVSSVTP 118  
 QY 116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPSTPAAPK 166  
 DB 119 APSPLSAAVSPSKLPEDDEPPARPPPPPPASVQAPFVMTTPPAPAPAAPSTPAAPK 178  
 QY 167 RG-SGSVDETLPAAPAAEPVTPSSAEKIMDLMEOPGNTVSSGQDFPSVLLETAASLPS 225  
 DB 179 RGSVGSVDETLPAAPAAEPVTPSSAEKIMDLMEOPGNTISAGQDFPSVLLETAASLPS 237  
 QY 226 LSPSTVTFKHEGYLGNLSAVSSSEGTIETLNEASKELPERATNPFVNRDLAEFSELY 285  
 DB 238 LSPLSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLTFESELY 297  
 QY 286 SEMGSPFKGSPKGSAILVENTKEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339  
 DB 298 SEMGSPFSVSPKASAVIVANPREIIVKNKDEEEKLSNNILHNQOQLPTALTCLKVED 357  
 QY 340 RVVSPKTMIDIFENQMSVVAVRBEYADFKEFQOAWKVDTYEGSRDVLAA----RANV 395  
 DB 358 EVVSEKAKDSFNKRKVAEAPRBEYADFKEFVWEVKDSKEDS-DMLAAGGKIESNL 416  
 QY 396 ESKVDRKCLLEDSLEQKSLGKDSERNEADSPSTPEPVKDSRAVITCASFT-SATESTT 454  
 DB 417 ESKVDKCFADSLQTNHEKDSSESSNDTSPSTPEGIDKDSGAVITCAPFPAATESIA 476  
 QY 455 ANTFFLLEDHTSENKTDEKKIIEERKAQIITEK-TSPKTSNPLVAVQDEADYVTDILS 513  
 DB 477 TNIFPLLDGPTSENKTDEKKIIEERKAQIVTEKNTSTKTSNPLVAAQDSEYDVTNLT 536  
 QY 514 KYTEAAVSNMPEGLTPDLVQEAECESLNEATGKTAYETKVDLVOTSEAIQESLYPTAQL 573  
 DB 537 KYTEEVVANNMPEGLTPDLVQEAECESLNEVTGKTAYETKMDLVQTSFVWQESLYPAAQL 596  
 QY 574 CPSEFEAEATPSPVLPDIIVMEAPLNSLPSAGASVQPSVPLEAPPVPSYDSIKLEPEN 633  
 DB 597 CPSEFESEATPSPVLPDIIVMEAPLNSVPSAGASVIQPSSPLEA--SSVNYESIKHEPEN 655





836	STAVYNDLUFISKEAQIRETETSDSPTEIIDEPFTLISSKTDTSFKLAREYTDLEVS	895
869	DKSEIANIQSGADSLPCLEUPCDLUSFKXNIYPK--DEVHVSDEFSENKSSVSKASISPSNV	926
896	HKSEIANAPDGAAGSLPCTELPHDILSLKNIOPKVEKISFSDDFSKNGSATSKVLLLPDV	955
927	SALEPQTEMGSIKSVKSLITKEAEKKLPSTDYKEDORSLSAVLSAELSKTSVVDDLLYWRDIK	986
956	SALATQAEIESIYKPKVLKXAEKKLPSTDYKEDRSPSAFSAELSKTSVVDDLLYWRDIK	1015
987	KTGVVFGASIFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSEGHFPA	1046
1016	KTGVVFGASIFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSEGHFPA	1075
1047	YLSSEVAISELVOKYSNSALGHVNSITIKELRRLFLVDDLVDSLKPAVLMMVFTYVGCALF	1106
1076	YLSSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKPAVLMMVFTYVGCALF	1135
1107	NGUTLLILALISFSPVPIVERHQVQIDHYLGLANKSVKQAMAKIOAKIPGLKRRKAD	1163
1136	NGUTLLILALISFSPVPIVERHQVQIDHYLGLANKSVKQAMAKIOAKIPGLKRRKAE	1192

RESULT 15  
AAB82349  
ID AAB82349 standard; protein; 1192 AA.

AC AAB82349;

DT 23-JUL-2001 (first entry)

Human NOGO-A protein.

ZK NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

OS Homo sapiens.

XX PN WO200136631-A1.

25-MAY-2001.

PF 14-NOV-2000; 2000WO-GB004345.

PR 15-NOV-1999; 99GB-00026995.

XX  
06CCT0000-ED0007; 0007-NY0-47 YJFA (SMIK / SMITHLINE BEECHAM PLC.  
XX  
XXFI  
XX  
MICHAŁOWICH D., PRINJNA R;

DR WPI; Z001-343822/36.  
DR N-PSDB; AAF90324.

New polypeptide d

gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.

PS Disclosure: Page 26-27: 25pp: English  
xx

CC The present sequence is that of human

CC known splice variant of the human NOG3  
CC invention relates to a novel splice va

provides NQO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilizing NQO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying

CC agonists and agonists for use in treating conditions associated with NQO  
CC -C imbalance, and diagnostic assays for detecting diseases associated  
CC with inappropriate NQO-C activity or levels  
XX  
SQ Sequence 1192 AA;

Query Match	75.2%;	Score 4398.5;	DB 4;	Length 1192;
Best Local Similarity	75.9%;	Pred. No. 4.3e-222;		
Matches 908; Conservative 104; Mismatches 146; Indels 39;				

	QY	1	MEDIDOSSLVSSSTDSPRRPPAPFKYQVTFPEDEDEDDEEEDDEDEDLEELLEVLERK	60
	Db	1	MEDDOQSPLVSSS--DSGPRPQPAPKYQVREPSDEB--EEEBEEEEDEDELEELLEVLERK	58
	QY	61	PAAGLSAAAVP--AAAAALLDFSSDVPAPRPGPLPAAPAAPAPEROPSWEERSPAA--P	115
	Db	59	PAAGLSAAPVPTAPACAPLMDFGNDFVPAPRPGPLPAAPVPAPEROPSWDPSPVSSTVP	118
	QY	116	APSLLPAAAVALPSKLPEDDPPARPPPPPAGASPLAE-----PAAPPSTPAAPAKR	166
	Db	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPASPVSQAEPVMTVPAPAPAAPPSTPAAPAKR	178
	QY	167	RG--SGSVDETFLPALPAASEPVITPSSAEKIMDLMEOPCNTVSSGOEDPSPVLLETAAASLPS	225
	Db	179	RGSOGSVDETFLPALPAASEPVIRSSAEN--MDLKEQFCNTISAGQEDFPSSLTETAASLPS	237
	QY	226	LSPSLTVTSFKEHGYLGNLSAVSSSEGTIBETLNEASKELPERATNPVNDRDLABFSLEY	285
	Db	238	LSPLSAASFKEHYLGNLSTVLTEGTUQNVSSEAKVKTLIIDRLDTBFSELEY	297
	QY	286	SEMGSSFKGSPGESAILVENTKEBIVVRISKOKED--LVCSAALHSPOESVPVG-----KED	339
	Db	298	SEMGSSFVSFSPAESAVIDANPREEIIIVKNODEEEKLVSNILHNQDELPTALTCLKVKED	357
	QY	340	RUVSPKTMWIDIFNMOMSVVAUPVREIYADPKPEQAWEVKDYTGEGSRDVLA--RANV	395
	Db	358	EYVSSBKAKDSFNKKRVAEAPNRREIYADPKPFERVMVEVKDSKEDS--DMLAAGCKIESNL	416
	QY	396	ESKVDRKCLSDLSUEOKSLGKDSGRNEDASFPTBPVKDSRAYITCASFT--SATSETT	454
	Db	417	ESKVDKCCPADSLQEQTNHEKDSSESSNDTTSFPTSPGIKDRCPAYITCAPFNPAATESIA	476
	QY	455	ANTFPALLEDBHTSENKTDEKKIEBERKAQIITEK--TSPKTSNPFVLVAQDSADYYVTDTLS	513
	Db	477	TNIFFPLGLDPTSENKTDEKKIEBKQAVITEKNTSTKTSNPFVLVAQDSETDYVTDTNL	536
	QY	514	KUTEAAVSNMPEGLTPDLVQEACESELNEATGHKIAYETKVDLVQTSEALQESLYPTAQOL	573
	Db	537	KUTEEVVANNPEGLTPDLVQEACESELNEVTGKIAYETKMIDLVTQSEVNESLYPYAAQL	596
	QY	574	CPSFREAEATPSPVLDPDIVMEAPLNLSLPSAGASVVQPSVSPLEAPPVPVSYSCLKLEPEN	633
	Db	597	CPSFESEATPSPVLDPDIVMEAPLNSAVFSAGASVIQPSSSPLUA--SSVNYESIUKHEPEN	655
	QY	634	PPPYEAMNVALKAL--GTKEGIKEPESFNAAVOETEAPYISIACDLIKETKLTSTEPSPDF	692
	Db	656	PPPYEAMSLSLKCVSGIKEEIKEPENINAALOSTEAPYISIACDLIKETKLSAEPAPDF	715
	QY	693	SNNYEITAKEKSVPEHAELIVEGOSPSSEPVDLPSDDSISEVPQTOBEAVMLMKESLTEVS	752
	Db	716	SDYSEMAKVQEPVPDHSSELVESSPSSEPVDLPSDDSIPDPQKQDETMVLVAKESLSETS	775
	QY	753	-ETVAQH-K--BERLSASPOLGKPYLESFQPNLHSTKDA--ASNIDIPTLTKEKESLOWEEF	809
	Db	776	FMSMIENKELKSALPPGGGKPYLESFKLSLONTXDTLLPDSBSTLSKKEKIPLOQUEEL	835
	QY	810	NTAIYENDDLLSSKEDIKETSETFSSDSPTEIIDEPPTFFVSAKDDS--PKLAKERYTDLEVS	868
	Db	836	STAVSYNDLLDFSKEAQIRETETFSSDSPTEIIDEPPTLISSKTDTSFKLAREYTDLEVS	895
	QY	869	DKSEIANIOSGADSLPCLELPCDLSPKNITYPK--DEVHVSDSEFSERNRSSVSKASISPSNV	926
	Db	896	HKSEIANAPDGAGSLPCTELPHDSLUNTOPKVEKISIPSDPSKONGSATSKVLLLPDVP	955

Qy	927	SALEPQTEMGSIVKSKSLTKBAEKKLP	SDTEKEDRSLSAVLGAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLKBAEKKLP	SDTEKEDRSPSAIFGAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAY	IALLSVTISPRIYKGVIOAIQKSDGHPRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAY	IALLSVTISPRIYKGVIOAIQKSDGHPRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTI	KELRRLFLVDDLVDSLKFAVLMMVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTI	KELRRLFLVDDLVDSLKFAVLMMVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQID	HYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHQVQID	HYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

Search completed: June 16, 2005, 13:10:59  
Job time : 174.944 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 43.9175 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-2  
Perfect score: 5848  
Sequence: 1 MEDIDQSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908	15.5	199	2	US-08-700-607-1
2	908	15.5	201	4	US-09-949-016-9124
3	789.5	13.5	776	2	US-08-700-607-5
4	789.5	13.5	776	4	US-09-949-016-6998
5	724.5	12.4	439	4	US-09-949-016-9180
6	716.5	12.3	356	2	US-08-700-607-6
7	685	11.7	208	2	US-08-700-607-7
8	671	11.5	267	2	US-08-700-607-8
9	625.5	10.7	192	4	US-09-949-016-8859
10	539.5	9.2	168	4	US-09-149-476-563
11	522.5	8.9	219	4	US-09-270-767-45132
12	519	8.9	241	2	US-08-700-607-3
13	490	8.4	588	4	US-09-949-016-7290
14	387.5	6.6	127	4	US-09-513-999C-5000
15	302.5	5.2	8991	4	US-08-714-741-32
16	288	4.9	2468	4	US-09-976-594-726
17	288	4.9	2468	4	US-09-538-092-1135
18	288	4.9	2522	4	US-09-949-016-10237
19	286	4.9	68	4	US-09-513-999C-6304
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21	282.5	4.8	1219	4	US-09-344-624-4
22	279.5	4.8	1786	3	US-08-973-462-8
23	275.5	4.7	2753	4	US-09-949-016-7659
24	275.5	4.7	2753	4	US-09-949-016-7660
25	275.5	4.7	3924	4	US-09-538-092-1246
26	267	4.6	1781	4	US-09-961-403-13
27	265.5	4.5	1780	1	US-08-769-309A-5

Sequence 5, Appli  
Sequence 4463, Ap  
Sequence 911, App  
Sequence 4600, Ap  
Sequence 4601, Ap  
Sequence 647, App  
Sequence 4, Appli  
Sequence 7861, Ap  
Sequence 10933, A  
Sequence 6978, Ap  
Sequence 10925, A  
Sequence 6890, Ap  
Sequence 330, App  
Sequence 8902, Ap  
Sequence 8903, Ap  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 7, Appli

28 265.5 4.5 1780 3 US-08-994-570-5  
29 265 4.5 2137 3 US-09-134-001C-4463  
30 259.5 4.4 1020 4 US-09-538-092-911  
31 256.5 4.4 75 4 US-09-621-976-4600  
32 256.5 4.4 75 4 US-09-621-976-4601  
33 255.5 4.4 1140 4 US-09-538-092-647  
34 254.5 4.4 1596 4 US-08-978-277A-4  
35 252 4.3 114 4 US-09-513-999C-7861  
36 251.5 4.3 3913 4 US-09-949-016-10933  
37 250.5 4.3 4377 4 US-09-949-016-6978  
38 239.5 4.1 1344 4 US-09-949-016-10925  
39 238.5 4.1 1341 4 US-09-949-016-6890  
40 238 4.1 1306 4 US-09-538-092-330  
41 237 4.1 1878 4 US-09-949-016-8902  
42 237 4.1 1878 4 US-09-949-016-8903  
43 233 4.0 1142 2 US-08-993-118-7  
44 233 4.0 1142 3 US-08-845-528C-7  
45 233 4.0 1142 4 US-09-066-281B-7

## ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: Consensus  
US-08-700-607-1

Query Match 15.5% Score 908; DB 2; Length 199;  
Best Local Similarity 96.3%; Pred No. 1.5e-50;  
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 973 KTSVVDLLYMRDKKTVGFGASILLLSLTVFSIVSTAYIALALLSVTISFRIYKGV 1032

Db 9 KDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGYI 68  
QY 1033 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKF 1092  
Db 69 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKF 128  
QY 1093 AVLMMVFTVVGALFNGLLTLLIALISLFSIPVIYERHQVIDHYLGLANKSVKDMAKIQ 1152  
Db 129 AVLMMVFTVVGALFNGLLTLLIALISLFSVPVIYERHQVIDHYLGLANKSVKDMAKIQ 188  
QY 1153 AKIPGLKRAKAD 1163  
Db 189 AKIPGLKRAE 199

RESULT 2  
US-09-949-016-9124  
; Sequence 9124, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9124  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9124

Query Match 15.5%; Score 908; DB 4; Length 201;  
Best Local Similarity 96.3%; Pred. No. 1.5e-50;  
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 973 KTSVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGYI 1032  
Db 11 KDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGYI 70  
QY 1033 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKF 1092  
Db 71 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKF 130  
QY 1093 AVLMMVFTVVGALFNGLLTLLIALISLFSIPVIYERHQVIDHYLGLANKSVKDMAKIQ 1152  
Db 131 AVLMMVFTVVGALFNGLLTLLIALISLFSVPVIYERHQVIDHYLGLANKSVKDMAKIQ 190  
QY 1153 AKIPGLKRAKAD 1163  
Db 191 AKIPGLKRAE 201

RESULT 3  
US-08-700-607-5  
; Sequence 5, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 776 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307107  
US-08-700-607-5  
Query Match 13.5%; Score 789.5; DB 2; Length 776;  
Best Local Similarity 31.2%; Pred. No. 4.1e-42;  
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;  
QY 487 TSPKTSNPNFLVAVQDSEADYVTTDTLSKVTRAAVSNMPEGLTPDLVQACSELNEATGT 546  
Db 65 SGPARQSP--VAMETASTGVAGVSSAMDHPTSTTSKDGEG-----SCVTSLLI-----S 110  
QY 547 KIATYETKVDLVQTSEAIQ--ESLYPTAQLCPSEAEATPSPVLPDI--VMEAPLNS---- 599  
Db 111 DICYPQEDSYFTGILQKENGHVITSESP---BELGTPGSLPDPVGIESRGLFSSDSG 167  
QY 600--LLPSAGASVVPQSVSPLEAPPVSY-----DSIKLEPENPPYEEA-----M 641  
Db 168 IEMTPAESTEVNKLADPLDQMKAEAYKVIDITREEVKHQHHELEDKDLDFKNKDT 227  
QY 642 NVALKALGTGKGIKEPE-----SFNAVQTEAPYISACDLIKETKLSTE--PSP 690  
Db 228 DISIK---PEGVREPDKPAPVEGKIIKHLLLESTFAPYID---DLSEEQRAPQITTP 280  
QY 691 DFSNYSYETAKESVPEHAELVEDSSPESEPVDLF--SDDSIPEV---POTQEEAVMLMK 745  
Db 281 VKITUTEIE-----PSVETTTQKTPKQDILCLKPSDPTVTVTVSPEDDSDSPSIPTP 334  
QY 746 ESLTEVSETVAQHK-----EERLSASPOLGKPYLESFQ-----NLHSTKDAASND---- 792  
Db 335 SSGTEPSAAESQKGSISEDELITAIKEAKGLSVTAENPRPVGQLADRPEVKARSGPPT 394  
QY 793 IPTLTKEKIKLQMEEFNTAYISNDDLLSSKEDI----- 827  
Db 395 IPSPLDHEASSAESGDSIELVSEDPM--AAEDALPSGVSVFSGHVGPPSPSPASIQVS 452  
QY 828---KESETFSDSSPIEIIDEPFTFVSAXDDSPKLAKYVTDLEVSQKSEI-----ANIQSG 879  
Db 453 ILREEREAELDS---ELIIESCDASSASEEPKRDQSDPPMKPSALDAIRETGTVAER 509  
QY 880 ADSLPCLELPCDLSFKNIYPKDEHVSDSEFSENRSVSKASISPSNVSALEPQTEMGSTIV 939  
Db 510 APSRRGLAEPG--SFLD--YPSTEPQGPPEL-----PPGDGALEPETPM----- 549



Qy 940 KSKSLTKEAEKKLPDSSTKEBDRSLSAVLSAE-----LSKTSVVDLLLYWRD 984  
Db 550 -----LPRKPEDSSNSQSPAATKGGPLGPGAPPPLLFLNKKQKADLLLYWRD 597  
Qy 985 IKKTGVVFGASIFLLLSLTVFSIVSAYIALALASVTSIFRIYKGVQIAOKSGEGHPF 1044  
Db 598 IKQTGVFGSFLLLLSLTVFSIVSAYIALALASVTSIFRIYKGVQIAOKSGEGHPF 657  
Qy 1045 RAYLESEVAISEELVQKYSNAGLGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 1104  
Db 658 KAYLELEITLSEQIQKYTDCLQFVNSTKLSELRLFLVQDLVDSLKFAVLMWLLTYVGA 717  
Qy 1105 LFNGLTLILALISLFSIPVYERHQVQIDHYGLANKSVKDMAMAKIOAKIPGLKRRKAD 1163  
Db 718 LFNGLTLILMAVSMFTLPVVVYVHQADQIDYGLVTRHINAVVAKIOAKIPGAKRHA 776

RESULT 4  
US-09-949-016-6998  
; Sequence 6998, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6998  
; LENGTH: 776  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6998

Query Match 13.5%; Score 789.5; DB 4; Length 776;  
Best Local Similarity 31.2%; Pred. No. 4.1e-42;  
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

Qy 487 TSPKTSNPFVAVQDSEADYVTTDLTSKVTEAANMPEGLTDLVQACBSSELNEATGT 546  
Db 65 SGPARQSP--VAMETASTGAVGVSSAMDHFTSTTSKDGEG-----SCYTSLI---S 110  
Qy 547 KIAYETKVDLVQTEAIO-ESLYPTAQLCPSEAEATPSVLPDI--VMEAPLNS---- 599  
Db 111 DICVPPQEDSTYFTGILQKENGHVITSESP---ELGTGPGSLPDVPGIESKGLFSSDSG 167  
Qy 600 --LLPSAGASVQVSPSLEAPPVSY-----DSIKLEPNPPPEEA-----M 641  
Db 168 IEMTPAESTEVNKILADPLDQMAEAYKVIDITRPEEVKHQHQHPELEDKLDLFPNKDT 227  
Qy 642 NVALKALGTKEGIKEPE-----SFNAAVQTEAPYISIACDLIKETKLSTE-PSP 690  
Db 228 DISIK----PEGVREPDKPAVPEGKIIKHLLLEESTFPAYID--DLSEEQRRAPQITTP 280  
Qy 691 DFSNYSRIAKEKSVPEHAELVDSSEPEVDLP-SDDSIPEV----PQTQEEAVMLMK 745  
Db 281 VKITLTIE-----PSVETTTQKTPBKQDICKLPSDPTVPTVTSPEPDDSPGSI 334  
Qy 746 ESLTEVSETVAQHK-----EERLSASPGLKPYLESFQP-----NLHSTKDAASND 792  
Db 335 SSGTSPSAESQKGSISEDLITAIKAKGLSYETAENPRPVQGLADRPVKARSGPPT 394  
Qy 793 IPTLTKEKIKSLQWEEFNATYISNDDLLSSKEDI----- 827

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395 IPSPLDHEAASAGSGDSEIELVSEDPM--AAEDALPSGYVSFGVHGPPPPSPASPSIQYS 452
828 ---KESETFSDSSPIEIIIDFPTFVSADQSPKLAKKEYTDLVLESDKSEI-----ANIQSG 879
453 ILREEREAEUDS---ELIIESCDASSASESPKREQDSPPMKPSALDAIREETGVRAEER 509
880 ADSLPCLLEPCDLSFKNIYIPKDEVHVHSDSEFSENKSSVKASISPSNVSALEPQTEMGSIV 939
510 APSRRGLAEPFG--SFLD-YPSTEPQGPPEL-----PFGDGALEPETPM----- 549
940 KSKSLTKAEKKLPSPDTEKEDRSLSAIVSAE-----LSKTSVVDLLVWRD 984
550 -----LPRKPESSSSNQSPAATKPGCPGLGAPPPPLFLFNKQKADULLVWRD 597
985 IKRTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPF 1044
598 IKGTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPF 657
1045 RAYLESEVAISEELVQKYSNALSCHVNSTTKELRRLFLVDDLVDLSLKFVLMWVFTYVGA 1104
658 KAYLELEITLSQEQIQKYTDCLQFYVNSTTKELRRLFLVQDLVDLSLKFVLMWVFTYVGA 717
1105 LFNGLTLLIILALISLPSIPVYSEHVOQIDHYLGLANKSVKDMAKIQAKTGLKRRKAD 1163
718 LFNGLTLLLMVMSMFTLPVYVYKHOAQIDQYLGVLVTHINAVVAKIQAKTGPAGRRHAE 776

RESULT 5
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180

Query Match 12.4%; Score 724.5; DB 4; Length 439;
Best Local Similarity 38.04; Pred. No. 2.6e-38;
Matches 190; Conservative 64; Mismatches 135; Indels 111; Gaps 13;

Qy 713 EDSPSEPVDLFSDDSIPEVPQTQBEAVMLMKESLTVESVTVAQHKERLSASPQL-- 770
Db 2 EPAASOSQKGSISED-----ELITAKEKGLSVETAENPPVQLADRPVKA 51
Qy 771 --GKPYLESFPQNLHSTKDAASNDIPTLTKEKXISLQMEFNTAIYNSDDLSS----- 822
Db RSGPPTIPS--PLDHEASSAESGD-----SBIELVSEDPMAA---EDALPSGYVSFG 98
Qy 823 -----KEDIKSETSDSSPPIIIDFPTFVSADQSPKLAKKEYTDLVLESDKSEI 863
Db HVGPGPPSPASPSIQYSILFEAREALDS-----ELIIESCDASSASESPKREQDSP 151
Qy 864 DLEVSDKSEI-----ANIQSGADSLPCLLEPCDLSFKNIYIPKDEVHVHSDSEFSENKSSVKASISPSNVSALEPQTEMGSIV 918
Db 152 PMKPSALDAIREETGVRAEERASRRGLAEPFG--SFLD-YPSTEPQGPPEL----- 199
Qy 919 ASISPSNVSALEPQTEMGSIVKSKLTKAEKKLPSPDTEKEDRSLSAIVSAE----- 970

```

Query Match	12.4%	Score	724.5	DB	4	Length	439
Best Local Similarity	38.0%	Pred. No.	2.6e-38				
Matches	190	Conservative	64	Mismatches	135	Indels	111
Gaps	13						
Qy	713	EDSSPSEPVDLFSDPSDISEVPTQTEAVALMKESLIEVSETVAQHKERLSASPOEL	--	770			
Db	2	EPSAASQKGSI	SED-----ELITAIKEAKGLSVETAENRPVQQLADREVKA	51			
Qy	771	--GKPYLESFQPNLHSTKDAANDIPTLTTKKISLQMEEFNTATYNSDDLLSS	-----	822			
Db	52	RSQPPTIPS--PLDHEASSAEGD-----SEIELVSDPMAA	-----EDALPSGVYVFG	98			
Qy	823	-----KEDKIKESETFSDSPPIEIIDEPPTFVSAKDDSPKLAKBYT	863				
Db	99	HVGPGPPSPASPSIQYSLILREERAELDS-----ELIIESCDASSASESPKREQDSP	151				
Qy	864	DLEVSQSKI-----ANIQSGADSLPCLELPCDLSPKNIYPKDEVHVSDSEFNSSVSK	918				
Db	152	PMKPSALDAIREBTGVRAERAPSRRLGAEPG--SPLD--YPSTEQPGPEL	-----	199			
Qy	919	ASISPNVNSALEPQTEMGSIIVKSKSLTKEAEKKLPSDTEKDRSLSAVLSAE	-----	970			

[illegible]

## RESULT 6

US-08-700-607-6  
; Sequence 6, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-L  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.

ZLFI: 3504  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/700,607  
 FILING DATE: Filed Herewith  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0114 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4186  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 356 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 307309  
 US-08-700-607-6

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Query Match      12.3%; Score 716.5; DB 2; Length 356;
Best Local Similarity 46.1%; Pred. No. 6.2e-38;
Matches 164; Conservative 48; Mismatches 89; Indels 55; Gaps 7;

828 KSETFSDSPRIIDFFPTFVSAKDDSPKLAKEYTDLFVSDKSEI-----ANIQSGADS 882
QY

36 EREAEALDS---ELIIESDASSGESPKRQDDSPMKPSALDAIREETGVRAEEAPS 92
DB
```

[illegible]

## RESULT 7

US-08-700-607-7  
Sequence 7, Application US/08700607  
Patent No. 5858708  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Au-Young, Janice  
APPLICANT: Goli, Surya K.  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4186
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307311
US-08-700-607-7

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Query Match      11.7%; Score 685; DB 2; Length 208;
Best Local Similarity 67.0%; Pred. No. 2.9e-36;
Matches 128; Conservative 32; Mismatches 31; Indels 0; Gaps 0;

QY   973 KTSVDDLXWRDIKKTGVVFSGASFLLLSLTTFESIVSTAYIALALLSVTISPRIYGV I 1032
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db    18 KSQAIDLLXWRDIKQTGIVFGFGLLLFSLTQSFVSWVAYLALAAISATISPRIYKSVL 77

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Qy	1033	QAIOKSDGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRLFLVDLVDLSKF	1092
Dd	78	QAVQKTDEGHPFRAYLEITLTSQEIQKYTDCLQFYVNSTKLRELRLFLVQDLVDLSKF	137
Qy	1093	AVLMWFTYTGALFNGLTLLILALISLFSPIVYERHQVIDHYGLANKSVKDAMAKIQ	1152
Dd	138	AVLMWLLITYGALFNGLTLLMLMAVSMFTPLPVVYVKHQAQIDQYGLVRTHINAVAKIQ	197
Qy	1153	AKTIPGLKKRAD	1163
Dd	198	AKTFPGAKRHAE	208

## RESULT 8

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US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: 20 NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 281046  
US-08-700-607-8

	Query Match	11.5%	Score 671;	DB 2;	Length 267;	
	Best Local Similarity	66.3%;	Pred. No. 3.3e-35;			
	Matches 124;	Conservative 33;	Mismatches 30;	Indels 0;	Gaps 0;	
<hr/>						
QY	973	KTSVDLLLYWRDIDKKTGVFGASFLFLLSLTVFSIVSVTAYIALLSVTISFRYYGVI	1032			
	:	: : : : : :	:	:	:	:
	:	: : : : : :	:	:	:	:
Dd	9	KSQAIDLILYWRDIKQTGI VFGSFLILFSLTQFSVSWWAYLAAALSAATISFRYYKSVL	68			
<hr/>						
QY	1033	QATQKSDGEHPFPAYLESEVAISEELVQKYSNGALGHVNSTIKELRRLFLVDLDVLSKF	1092			
	:	: : : : : :	:	:	:	:
	:	: : : : : :	:	:	:	:
Dd	69	QAVQKTDEGHPFKAYLEILTLSQEIQKYTDCLQLYVNSTKLKLRRLFLVDLVLSKF	128			
<hr/>						
QY	1093	AVLMWFTYYGALPENGTLTLLIALLISLFSIPVYERHQVIDHYVLGLANKSVKDAMAKIQ	1152			
	:	: : : : : :	:	:	:	:
	:	: : : : : :	:	:	:	:

```

Db      129  AVLWMLITYYVGALENGLTLLLMVVSMFTLPVVTVYKHOAQVDQYLGLVVRTHINTVVAKIQ 188
Qy      1153 AKIPGLK 1159
          ||||| :
Db      189 AKIPGAR 195

RESULT 9
US-09-949-016-8859
; Sequence 8859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

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Gaps	1;						
Qy	975	SVVDLLVWRDIKKTGVVFGASFLLSLTVFVSIVSTAYITALALLSVTISPRIYKGVIOA	1034				
Db	3	SVHDLIFWRDVKTGPFVGTLLIMLLSLAFAFSIVSVSYLILALLSVTISPRIYKSVIOA	62				
Qy	1035	IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTTKELRRLFLVDLVDLSKPAV	1094				
Db	63	VQKSEEGHPKPYALVDVDTLSSEAFNHYNMAAMVHINRAKLITRLFLVEDVDSLKLAV	122				
Qy	1095	LMWFTVVGALFNGLTLLIALLSLFSIPVYERHQVQIDHYILGLANKSVKDMAKTOAK	1154				
Db	123	FWMLMTVGVAFNGITULLIALLBELIFSVPVIEKIKTQIDHYVGIARDQTKSIVEKIOAK	182				
Qy	1155	IPGL-KRKAD	1163				
Db	183	LPGIKKKAE	192				

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RESULT 10
US-09-149-476-563
Sequence 563, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07

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2	EARLIER APPLICATION NUMBER: 60/048,974	
3	EARLIER FILING DATE: 1997-06-06	
4	EARLIER APPLICATION NUMBER: 60/056,886	
5	EARLIER FILING DATE: 1997-08-22	
6	EARLIER APPLICATION NUMBER: 60/056,877	
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11	EARLIER FILING DATE: 1997-08-22	
12	EARLIER APPLICATION NUMBER: 60/056,630	
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57	EARLIER FILING DATE: 1997-05-23	
58	EARLIER APPLICATION NUMBER: 60/047,585	
59	EARLIER FILING DATE: 1997-05-23	
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62	EARLIER APPLICATION NUMBER: 60/047,590	
63	EARLIER FILING DATE: 1997-05-23	
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65	EARLIER FILING DATE: 1997-05-23	
66	EARLIER APPLICATION NUMBER: 60/047,589	
67	EARLIER FILING DATE: 1997-05-23	
68	EARLIER APPLICATION NUMBER: 60/047,593	
69	EARLIER FILING DATE: 1997-05-23	
70	EARLIER APPLICATION NUMBER: 60/047,614	
71	EARLIER FILING DATE: 1997-05-23	
72	EARLIER APPLICATION NUMBER: 60/043,578	
73	EARLIER FILING DATE: 1997-04-11	

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EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 9.2%; Score 539.5; DB 4; Length 168;  
Best Local Similarity 59.3%; Pred. No. 4.3e-27;  
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;  
Qy 998 LLLSLTVFSIVTAYIALALLSVTSPIRYKVIQAIQKSDGHPFRAYLESEVASEE 1057  
Db 1 MLLSLAAPSIVSVSYLLALLSVTSPIRYKVIQAVQKSEEGHPFKAYLDVDTLSSE 60  
Qy 1058 LVQKYSNSALGVNSTIKELRELFLVDLSLKFVLMVFTYVGVLFNGLTLLIALI 1117  
Db 61 AFHYMNAAMVHINRAKLIIRLFVEDLVDLSLKFVLMVFTYVGVLFNGLTLLIALI 120  
Qy 1118 SLFSPVYERHQQVDHYLGANKSVKDMAKIQAKIPGL-KRKAD 1163  
Db 121 LIFSVPVYKQIDHYGVGIARDQYKSVIEKIQAKLPGIAKKAE 167

RESULT 11  
US-09-270-767-45132  
Sequence 45132, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 45132  
LENGTH: 219  
TYPE: PPT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-45132

Query Match 8.9%; Score 522.5; DB 4; Length 219;

Best Local Similarity 47.8%; Pred. No. 7.8e-26;  
Matches 97; Conservative 48; Mismatches 55; Indels 3; Gaps 1;  
Qy 957 EKEDRSLSA---VLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY 1013  
Db 1 EHRSSVGKPNLNRKXSNRLLESLLYWRDVKGSGIVFGAGLITLAAISFSVISVPAY 60  
Qy 1014 IALALLSVTSIFRIYKVIQAIQKSDGHPFRAYLESEVASEEVLQKYSNSALGVNST 1073  
Db 61 LSLTLFETVAFRIYKSVTQAVKTNEGHPKDYLEDLTLSEKVNQIAGVAHNGF 120  
Qy 1074 IKELRRLFLVDLVDLSLKFVLMVFTYVGVLFNGLTLLIALISLSPVYERHQQV 1133  
Db 121 ISELRLFLVEDIIDSIKFGVILMVFTYVGVLFNGMTLVILAFVSLFTLPKVYNNKQSI 180  
Qy 1134 DHYLGANKSVKDMAKIQAKIP 1156  
Db 181 DTHLDLVRSLKLTETDKIRVAIP 203

RESULT 12  
US-08-700-607-3  
Sequence 3, Application US/08700607  
Patent No. 5858708  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Au-Young, Janice  
APPLICANT: Goli, Surya K.  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: THPIN0801  
CLONE: 31870  
US-08-700-607-3

Query Match 8.9%; Score 519; DB 2; Length 241;  
Best Local Similarity 59.4%; Pred. No. 1.5e-25;  
Matches 95; Conservative 33; Mismatches 32; Indels 0; Gaps 0;  
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Db 44 SSCAVHDLIXWRDVKKTGFGVFGTLLMLSLAAPSIVSVSYLLALLSVTSPIRYKSV 103

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Qy 1032 IQALQKSDGEGHFFRAYLSEVAISELWOKYNSNALGHVNSTIKELRLRLFLVDDLVDLSLK 1091
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Qy 1092 FAVLMWFTYVYGALFNGTLTLILALISLFSPIVYERHOV 1131
Db 164 LAVFWMLTYVGVAFNGTTLILAEELLIXSPIVYXKYK 203

RESULT 13
US-09-949-016-7290
; Sequence 7290, Application US/099490016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7290
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290

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Best Local Similarity 28.3%; Pred. NO. 4e-23;
Matches 160; Conservative 76; Mismatches 202; Indels 128; Gaps 17;

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Qy 725 PSDSIPVPQTOEAVMLMKESLTVSETVAQHKEERLSASPOELGKPYL-ESQPQNLH 783
Db 110 IAFQGVGSGGRDSTARPPQCRSVSEPRDQHPQPSLIGDSLESI--PSLSQSPQGR 167
Qy 784 STKDAASNDIPTLKKEKISLQMBEFNTALYSNDLLSKEDKIKESFTFSDSSPIEIID 843
Db 168 GDPDTAP--PSEPLEDLRLDHLGWARGT---GSGED---SSTSSTPLE--- 212
Qy 844 EFPTFVSAKDSPLAKETDTLEVDSKSEIANIQSGADSLPCELEFLCDLSFKNIYPKDEV 903
Db 213 -----DEEP---QEPNRLTGEAGE-----EL-DLRLRLAQPSPE 244
Qy 904 HVSDEFNSRNSVSKASISP-----SNVSALEPQTE----- 934
Db 245 VLTPLQSPGSGTPQAGTSPSRSDNSNGPEEPLEEEBEEKQWGPLEREFPVRQCCLDSTDQ 304
Qy 935 -----MGSIVK--SKSLTKAEKKLP-----S 954
Db 305 LEFTVEPRLLTGAMEWLKTSLLAVYKTVPILELSPPLMTAIGWVQRGTPPTPVLRLVLL 364
Qy 955 DTEKEDRSLSAVLSAELSK---TSVVDLLYWRDIKKTGVVFGASLPLLLSLTVFSIVSVT 1011
Db 365 KWAKSPRS-SGVPSLSLGADMGSKVADLLYWKDTTSGVFTTGLMVSLCLLHFSIVSA 423
Qy 1012 AVIALALLSVTISFRIYKGVIOAIKSDGEGHFFRAYLSEVAISELWOKYNSNALGHVN 1071
Db 424 AHLALLLCGTHLSLAVYRKVQAVIRGQANPQAYLDVDTLTLTQETRLSHQITSRV 483
Qy 1072 STIKELRLFLVDDLVDLSLKFAVLMWFTYVYGALFNGTLTLILALISLFSPIVYERHOV 1131
Db 484 SAAQTOLRHFFLVEDLVDLSLKALLPFIYLTFTVGAIFNGLTLLIGVIGFTIIPLLYRHOA 543

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:29:05 ; Search time 150.865 Seconds  
(without alignments)  
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Title: US-09-830-972-2

Perfect score: 5848

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Searched: 1714042 seqs, 383979560 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications AA:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	5312.5	90.8	1162	16	US-10-427-741-10
5	5307	90.7	1163	15	US-10-267-502-431
6	4403.5	75.3	1192	9	US-09-758-140-6
7	4403.5	75.3	1192	9	US-09-972-599A-6
8	4403.5	75.3	1192	14	US-10-060-036-71
9	4398.5	75.2	1192	9	US-09-789-386-2
10	4398.5	75.2	1192	9	US-09-893-348-23
11	4398.5	75.2	1192	15	US-10-267-502-429

12	4398.5	75.2	1192	16	US-10-327-213-9	Sequence 9, Appli
13	4398.5	75.2	1192	16	US-10-466-258-9	Sequence 9, Appli
14	4398.5	75.2	1192	16	US-10-810-653-23	Sequence 23, Appli
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22	1191	20.4	373	14	US-10-060-036-72	Sequence 8, Appli
23	1191	20.4	373	15	US-10-408-967-8	Sequence 24, Appli
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31	908	15.5	199	16	US-10-810-653-25	Sequence 9, Appli
32	901	15.4	199	15	US-10-408-967-9	Sequence 467, App
33	899	15.4	199	11	US-09-978-360A-467	Sequence 4, Appli
34	888	15.2	289	9	US-09-789-386-4	Sequence 11, Appli
35	868	14.8	199	16	US-10-466-258-11	Sequence 93, Appli
36	801	13.7	777	14	US-10-205-219-93	Sequence 432, App
37	792	13.5	780	15	US-10-267-502-432	Sequence 5, Appli
38	789.5	13.5	776	15	US-10-660-946-5	Sequence 430, App
39	789.5	13.5	776	15	US-10-267-502-430	Sequence 1481, Ap
40	789.5	13.5	776	16	US-10-723-860-1481	Sequence 6, Appli
41	716.5	12.3	356	15	US-10-660-946-6	Sequence 2892, Ap
42	706.5	12.1	593	15	US-10-108-260A-2892	Sequence 7, Appli
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44	671	11.5	267	14	US-10-205-194-127	Sequence 8, Appli
45	671	11.5	267	15	US-10-660-946-8	

## ALIGNMENTS

### RESULT 1

US-09-893-348-18  
; Sequence 18, Application US/098933348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-893-348-18

Query Match 100.0%; Score 5848; DB 9; Length 1163;  
Best Local Similarity 100.0%; Pred. No. 1.9e-256;  
Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





QY 1015 ALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEBELVOKYSNSALGHVNSTI 1074  
DB 1014 ALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEBELVOKYSNSALGHVNSTI 1073  
QY 1075 KELRRLFLVDDLVDLSLKFVLMWVFTYVVGALFNGLLTLLILALISLFSIPVIYERHQVQID 1134  
DB 1074 KELRRLFLVDDLVDLSLKFVLMWVFTYVVGALFNGLLTLLILALISLFSIPVIYERHQVQID 1133  
QY 1135 HYLGLANKSVKDMAKIOAKIPGLKPKAD 1163  
DB 1134 HYLGLANKSVKDMAKIOAKIPGLKPKAE 1162

RESULT 4  
US-10-427-741-10  
; Sequence 10, Application US/10427741  
; Publication No. US20040191291A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023  
; CURRENT APPLICATION NUMBER: US/10/427,741  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 1162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-427-741-10

Query Match 90.8%; Score 5312.5; DB 16; Length 1162;  
Best Local Similarity 91.0%; Pred. No. 3.3e-232;  
Matches 1064; Conservative 37; Mismatches 55; Indels 13; Gaps 6;

QY 1 MEDIDQSSLVSSSTSPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDEDEDELEVLK 60  
DB 1 MEDIDQSSLVSSSADSPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLK 59  
QY 61 PAAGLSAAVPPAAAPLIDFSSDVPAPRGLPAAPAAERQPSWERSPAAAPSLP 120  
DB 60 PAAGLSAAVPP-AAAPLIDFSSDVPAPRGLPAAPPTAPERQPSWERSPAAAPSLP 118  
QY 121 PAAAVLPKLPEDDEPPARPPPPAGASPLAEPAPPTAPAKRRGSGSVDETLFALP 180  
DB 119 PAAAVLPKLPEDDEPPAR-PPAPAGASPLAEPAPPTAPAKRRGSGSVDETLFALP 176  
QY 181 AASEPVIPSSAKIMDLMEQNGNTVSSGQEDFPFVLLLETAASLPSLSTVSKHEGYL 240  
DB 177 AASEPVIPSSAKIMDLMEQNGNTVSSGQEDFPFVLLLETAASLPSLSTVSKHEGYL 236  
QY 241 GNLSAVSSECTIETETINEASKELEPERATNPPFNRDLAEPFSELEYSEMSSFGPKGES 300  
DB 237 GNLSAVASTEGETIETETINEASKELEPERATNPPFNRDLAEPFSELEYSEMSSFGPKGES 296  
QY 301 AILVENTKEIVRSKDKEDLVCSAALHSPQESP-----VGKEDRVVSPKEMTDFNEMQ 355  
DB 297 AMLVENTKEIVRSKDKEDLVCSAALHNPQESPATLTVKVKEDGVMSEKMTDFNEMK 356  
QY 356 MSVAVPVRREYADFPFEQAWKQTYEGSRDVLAAARANVESKVRKCLDSLEQKSLGK 415  
DB 357 MSVAVPVRREYADFPFEQAWKQTYEGSRDVLAAARANVESKVRKCLDSLEQKSGHK 416  
QY 416 DSEGRNEDASFPSTPEPVKDSRAYITCASFTSATSTTANTFPFLEEDHTSENKTDKKI 475  
DB 417 DSESRNENASFPRTPLVLKDGSRAYITCDSFSATSTTANTFPFLEEDHTSENKTDKKI 476  
QY 476 ERKAQIITEKTSPTKSNPFLVAQDSEADYVTTDLNLSKVTEAVVATWPEGLTDPDLVQEA 535

DB 477 ERKAQIITEKTSPTKSNPFLVAIHDSADYVTTDLNLSKVTEAVVATWPEGLTDPDLVQEA 536  
QY 536 CESELNATGKIAYETKVDLVQVSEATQESLYPTAQICPSPERAEATSPVLDPVMEA 595  
DB 537 CESELNATGKIAYETKVDLVQVSEATQESLYPTAQICPSPERAEATSPVLDPVMEA 596  
QY 596 PLNSLLPAGASVQPSVPLEAPPVSYDSIKLEPENPPPPYEEAMVAKLKGTEGK 655  
DB 597 PLNSLLPAGASVQPSVPLEAPPVSYDSIKLEPENPPPPYEEAMVAKLKGTEGK 656  
QY 656 EPESFNAAVQETEADYISIACDLIKETKLSSTEPSPDFSNYSIAKFEKSVPEHAELVDS 715  
DB 657 EPESFNAAVQETEADYISIACDLIKETKLSSTEPSPDFSNYSIAKFEKSVPEHAELVDS 716  
QY 716 SPSEPVDLFSDDSIPVPOQTEEAAMLMKESLSEVSETVQAQK-ERLSASPOELGPKY 774  
DB 717 SPSEPVDLFSDDSIPVPOQTEEAAMLMKESLSEVSETVQAQK-ERLSASPOELGPKY 776  
QY 775 LESFQNLHSTKDAASNDIPTLTKEKISLQWEEENTAIYSNDDLLSSKEDKIKESSTFS 834  
DB 777 LESFQNLHSTKDAASNDIPTLTKEKISLQWEEENTAIYSNDDLLSSKEDKIKESSTFS 836  
QY 835 DSSPTIIDEPTFVSADKDPKLAKEYTDLSEVSKSEIANIQSGADSLPCLLEPCDLSF 894  
DB 837 DSSPTIIDEPTFVSADKDP--KEYTDLSEVSKSEIANVQSGANSLPCSELPCDLSF 893  
QY 895 KNIYPKDEHVHSDSEFSENRSVSKASISPSNVSALEPQTEMGSIKVSLSLTKAEKPLPS 954  
DB 894 KNTYKDEAHVSDSEFSEKRSVSKVPLLLPNVSALESQIEMGNIKPKVLTKEAEKPLPS 953  
QY 955 PTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYI 1014  
DB 954 PTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYI 1013  
QY 1015 ALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEBELVOKYSNSALGHVNSTI 1074  
DB 1014 ALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEBELVOKYSNSALGHVNSTI 1073  
QY 1075 KELRRLFLVDDLVDLSLKFVLMWVFTYVVGALFNGLLTLLILALISLFSIPVIYERHQVQID 1134  
DB 1074 KELRRLFLVDDLVDLSLKFVLMWVFTYVVGALFNGLLTLLILALISLFSIPVIYERHQVQID 1133  
QY 1135 HYLGLANKSVKDMAKIOAKIPGLKPKAD 1163  
DB 1134 HYLGLANKSVKDMAKIOAKIPGLKPKAE 1162

RESULT 5  
US-10-267-502-431  
; Sequence 431, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Galant, Ron  
; APPLICANT: Kim, Jaeseob  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 431  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-267-502-431

Query Match 90.7%; Score 5307; DB 15; Length 1163;  
Best Local Similarity 91.1%; Pred. No. 5.8e-232;  
Matches 1066; Conservative 34; Mismatches 56; Indels 14; Gaps 7;

QY 1 MEDIDQSSLVSSSTSPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60  
DB 1 MEDIDQSSLVSSSADSPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDELEVLK 59

Qy 61 PAAGLSAAVPPAAAPLLDFSSDSVPPAPRGPLPAAAPPAEROPSWERSPAAPSLP 120  
Db 60 PAAGLSAAVPP- AAAPLLDFSSDSVPPAPRGPLPAAAPTAPEROPSWERSPAAPSLP 118  
Qy 121 PAAAVLPKGLPDDPPAPPPPPAGASPLAEPAPSTPAAPKRRGSGVDLTFALP 180  
Db 119 PAAAVLPKGLPDDPPAP- PPAAGASPLAEPAPSTPAAPKRRGSGVDLTFALP 176  
Qy 181 AASEPVPSSAEKINDLMEQNCNTVSSGOEPFSSVLLLETAASLSPLSTVSKHGYL 240  
Db 177 AASEPVPSSAEKINDLMEQNCNTVSSGOEPFSSVLLLETAASLSPLSTVSKHGYL 236  
Qy 241 GNLASVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKSPKGES 300  
Db 237 GNLASVASTEGTIEETLNEASRELPERATNPFVNRDESAEFVLESEMGSSFNKSPKGES 296  
Qy 301 AILVENTKEEVIVRSKOKEDLVCSAALHSPOESP-----VKBERVVSPEKTMDFINEMQ 355  
Db 297 AMLVENTKEEVIVRSKOKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDFINEMK 356  
Qy 356 MSVAVPVEEYADPKPFQOAEVKDITYGSRDVLAAARANVESKVDKCLEDSLQKSLGK 415  
Db 357 MSVAVPVEEYADPKPFQOAEVKDITYGSRDVLAAARANVESKVDKCFEDLSLQKSHGK 416  
Qy 416 DSEGRNEDASPPSTPEPVKDSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKI 475  
Db 417 DSESENENASFPSTPELVKDSRAYITCDSFTSATESAANI FVLEDTHTSENKTDEKKI 476  
Qy 476 BERKAAIITTEKTSPTKSNPFLVAVODSEADYVTTDTLSKVTEAAVSNMPEGLTDPDLVQEA 535  
Db 477 BERKAAIITTEKTSPTKSNPFLVAIHDSADYVTTDTLSKVTEAAVAVATMPEGLTDPDLVQEA 536  
Qy 536 CESELINEATGKIAYETKVDLVQTSSEATQESLYPTAQICPSFEAEATPSVPLVDIIMEA 595  
Db 537 CESELINEATGKIAYETKVDLVQTSSEATQESIYPTAQICPSFEAEATPSVPLVDIIMEA 596  
Qy 596 PLNSLLPAGASVVPQSPVLEAPPVSDYSGIKLEPENPPPYEAMNVALKALGTKEGK 655  
Db 597 PLNSLLPSTGASVQASPLSEVPSPYDGIKLEPENPPPYEAMNVALKTSDAKEIK 656  
Qy 656 EPESFNAAVQTEAPYISIACDLIKETKLSSTEPSPGFSNYSEIAKFKSVPEHAELVEDS 715  
Db 657 EPESFNAAVQAEAPYISIACDLIKETKLSSTEPSPGFSNYSEIAKFKSVDPDCHLVDDS 716  
Qy 716 SPSEPVDLFDDSDIPEVPQTEAEAVMLMKESLTVSETVTAQHK- EERLSASPOELGKPY 774  
Db 717 SPSEPVDLFDDSDIPEVPQTEAEAVMLMKESLTVSETVTVQHKHERLSASPOEVGKPY 776  
Qy 775 LESFQPNLHSTKDAASNDIPTLTTKKEKISLOWERFNTAIYGNDDLLSSKEDKIKESFTFS 834  
Db 777 LESFQPNLHITKDAASNEIPTLTTKKETISLOWEFNTAIYGNDDLLSSKEDKMKESFTFS 836  
Qy 835 DSSPIEIIIDPPTFVSAKDDSPKLAKETDLEVSDKSEIANIQSGADSLPCLCPLDSF 894  
Db 837 DSSPIEIIIDPPTFVSAKDDSP---KEYTDLVSNKSEIANVQSGANSLPCLCPLDSF 893  
Qy 895 KNIYPKDEVHVSDESENRSSVSKASISPSNVSALEPQTEMGSIKSLTKAEKCLPS 954  
Db 894 KNTYPKDSAHVSDSEKRSRSVSKVPLLLPNVSALESQIENGNTVKPKVLTKAEKCLPS 953  
Qy 955 DTEKEDRLSVALESLKTSVDLLIYWRDIKKTGW- FGASLFLILLSLTVFSIVSVTAY 1013  
Db 954 DTEKEDRLTAVLSAELNKTSDVLLIYWRDIKKTGVYFGASLFLILLSLTVFSIVSVTAY 1013  
Qy 1014 IALALLSVTISFRIYKGVIAQKSDSEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNST 1073  
Db 1014 IALALLSVTISFRIYKGVIAQKSDSEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNST 1073  
Qy 1074 IKELRRLFLVDDLVDLSLFAVLMVFTTVGALFNGLTLLIILALSLSIPVIYERHQVQI 1133  
Db 1074 IKELRRLFLVDDLVDLSLFAVLMVFTTVGALFNGLTLLIILALSLSIPVIYERHQVQI 1133

Qy 1134 DHYGLANKSVKDAWAKIQAKIPGLKERKAD 1163  
Db 1134 DHYGLANKSVKDAWAKIQAKIPGLKERKAE 1163  
RESULT 6  
US-09-758-140-6  
; Sequence 6, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.  
; TITLE OF INVENTION: No. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-140-6  
Query Match 75.3%; Score 4403.5; DB 9; Length 1192;  
Best Local Similarity 75.9%; Pred. No. 4.8e-191;  
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;  
Qy 1 MEDIDQSSLSVSSSDSPRPAPKQYQVTEPEDEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60  
Db 1 MEDIDQSPLVSS--DSPRPQAPKQYQVREPEDEE-EEEEEEDEDEDELEVLERK 58  
Qy 61 PAAGLSAAVPP--PAAAPLLDFSSDSVPPAPRGPLPAAAPPAEROPSWERSPAA---P 115  
Db 59 PAAGLSAAVPTAPAAAGAPLMDFGNDVFPAPRGPLPAAAPVAPERQSPVSVSTVP 118  
Qy 116 APSLPPAAAVLPKGLPDDPPAPPPPPAGASPLAE-----PAAPPSTPAAPKR 166  
Db 119 APSLPSAAVSPSKLPDDPPAPPPPPPPASVSPQAEVMTPPAPAPAPSTPAAPKR 178  
Qy 167 RG-SGSDVETILPALPAASEPVI PSSAEKINDLMEQNCNTVSSGOEDPESVLETAASLPS 225  
Db 179 RGSAGSVDETILPALPAASEPVI RSSAEN-MDLKEQPGNTISAGQEDPESVLETAASLPS 237  
Qy 226 LSPLSVTSFKBHGVLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSLEY 285  
Db 238 LSPLSAASFKBHEYVGNLSVLPTEGTLQENVSEASKEVSEKAKTLLIDRLDTFSELEY 297  
Qy 286 SEMGSSFKGPKGESAILVENTKEEVIVRSKOKED-LVCSAALHSPOESPVG-----KED 339  
Db 298 SEMGSSFSVPKAEASVIVANPREEIIIVKNKDEBEKLVSNLHNNQOELPTALTCLKVKED 357  
Qy 340 RVVSPKTMDFINEMQNSVAVPVEEYADPKPFQOAEVKDITYGSRDVLAA-----RANV 395  
Db 358 EYVSSEKAKDSFKRVAPEAPMREYADPKPFVWVVEVKDSKEDS-DMLAAGKIKESNL 416  
Qy 396 ESKVDKCLEDSLQKSLGKDSGRNEDASFPSTPEPVKDSRAYITCASFT-SATESST 454  
Db 417 ESKVDKLCFADSLSEQTHKDSSSNDTSPSTPEGIKORSAGYITCAPENPATSEIA 476  
Qy 455 ANTFPPLLEDHTSENKTDEKKIEERKAAQIITEK-TSPKTSNPFLVAVODSEADYVTTDTLS 513  
Db 477 TNIFPPLGDPSTSENKTDEKKIEEKAAQIVTEKNTSTKTSNPFLVAAQDSEDTYVTTDNL 536  
Qy 514 KVTEAAVSNMPEGLTDPDLVQEAASELNEATGKIAYETKVDLVQTSSEATQESLYPTAQOL 573  
Db 537 KVTEEVVANMPEGLTDPDLVQEAASELNEVTGTKIAYETKMDLVQTSSEVQESLYPAAQOL 596

QY 574 CPSFEAEATPSVLPDIWMEAPLNSLLPSAGASVVPQSVSPLEAPPVSYDSIKLEPEN 633  
 DB 597 CPSFESEATPSVLPDIWMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKEHEN 655  
 QY 634 PPPEEAMNVALKAL-GTKEGIKEPESFNAAQVETAPYISACDLIKETKLSSTPSDF 692  
 DB 656 PPPEEAMSVLKVGIGIKKEPENINAALQETAPYISACDLIKETKLSAPAPDF 715  
 QY 693 SNYSEIAFEKSVPEHAELVEDSSPESEPVDFSDSIPEVPQTOEEAVMLKESLTVS 752  
 DB 716 SDYSEMAKVQVPDHSSELVEDSSPESEPVDFSDSIPEVPQKQDETVMVKESLTETS 775  
 QY 753 -ETVAQHK-EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLOMBEF 809  
 DB 776 FESMIEYENKEKLSALPPGEGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMBEL 835  
 QY 810 NTAIYNSNDLLSKEDKIKESSTFSDSPIEIIDFPTFVSAKDD-PSKLAKETDLEVS 868  
 DB 836 STAVYNSNDLFTSKAQIRETETTFSDSPIEIIDFPTLISSTKTSFSLAREYDLEVS 895  
 QY 869 DKSEIANIQSADSLPCLPELPCDLGPKNTYK--DEVHVSDFSENRSVSKASISPSNV 926  
 DB 896 HKSEIANAPDGAGSLPCTELPHDLNLKNTQPKVEEKISFSDDFSKNGSATSKVLLLPDV 955  
 QY 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSTTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986  
 DB 956 SALATQAEIESIVKPKVLKAEKKLPSTTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015  
 QY 987 KTVGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRA 1046  
 DB 1016 KTVGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRA 1075  
 QY 1047 YLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDLSLKFVAVLMMVFTYVGALF 1106  
 DB 1076 YLESEVAISEELVQKYSNLSALGHVNCTIKELRRLFLVDDLVDLSLKFVAVLMMVFTYVGALF 1135  
 QY 1107 NGTLTLLIALISLFSPTVIYERHQQIDHYLGANKSVKDAKIQAKTIGLKRKAD 1163  
 DB 1136 NGTLTLLIALISLFSVPVIYERHQAQIDHYLGANKVNDAMAKIQAKTIGLKRKAE 1192  
 RESULT 7  
 US-09-972-599A-6  
 ; Sequence 6, Application US/09972599A  
 ; Patent No. US20020077295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STRITTMATTER, STEPHEN M.  
 ; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
 ; FILE REFERENCE: C077 CIP US  
 ; CURRENT APPLICATION NUMBER: US/09/972,599A  
 ; CURRENT FILING DATE: 2001-10-06  
 ; PRIOR APPLICATION NUMBER: PCT/US01/01041  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 09/758,140  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 60/236,378  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: 60/207,366  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/175,707  
 ; PRIOR FILING DATE: 2000-01-12  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-972-599A-6

Query Match 75.3%; Score 4403.5; DB 9; Length 1192;  
 Best Local Similarity 75.9%; Pred. No. 4.8e-191;  
 Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

QY 1 MEDIDQSSIVSSSTDSPPRPPAPFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60  
 DB 1 MEDLDQSLVSS--DPPRPQPAFKYQVREPEDEE-EEEEEEDEDEDEDELEVLERK 58  
 QY 61 PAAGLSAAAVP--PAAAAPLIDFSSDVPAPRGPPLPAAPPAAPRQSWERSPAA---P 115  
 DB 59 PAAGLSAAAVPPTAPPAAGAPLMDFGNDVFPAPRGPPLPAAPPVAPRQSWDSFSSVSTVP 118  
 QY 116 APSLPAAAVLPSKLPEDDEPPARPPPPAGASPLAE-----PAAPESTPAAPKR 166  
 DB 119 APSPLSAAAVSFKLPEDDEPPARPPPPASVPOAEPVMTTPPAPAPAAPSTPAAPKR 178  
 QY 167 RG-SSVDETLFPALPAASEPVISSAEKIMDLMEQPGNTVSSGQDDFSSVLLETAASUPS 225  
 DB 179 RGSSGVDETLPALPAASEPVISSAEN-MDLKEQPGNTISAGQDDFSSVLLETAASUPS 237  
 QY 236 LSPSLTVFKEHGYLGNLSAVSSSGTTEETLNEASKELPERATNPFVNRDLAEFSELEY 285  
 DB 238 LSPLSAASFKEHYLGNLSTVLPTEGTLOENVSEASKSEKAKTLLIDRDLTEFSELEY 297  
 QY 286 SEMGSPFKGSPKESAILVENTKEEVIYRSKDKED-LVCSAALHSPQSPVPG-----KED 339  
 DB 298 SEMGSPFSPKASAVIVANPREIIVKNKDEEKLVSNNILHNQBELPTALTALTKLVKED 357  
 QY 340 RVVSPKTMDFENEMQSVVAPVREYADFKPFEQAWKVKOTYEGSRDVLAA---RANV 395  
 DB 358 EYVSEKAKDSFKNEKRVAVEAPMREYADFKPFERVWEVKOSKEDS-DMLAAGGKIESNL 416  
 QY 396 ESKVDRKCLEDSLEQKSLGKDSSEGNEDASFPSTPEPVKDSRAYITCASFT--SATESIT 454  
 DB 417 ESKVKKCFADSLQETNHEKSESNDSTSPSTPEGIKDRSGAVITCAPFNPATESIA 476  
 QY 455 ANTPLLLEDHTSENKTDKKEERKAKIITEK-TSPKTSNPFLVAVQSEADYVTTDTLS 513  
 DB 477 TNIPLLGDPSTSENKTDKKEEKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNL 536  
 QY 514 KUTEAAVSNMPEGLTPDLVQACESEFNEATCTKIAYETKVDLVOTSAIOESLPTAQL 573  
 DB 537 KUTEVAVNMPEGLTPDLVQACESELNEVTGTKIAYETKMDLVOTSEVMQESLPPAAQL 596  
 QY 574 CPSFEAEATPSVLPDIWMEAPLNSLLPSAGASVVPQSVSPLEAPPVSYDSIKLEPEN 633  
 DB 597 CPSFESEATPSVLPDIWMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKEHEN 655  
 QY 634 PPPEEAMNVALKAL-GTKEGIKEPESFNAAQVETAPYISACDLIKETKLSSTPSDF 692  
 DB 656 PPPEEAMSVLKVGIGIKKEPENINAALQETAPYISACDLIKETKLSAPAPDF 715  
 QY 693 SNYSEIAFEKSVPEHAELVEDSSPESEPVDFSDSIPEVPQTOEEAVMLKESLTVS 752  
 DB 716 SDYSEMAKVQVPDHSSELVEDSSPESEPVDFSDSIPEVPQKQDETVMVKESLTETS 775  
 QY 753 -ETVAQHK-EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLOMBEF 809  
 DB 776 FESMIEYENKEKLSALPPGEGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMBEL 835  
 QY 810 NTAIYNSNDLLSKEDKIKESSTFSDSPIEIIDFPTFVSAKDD-PSKLAKETDLEVS 868  
 DB 836 STAVYNSNDLFTSKAQIRETETTFSDSPIEIIDFPTLISSTKTSFSLAREYDLEVS 895  
 QY 869 DKSEIANIQSADSLPCLPELPCDLGPKNTYK--DEVHVSDFSENRSVSKASISPSNV 926  
 DB 896 HKSEIANAPDGAGSLPCTELPHDLNLKNTQPKVEEKISFSDDFSKNGSATSKVLLLPDV 955  
 QY 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSTTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986  
 DB 956 SALATQAEIESIVKPKVLKAEKKLPSTTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015  
 QY 987 KTVGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRA 1046  
 DB 1016 KTVGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRA 1075  
 QY 1047 YLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDLSLKFVAVLMMVFTYVGALF 1106



Db 1076 YLESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDDLSLKFAVLMMVFTVVGALF 1135  
Qy 1107 NGLTLILALISLPSIPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAKAD 1163  
Db 1136 NGLTLILALISLPSIPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAE 1192

RESULT 8  
US-10-060-036-71  
; Sequence 71, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Daxin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yugu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060.036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-060-036-71

Query Match 75.3%; Score 4403.5; DB 14; Length 1192;  
Best Local Similarity 75.9%; Pred. No. 4.8e-191; Indels 39; Gaps 20;  
Matches 909; Conservative 104; Mismatches 145;

Qy 1 MEDIDQSLVSSSTDSPPRPAPKQYQVTPEDDEDEDEDEDEDEDEDEDEDEDELEVLK 60  
Db 1 MEDIDQSLVSS--DSPPRPAPKQYQVTPEDDE--EEEEEEEEDEDEDELEVLK 58

Qy 61 PAAGLSAAV--PAAGPLDFFSDSVPPAPRGLPAAPPAAPRQSWERSPAA---P 115  
Db 59 PAAGLSAAVPTAAGALMDFGNDFFVPPAPRGLPAAPPAAPRQSWDPSPVSTVP 118

Qy 116 APSLPPAAVLPSKLPEDDEPPARPPPPAGASLAE-----PAAPSPPAAPKR 166  
Db 119 APSLPPAAVPSKLPEDDEPPARPPPPASVSPQAEPPVTPPAPAPAPSPPAAPKR 178

Qy 167 RG-SGSDVDTLFAAPASEPVPISAEKIMDLMEQPGNTVSSGOEDFPVSLLETAASLPS 225  
Db 179 RGSQSDVDTLFAAPASEPVPISAEKIMDLMEQPGNTVSSGOEDFPVSLLETAASLPS 237

Qy 226 LSPLSTVSKHGYNIGNSAVSSSEGTTEETINRASKELPERANPFWNRDLAESELEY 285  
Db 238 LSPLSAASFKEHYGLNLSVLTPTGTLQENVSEASKEVSEKAKTLIDRLDTBFSELEY 297

Qy 286 SEMGSSFKGSPKESAILVENTKEVIVRSKED-LVCSAALHSPQESVPG-----KED 339  
Db 298 SEMGSSFSVSPKASAVIANPREIIVKNDEBEKLVNNILNQBELTALTKLVKED 357

Qy 340 RVWSPKTMDFNEMQMSVAVPVEEYADFPFQAEVMDKTYEGSRDLAA-----RANV 395  
Db 358 EVVSEKAKDSFNEKRVAVAPMEYADFPFQAEVMDKTYEGSRDLAA-----RANV 416

Qy 396 ESKVDRKCLDSLEQKSLGKDSSEGNEDASFPSTPEPVKDSRAYITCASFT--SATESTT 454  
Db 417 ESKVDKCFADSLQETNKEKDSSEGNEDASFPSTPEPVKDSRAYITCASFT--SATESTT 476

Qy 455 ANTPFLLEDHTSENKTKDEKKEKAAQIITEK--TSPTKSNPFLAVDSEADYVTTLS 513  
Db 477 TNIPFLLEDHTSENKTKDEKKEKAAQIITEK--TSPTKSNPFLAVDSEADYVTTLS 536

Qy 514 KVTEAAVSNMPEGLTPDLVQACESELNEATGTIAVETKVDLVQTSIAQIESLYPTAQL 573

Db 537 KYTEEVANMEGLTPDLVQACESELNEATGTIAVETKVDLVQTSIAQIESLYPTAQL 596  
Qy 574 CPSPFEAEATSPVLPDIIVMEAPLNSLLPSAGASVQSPVSPLEAPPVSDSKLEPEN 633  
Db 597 CPSPFEAEATSPVLPDIIVMEAPLNSLLPSAGASVQSPVSPLEAPPVSDSKLEPEN 655  
Qy 634 PPYPVEAMNVALKAL-GTKEGKEPESFNAAVQTEAPYISIACDLIKETKLSSTEPSPDF 692  
Db 656 PPYPVEAMNVALKAL-GTKEGKEPESFNAAVQTEAPYISIACDLIKETKLSSTEPSPDF 715  
Qy 693 SNYSEIAKFEKSPVEHAELVEDSSPSEPDVLFSDDSIPEVPQTEBEAVMLKESLTVS 752  
Db 716 SDYSEMAKVEQVPDHSSELVEDSSPSEPDVLFSDDSIPEVPQTEBEAVMLKESLTVS 775  
Qy 753 -ETVAQHK-BERLSASQELGKPYLESFQPNLHSTKOA-ASNDIPTLTKKKISLQWREF 809  
Db 776 FESMIEYENKELKALPPEGKPYLESFQPNLHSTKOA-ASNDIPTLTKKKISLQWREF 835  
Qy 810 NTAIYSNDLLSSKEDKIKESFSDSSPTEIIDFPTFVSADDS-PKLAKEYTDLRVS 868  
Db 836 STAVISNDLLFISKEAQIRETETFSFSDSPTEIIDFPTLSSKTSFSLARETDLRVS 895  
Qy 869 DKSEIANIQSGADSLPCLLEPCLSLFKNIYK--DEVHVSDEFSENSSVSASISPSNV 926  
Db 896 HKSEIANAPDAGSLPCTELPHDLSLKNIQPKVEKISFSDDFSKNGSATSKVLLLPDV 955  
Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986  
Db 956 SALATQAEIESIVKPKVLKVEAEKKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 1015  
Qy 987 KTGWFVGSALFLLLSLTVFSISVTVAYIALALLSVTISFRIYKGVIOAIQKSDGHPRA 1046  
Db 1016 KTGWFVGSALFLLLSLTVFSISVTVAYIALALLSVTISFRIYKGVIOAIQKSDGHPRA 1075  
Qy 1047 YLESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDDLSLKFAVLMMVFTVVGALF 1106  
Db 1076 YLESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDDLSLKFAVLMMVFTVVGALF 1135  
Qy 1107 NGLTLILALISLPSIPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAKAD 1163  
Db 1136 NGLTLILALISLPSIPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAE 1192

RESULT 9  
US-09-789-386-2  
; Sequence 2, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2

Query Match 75.2%; Score 4398.5; DB 9; Length 1192;  
Best Local Similarity 75.9%; Pred. No. 8.1e-191;  
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;







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Db 1076 YLESEVAISEELVQKYSNALGHVNCITIKELRRLFLVDDLSLKPAVLMMWFTYVGALF 1135
QY 1107 NGTLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI PGLKRKAD 1163
Db 1136 NGTLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI PGLKRKAE 1192

RESULT 12
US-10-327-213-9
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9

Query Match 75.2%; Score 4398.5; DB 16; Length 1192;
Best Local Similarity 75.9%; Pred. No. 8.1e-191;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

QY 1 MEDIDQSSLVSSSTDGPPPPAFKQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEVELEK 60
Db 1 MEDDQSLPVSSS-DSPRPQPAFKQFVREPEDEB-EDEEEDDEDEDEDELEVELEK 58
QY 61 PAAGLSAAAVP--PAAALDLDSSDSVPPAPRGPLPAAPPAAPAPQPSWERSPAA---P 115
Db 59 PAAGLSAAVPPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPAPQPSWDSVSTVP 118
QY 116 APSLPPAAAVLPSKLPEDDEPPAPPPPPAGASPLAE-----PAAPSTPAAPKX 166
Db 119 APSPLAAAVSPSKLPEDDEPPAPPPPPPPASVPOAEVPTWTPAPAPAPSTPAAPKX 178
QY 167 RG-SGSDVDTLFPALPAASEVPIVSSAEKIMDLMEQPGNTVSSQGEDFPVSLLETAASLPS 225
Db 179 RGSSGSDVDTLFPALPAASEVPIVSSAEN-MDLKEQPGNTISAGQEDFPVSLLETAASLPS 237
QY 226 LSPSLTVSKHGHLGNLGNLAVSSSEGTIBETLNEASKELPERATNPFVNRDLAFSELEY 285
Db 238 LSPLSAASFKEHYLGNLSTVLPTGTLQENVSEASKEYSEKAKTLLIDRLTFESELEY 297
QY 286 SEMGSSFKGSPKGESAILVENTKEEIVRSKQED-LVCSAALHSPQESVPG-----KED 339
Db 298 SEMGSSFSVSPKAEAVIANPREETIVKNQDEEKLVSNNILHNOQELPTALTUKVKED 357
QY 340 RVVSPKTMIDIFNEMQSVVAVPVEEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV 395
Db 358 EVVSESEKAKDSFNEKRVAVEAPMREYADFKPFEVWEVKDSKEDS-DMLAAGGKIESNL 416
QY 396 ESKVDKRLCDSLEQSLKQSDSGRNEADAFSTPEPVKDSSPAYITCASFT-SATESST 454
Db 417 ESKVDKRCFADSLQTNHEKQSSNDSTSPSTPEGIKDRPGAYITCAPFNPAAATESIA 476
QY 455 ANTFPLEDHTSNKTKDEKKIEBKQAIIIEK-TSPKTSNPFVLAVQDGEADVVTITDLS 513
Db 477 TNIFPLGDTSNKTKDEKKIEBKQAIIIEKQAIVTEKNTSTKSNPFVLAVQDSETDVTITDNL 536
QY 514 KVTEAAVSNMPEGLTDPDLVQACESELNATGKIAYETKVDLVQVTSIAQESLYTAQL 573
Db 537 KVTEEVVANNPEGLTDPDLVQACESELNVTGKIAYETKMDLVQVTSVQESLYPAAQL 596
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QY 574 CPSFEAEATSPVLPDVIWMEAPLNSLLPSAGASVQPSVSPLEAPPVPPVSDYSIKLEPEN 633
Db 597 CPSFESEATSPVLPDVIWMEAPLNSAVFSAGASVIQFSSSSPLEA-SSVNESIKHEPEN 655
QY 634 PPPEEAMNVALKAL-GTKEGKEPESFNAAVQETEAPYISIACDLIKETKLSSTPSPDF 692
Db 656 PPPEEAMSVSLKKVSGIKKEIKEPENINAAALQETEAPYISIACDLIKETKLSASPADF 715
QY 693 SNYSIAKPEKSVPEHAELVEDSSPESBPVDLFDSDSIPEDVQTOBEAVMLKESLITEVS 752
Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSPVDLFDSDSIPDPVQKQDETVMVKESLITETS 775
QY 753 -ETVAQHK-EELSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMBEF 809
Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKOTLLPDEVSTLSEKKEKIPQMEEL 835
QY 810 NTAYISNDDLLSSKEDKIKESFTFSDSPIETIIDEFTFVSAKODS-PKLAKEYTDLLEVS 868
Db 836 STAVYSNDDLFISKQAQIRETETFTSDSPIETIIDEFTLISSTDSFKLAKEYTDLLEVS 895
QY 869 DKSEIANIQSGADSLPCLELPCDLSFKNIYPK-DEVHVSDFSENRSVSKASISPSNV 926
Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDV 955
QY 927 SALEPQTMGSIVKSKSLTKEAEKLPSTDEKEDSLSAVLSAELSKTSVVDLLYWRDIK 986
Db 956 SALATQAEIESIVKPKVLKEAEKLPSTDEKEDSPSAIFSAELSKTSVVDLLYWRDIK 1015
QY 987 KTGVSFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRA 1046
Db 1016 KTGVSFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRA 1075
QY 1047 YLESEVAISEELVQKYSNALGHVNCITIKELRRLFLVDDLSLKPAVLMMWFTYVGALF 1106
Db 1076 YLESEVAISEELVQKYSNALGHVNCITIKELRRLFLVDDLSLKPAVLMMWFTYVGALF 1135
QY 1107 NGTLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI PGLKRKAD 1163
Db 1136 NGTLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI PGLKRKAE 1192

RESULT 13
US-10-466-258-9
; Sequence 9, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-258-9

Query Match 75.2%; Score 4398.5; DB 16; Length 1192;
Best Local Similarity 75.9%; Pred. No. 8.1e-191;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

QY 1 MEDIDQSSLVSSSTDGPPPPAFKQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEVELEK 60
Db 1 MEDDQSLPVSSS-DSPRPQPAFKQFVREPEDEB-EDEEEDDEDEDEDELEVELEK 58
QY 61 PAAGLSAAAVP--PAAALDLDSSDSVPPAPRGPLPAAPPAAPAPQPSWERSPAA---P 115
Db 59 PAAGLSAAVPPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPAPQPSWDSVSTVP 118
QY 116 APSLPPAAAVLPSKLPEDDEPPAPPPPPAGASPLAE-----PAAPSTPAAPKX 166
Db 119 APSPLAAAVSPSKLPEDDEPPAPPPPPPPASVPOAEVPTWTPAPAPAPSTPAAPKX 178
QY 167 RG-SGSDVDTLFPALPAASEVPIVSSAEKIMDLMEQPGNTVSSQGEDFPVSLLETAASLPS 225
Db 179 RGSSGSDVDTLFPALPAASEVPIVSSAEN-MDLKEQPGNTISAGQEDFPVSLLETAASLPS 237
QY 226 LSPSLTVSKHGHLGNLGNLAVSSSEGTIBETLNEASKELPERATNPFVNRDLAFSELEY 285
Db 238 LSPLSAASFKEHYLGNLSTVLPTGTLQENVSEASKEYSEKAKTLLIDRLTFESELEY 297
QY 286 SEMGSSFKGSPKGESAILVENTKEEIVRSKQED-LVCSAALHSPQESVPG-----KED 339
Db 298 SEMGSSFSVSPKAEAVIANPREETIVKNQDEEKLVSNNILHNOQELPTALTUKVKED 357
QY 340 RVVSPKTMIDIFNEMQSVVAVPVEEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV 395
Db 358 EVVSESEKAKDSFNEKRVAVEAPMREYADFKPFEVWEVKDSKEDS-DMLAAGGKIESNL 416
QY 396 ESKVDKRLCDSLEQSLKQSDSGRNEADAFSTPEPVKDSSPAYITCASFT-SATESST 454
Db 417 ESKVDKRCFADSLQTNHEKQSSNDSTSPSTPEGIKDRPGAYITCAPFNPAAATESIA 476
QY 455 ANTFPLEDHTSNKTKDEKKIEBKQAIIIEK-TSPKTSNPFVLAVQDGEADVVTITDLS 513
Db 477 TNIFPLGDTSNKTKDEKKIEBKQAIIIEKQAIVTEKNTSTKSNPFVLAVQDSETDVTITDNL 536
QY 514 KVTEAAVSNMPEGLTDPDLVQACESELNATGKIAYETKVDLVQVTSIAQESLYTAQL 573
Db 537 KVTEEVVANNPEGLTDPDLVQACESELNVTGKIAYETKMDLVQVTSVQESLYPAAQL 596
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Job time : 156.865 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 34.9713 seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-2  
Perfect score: 5848  
Sequence: 1 MEDIDQSSVSSSTDSPPR.....VKDAMAKIQAKIPGLKRRAD 1163

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	789.5	13.5	776	2 A46583	neuroendocrine-spe
2	685	11.7	208	2 A60904	neuroendocrine-spe
3	671	11.5	267	2 A60021	tropomyosin-relate
4	517	8.8	2484	2 T26216	hypothetical prote
5	503.5	8.6	2607	2 T26215	hypothetical prote
6	328.5	5.6	5327	2 T13564	microtubule-associ
7	322	5.5	7962	2 I38346	elastic titin - hu
8	320	5.5	222	2 T26213	hypothetical prote
9	304.5	5.2	873	2 A47283	calphotin - fruit
10	302.5	5.2	1829	2 T24583	hypothetical prote
11	295.5	5.1	865	2 A47282	calcium-binding pr
12	292	5.0	3507	2 T34513	hypothetical prote
13	291.5	5.0	2364	2 A56577	microtubule-associ
14	288.5	4.9	971	2 T19431	hypothetical prote
15	284	4.9	2464	1 QRMSP1	microtubule-associ
16	281	4.8	3488	2 T34418	hypothetical prote
17	279.5	4.8	1262	2 T22523	hypothetical prote
18	277	4.7	1621	2 A82255	hypothetical prote
19	275.5	4.7	3924	2 S37431	ankyrin 2, neurona
20	275	4.7	1299	2 T47182	hypothetical prote
21	273.5	4.7	1029	2 T30351	mucin-like protein
22	273.5	4.7	1274	2 T16251	hypothetical prote
23	273	4.7	1558	2 B71603	RESA-H3 antigen pF
24	272.5	4.7	3534	2 T42567	tegument protein 2
25	270	4.6	1230	2 T22458	hypothetical prote
26	269.5	4.6	2187	2 T30826	nascent polypeptid
27	267	4.6	1684	2 JW0057	gravin - human
28	265.5	4.5	1828	2 A40115	microtubule-associ
29	263	4.5	1825	2 S13507	microtubule-associ

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human  
N:Contains: neuroendocrine-specific protein, splice form B  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; J. Biol. Chem. 268, 13439-13447, 1993  
A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe  
A:Reference number: A46583; MUID:93293865; PMID:7685762  
A:Accession: A46583  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-776 <ROE1>  
A:Cross-references: UNIPROT:Q16799; GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A:Accession: I60903  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 421-776 <ROE2>  
A:Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C:Genetics:  
A:Gene: GDB:RTN1; NSP  
A:Cross-references: GDB:203968; OMIM:600865  
A:Map position: 14q21-14q22

Query Match 13.5%; Score 789.5; DB 2; Length 776;  
Best Local Similarity 31.2%; Pred. No. 8.5e-25;  
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;  
Qy 487 TSPKTSNPFVLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGITPDVQVQACESELNATGT 546  
Db 65 SGPARQSP--VAMETASTAGVSSAMDHFTSTTKDGE-----SCYSLI-----S 110

Qy 547 KIAYETKVADVQVSEAIQ-ESLYPTAQLCPSEFAEATPSPVLPDI--VMEAPLNS----- 599  
Db 111 DICYPPOEDSTYFGILQKENGHVITISEP---BELGTPGSLPDVPGIESRGLFSSDSG 167

Qy 600 --LLPSAGASVQVSPSFLAPPVSY-----DSIKLEPENPPPYEEA-----M 641  
Db 168 IEMTPAESSTEVNKTLADPLDQMAEAYKYIDITRPEEVKQHQHPELEDKDLDFKNKDT 227

Qy 642 NVALKALGTGEGIKEPE-----SFNAAVQETAPYISACDLIKETKLSTE--PSP 690  
Db 228 DISIK-----PEGVREPKPAPVEGKIIKHLLESTFAPYID---DLSEORRAPQITTP 280

Qy 691 DFSNYSIAKFEKSVPSHAELVEDSSPESPDVLF-SDDDSIPEV----PQVEEAVMLMK 745  
Db 281 VKITLTIE-----PSVETTTQETPEKQDICLKPSPDIVPTVTVSEPEDDSFGSITPP 334  
Qy 746 ESLTEVSETVAQHK-----EERLSASQELGKPYLESFQP-----NLHSTKDAAND----- 792

neurofilament trip  
neurofilament trip  
fimbriae-associate  
nestin - golden ha  
neurofilament trip  
hypothetical prote  
microtubule-associ  
microtubule-associ  
hypothetical prote  
protein UNC-89 - C  
cytadherence-acces  
versican precursor  
367K tegument prot  
hypothetical prote  
microtubule-associ  
ankyrin 3, long sp





Db	1615	QVQRIPIEVEQATPIQPPRPKSE----	LPKAKPDDDSKSRVRFAPLNIKIGRTY	1670
Qy	206	SSQOEPPSVLLTAASPLSLSTVSFKHEGYLGNLSAVSSSEGTIETINEASKELP	265	
Db	1671	SEEQOK-----ELVESLE--RPLTIIT--	-----QOKPP	1695
Qy	266	ERAT-----NPFVNRDLAFSELEYSEMSSFKGSPKGSAILVENTKEVIVRSKQKE	319	
Db	1696	EKPTEDIGALSPLSPNTLAEYEEVPMQDOS	-----	1726
Qy	320	DLVCSAALHSPQSPVKCEDRVVSPKTMIDIFNEMQ--MSVAVPVREYADFKPEQAVEV	378	
Db	1727	-----VPHSPQE-----KQBEI--EALSEIIEEPQAMKEVE-----KVESAPE--	1763	
Qy	379	KDTYEGSRDVLAAARANVESKVRKCLDEDSL--EOKSLGKDSGRNEDASPPSPPEVKOS	436	
Db	1764	KD-----NESLEAPEIINEPIRVLVETKMGCKSLNED-----NDD-----	1801	
Qy	437	SRAYITCASFTSATESGTANTFPLEDHTSENKTEKKIIEERKAQIITEKTSPTKSNPFL	496	
Db	1802	-----DDGSECLDSIGDLSE--	-----TIQRFN	1824
Qy	497	VAVQDSEADVYTTLSKVT-----EAAVSNMPEGLTPDLVQACSEIENEGTKI	548	
Db	1825	TSDDPS-----IRDSFSSISSFGDRKFRTAIENIRQDLLP-----	1862	
Qy	549	AVETKYDLVQTSIAQESLYPTAQLCPSPEEAZATSPVLDPDVMBAPLNSLLPSAGASV	608	
Db	1863	-FOSSV-----SQYLRSFNPSQOL-----LVTNLSMDSP--SDLSPNA-----	1898	
Qy	609	VQPSVSPLEAPPVSYDSI-----KLEPENPPPYEAMNVALKALGTKEGKEPESFNAA	663	
Db	1899	-----PPVGPPENTAQFLKQLQEDRPSAEGSID-----SSGFKVD--HEG	1937	
Qy	664	VQTEAPYISACDLKTKETKLTSTEPDPF-----SNYSIAKFEKSVP	707	
Db	1938	LDEFAAPPVH--DPMQKSVFGSLGSDMKPGSQDDGFVPIERNEANEATLKNQKMSH	1994	
Qy	708	HAEVLVDS-----SPESEBVDLFDSDSIPEVPQTQEA--MLMKSLTE	750	
Db	1995	HNDVIEKNYNDNAPTAALLESPIAEARKLVQAVESASEYKQAVDSGDEIGRELLDN	2054	
Qy	751	VSETVAQHKE-----ERLSASPOELGKPYLESFQP	780	
Db	2055	VEQKIEQVKPEIVDSLHKAYDGVGFVHETVPNAVDDFVREAEKQLPESVPVEKIEPTEP	2114	
Qy	781	--NLHSTKDAAANDIPTLTKEKISIQMESFNATAYSNDDLLSKEDK-----IKES	830	
Db	2115	LVDIHDITVKVHDEVONFLAREP-----TPPFETDDVAPLSDDKPQFGNQTPPEDE	2165	
Qy	831	ETPESDSSPIEIDEPFFVFSKDDSPKLAKKEYTDLEVSCKSEIANTIQSGA---DSLPL	886	
Db	2166	TFPDRKGPLTIPBEVEKAAAQOND--LDDFPLVTSNTGAAGFAVGAAGAAVESLTEE	2222	
Qy	887	ELPCDLSEFKNI-----YPKDEHVSDSEFSENRSVSKASISPNVSGA-----LEPQTEM	935	
Db	2223	EMEGHQKFEIVPPPPPKD--LSDE-----DVKPVTNLGPSSHHSHSSPH	2268	
Qy	936	GSIVKSKSLTKEAEKPLPSDTEKEDRSLSAVLSAELSKTSSVDLLYWRDIKKTGVVFGAS	995	
Db	2269	HSILKHG-----DAWIDFKTVPCCVLDVIYWRDAKSAIVLSLA	2308	
Qy	996	LFLLLSLTVFSVTVAYIALLSVTISFRIYKGVIOAQKSGDEGPPFRAYLESEVAIS	1055	
Db	2309	LLVLFLVAKPLTLTVVTVSYLLALGAAGAFRVFKYEAQIKKTDSHFSEIILAQTLP	2368	
Qy	1056	EELVOKYSNAGLHVNSTIKELRRLPLVDDVLSLFAVLMMVFTYVGAFLNGLTLLILA	1115	
Db	2369	QEKVHAQADVFEHATCIANKLKLIVFVESPLSIFGLVNSLTYIASWFSFTAILG	2428	
Qy	1116	LISLFSIPVIYERHQVIDHYLGLANKSVKDAWAKIQAKTIGLK	1159	

Db 2429 LLGVFVPKVYESNQEAIDPHLATISGHLKXNVQNIIDEKLPFLR 2472

RESULT 5

T26215

hypothetical protein W06A7.3a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T26215

R/Ainscough, R.

submitted to the EMBL Data Library, August 1996

A/Reference number: Z20173

A/Accession: T26215

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2607 <W1>

A/Cross-references: UNIPROT.Q23187; EMBL.Z78066; PIDN:CAB01522.2; GSPDB:GN00023;

A/Experimental source: clone W06A7

C/Genetics:

A/Gene: CESP:W06A7.3a

A/Map position: 5

A/Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match 8.6%; Score 503.5; DB 2; Length 2607;

Best Local Similarity 20.8%; Pred. No. 1.7e-12;

Matches 280; Conservative 181; Mismatches 481; Indels 407; Gaps 52;

QY 28 FVTEPDEE---DEEEDEEED-----DEDLEELEVL----- 57

Db 1437 FGTESEESQKADGNQENQEEEDVVAELPHPIQWRDEDVISQSLKSLVAEVCITDV 1496

QY 58 -----ERKPAAGLSAAVPAAPAAPI-LPSSDSVPPAPRGPLPAAPAAP--ERQPSW 108

Db 1497 DASVNEQDEESTLKILKVVFPSEPSLLEDTND--PKVIHVPILPMEPATWYLEMVEW 1554

QY 109 -----ERSPAAPAPSLPPAAAVLPS-----KLP-EDDEPPARPPPPPA 146

Db 1555 IIAVAVKEVSEMEVVTSEISEMAPQVSESTCPPEPLADLKLPEVDEKTPPEPFPVVP 1614

QY 147 GASPLAEPAPPTPAAPKRGSGSVDTLFPALPAASEPVIPS--SAEKIMDLMEQGNTV 205

Db 1615 QVQERIIPVEVQAPTIQPPRPAPKSE---LPKVAKPLDDSKSRVRFAPINIKLGRY 1670

QY 206 SSGQEDPPSVLLETAASLPSLSTVTSFKEHGYLGNLSAVSSSEGTIETLINEASKLP 265

Db 1671 SEEQK-----ELVESLE-RPLTIIT-----QQKPP 1695

QY 266 ERAT-----NPFVNRDLAFSELEYSEMSSFKGSPKGSAILVENTKEEVIVRSKDE 319

Db 1696 EKPTEDIGALSPLSPNTLAEEYEPMDM-QSVFHP-----QEQEIEALSEIIE 1746

QY 320 DLVCSAALHSPQES-PVGKEDRVVSPKTMDFNEMQMSVVPVREEVADFK---PFEQA 375

Db 1747 EQAMKEVAPVESAPKONESLAPE-----IINE-----PIRVLVETKIMGFGKSL 1795

QY 376 WEVKDTYEGSRDVLAAANVESKVDKRCLEDSLQKSLGKDS-----E 418

Db 1796 NEDNDDDDGSECLDSIGLSERTIQ-RFNTSIDDPISRRDSFSSISFGDRQKPRTAIE 1854

QY 419 GRNED-----ASPPTPEPVKDSRAVITCASFTSATESTT-----ANTFPLE 462

Db 1855 NIRQDLLPFQSSVSQYLRSSPNP---SQQLLVTLNLSMDSPDLSPNAPPVGFENTAQFLE 1911

QY 463 -----DHTSENKTDKKEEKRAQII-----TEXTSPKTSNPF 495

Db 1912 KLOQEDRPSAEGSIDSSGFEKVDHEGDEFAAPPDHPMQKSVFGSLGSDMKQSGQDQ 1971

QY 496 LVAVQDSEADYVT-----TDTLK-----VTEAAVSNMPEGLTPDLVQ 533

Db 1972 FVPIERNEAETLKKQKMSHHNDVIEKNYFNDNAPTALLSSPIAEARKLVQDAVE 2031

QY 534 EACE-----SELNEATGKIAYETKVDLVQVTSIAIQBSLYPTAQLCPSFBEAEATPSPVL 588

```

Db 2032 SASSEYKQAVDSGDEIGRELLDNVEQIEQVKEPIQVKEPIVDSLHKAAYDGVGDVHV-ETVNAV- 2089
Qy 589 PDVMEAPLNSLLPSAGASVQPSVSPLEAPPVSDYSIKLEPENPPPEEAMNVALKAL 648
Db 2090 DDVFREAE-----KOLPESVVP-----2106
Qy 649 GKKEGKPEPESFNAAVQETAPYISTACDLIK-----ETKLEPSPDFSNYSIEIAKPK 703
Db 2107 ----EKIETPE-----PLVDLHDTVDKVDHEDVNFRLREPTPPP-----2142
Qy 704 SVPEHAELVEDSPSEPEVDLSDSDSIPVOTQBEAVMLMESLT---EVSETVAQHK 760
Db 2143 -----TDDVAPLSDDKPQGNQT-PE-----EDETTFDRKGPLTIPBEVEKAAQAQNN 2189
Qy 761 ERLSASPQELGPKYLESFOPNLHSTKDA-----ASNDIPTLTKKKESLSLQMEFNTAI 813
Db 2190 D-----LDDDFPLVTSNTGAAGAAVGAAGAAAVESLITBEEMFGHQ--KFETVP 2234
Qy 814 YSNDLLSSKEDKIKESETFSSPIEIIDEPPTFVSADKDDSP--KLAKEYTDLEVSOKS 871
Db 2235 RPTPPKOISDEBVKPS-----TVNLGFSHHHPSPHHSILKHGDAMIDFKT 2284
Qy 872 EIANIQSG-----ADSLPCLE-----LPCDLSFKNIYKPKDEHV 904
Db 2285 VPPCAQNAFSGEIMFLLAFFVYLSCFASFPSKSLPLLDNLSLVVYLSISLI-----IH 2339
Qy 905 VSDE-----FSENRSVSKASISPSNVSA-----LEPOTMGSIYKSKSLTKKARK 950
Db 2340 VKHRRKFRWNEBQATMTSKLGAAGVGLYALIAFIVNIVLVRGLNVALVGVAVSAHEAYK 2399
Qy 951 KLPSDTEKEDRSLSVLSAELSKTSVVDLLYWRDICKTGWFGASIFLLLSITVFSIVSV 1010
Db 2400 LTKS-----SGVLRKKEVLDVYWRDACKSAIVLSLALLVFLVLAQYPLLTIV 2446
Qy 1011 TAYIALALISVTISFRIYKGVIOAQKSGDEGHFRAYLSEVAISEELYQKYSNSALGHV 1070
Db 2447 VTYSLLLALGAAGFRVFKVQAEIKKTSEHPFSEILLAQDLTLQEKVHAQADVFEHA 2506
Qy 1071 NTKIELRLFLVDLDSKFAVLMWVYTGALFNGUTLILIALISLIFSIPVYERHQ 1130
Db 2507 TCIANKKLKLVPESPLESIKGLVMSLTYIASWFSGFTLAILGLLGVFSVPKYVESNQ 2566
Qy 1131 VOIDHYVLGLANKSVKDAMAKIQAKIPGLK 1159
Db 2567 EALDPLHATISHLKNVQNIIDEKUPFLR 2595

RESULT 6
T13564
microtubule-associated protein homolog - fruit fly (Drosophila melanogaster)
N:Alternate names: hypothetical protein EG:4984.1
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13564
R:Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17689
A:Accession: T13564
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5327 <SPA>
A:Cross-references: UNIPROT:O76891; EMBL:AL031128; PIDN:CAA20006.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0025392
A:Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1
A>Note: EG:4984.1
C:Superfamily: Drosophila 576K microtubule-associated protein homolog

Query Match 5.6%; Score 328.5; DB 2; Length 5327;
Best Local Similarity 22.7%; Pred. No. 5.5e-05;
Matches 255; Conservative 176; Mismatches 453; Indels 238; Gaps 54;

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Db      7179  PAKKPEAPPKVPPEAP-KEVVPEKKVPVPPPKKPEVPPPTKVPEVPKAAVPEKKVPEAIPP 7237
QY      570  TAOLCPS--PEBAEATPS-----PV-LPDIVMEAPLNSLLPSAGASVWOPSVSPLE 617
Db      7238  KPSPPEPVEPEESESAPPKKPEVPVTVVPEVKVPEKKVPAAPPK--KPEVTPVK 7295
QY      618  AP-----PPVSY-----DSIKLEPENPPP--YEE 639
Db      7296  VPEAPKEVVPEKKVPVPPPKKPEVPPTKVPEVKVAVPEKKVPEAIPPKPESPPEPVFEE 7355
QY      640  AMNVALKALGTKEGIEKPEPSFNA-----VQTEAPYISTACDLIKETKLSTEP 688
Db      7356  PEEVALEE-PPAEVVEPEPEP--AAPQVTVPPKPNVPEKKAPAV-----VAKPELPPVK 7407
QY      689  SPDFSNSYETAKPEKVPSEHAEIVEDSSPESEPVDFLSDDSIPEVPQTOEAVMLMKESL 748
Db      7408  VPEVP--KEVVP-EKKVP-----LVVPKKPEAPA-----KVPEVP-----KEVV 7444
QY      749  TEVSETVAQHEERLSSASQSELGPKPYLGFPQNLHSTKDAASNDIPTLTKEKISLQMBE 808
Db      7445  PEKKVAVPKKPEVPVPAKVPEVKPKVLEE-KPAVPVPERAESPPPEVVEPEPEIAPEE- 7502
QY      809  FNTAIYNSDDLSSKEDK--IKESZ-----TFSSSPIIITDEPPTTFVSADKSDSKLA 859
Db      7503  -----IAPSEKPVPAEESPEVPPPAVPEEPKKIIPKPKVPVIKPEAPP-P 7550
QY      860  KEYTDLEVSDKSRIANIQSGADSLPCLELPCDLSEK-NIYPKDVHVHSDFSSENRSVSK 918
Db      7551  KSEPEKVKIEKPKLKRPPPPPPPPAPKEDVKEKIFQLKAIPKKKV-----PENPQVPEK 7604
QY      919  ASISPSNVSALEPQTEMGSIVKSKSLTKBAEKKLP--SDTEKEDRSLSAVL 967
Db      7605  VEITPLKVPGE-----KKVKRLPERKPEKEVVLKSVL 7640

RESULT 8
T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <WIL>
A;Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN000023
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP.W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

Query Match 5.5%; Score 320; DB 2; Length 222;
Best Local Similarity 32.1%; Pred.No.1.5e-06;
Matches 59; Conservative 47; Mismatches 78; Indels 0; Gaps 0;

QY      976  VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIAI 1035
Db      27  ILDDVIWRDAKKSAILVLSLALLVLFVLAKYPLLTVVTYSLLLAALGAAGAFVKCKVEAQI 86
QY      1036  QKSDGEHPFRAYLESEVALISEELVQKYSNAGHVNSTIKELRRLFLVDDVLSLKFVVL 1095
Db      87  KKTDSHPFSEILAQDLTLTPOEKVHAQADVFEHATCIANKLKKGVFVSPELSIKFGLV 146
QY      1096  MWVFTVVGALFNGLLTLLIALLSLFSIPVIYERHQVQIDHYLGLANKSVKDAKIAQAKI 1155
Db      147  LMSLTIIASWFSFGFTLAILLGLGVSPVKPYESQAIIDPHLATISLGHUKNVQNIIDDKL 1206
QY      1156  PGLK 1159

```











QY 920 SIS 922  
Db 907 SVS 909

RESULT 15  
QMSPI

microtubule-associated protein MAP1B - mouse  
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S07549; S44387; A33645  
R:Noble, M.; Lewis, S.A.; Cowan, N.J.  
J. Cell Biol. 109, 3367-3376, 1989  
A:Title: The microtubule binding domain of microtubule-associated protein MAP1B contains  
A:Reference number: A33645; MUID:90094539; PMID:2480963  
A:Accession: S07549  
A:Molecule type: mRNA  
A:Residues: 1-2464 <NO>  
A:Cross-references: UNIPROT:P14873; EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000  
R:Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.  
Arch. Biochem. Biophys. 310, 428-432, 1994  
A:Title: Binding of heat-shock protein 70 (hsp70) to tubulin.  
A:Reference number: S44387; MUID:94234720; PMID:8179328  
A:Accession: S44387  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 653-663, 'IC' <SAN>  
C:Superfamily: microtubule-associated protein MAP1B  
C:Keywords: microtubule binding; phosphoprotein; tandem repeat  
F:589-786/Domains: microtubule binding #status experimental <MTB>  
F:589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-694  
R:X-E/D-X)

F:1861-2064/Region: 17-residue repeats  
F:91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: ph  
F:147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (Co  
F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 284; DB 1; Length 2464;  
Best Local Similarity 20.7%; Pred. No. 0.0012;  
Matches 233; Conservative 159; Mismatches 424; Indels 312; Gaps 51;

QY 31 EPEDEDEDEDEED-----DEPLELE-----VLERKPAAG-----LSAAAVP 71  
Db 1009 EAEQSEEGEEDKAEDEEGVEPDKTEADYVMAVADKAAAGVTEQYGLGTSKQ 1068

QY 72 PAAAPLLDFSS-----DSVPPAPRGLPAPPAAPERQP-----SWERSPAAPA 116  
Db 1069 PGIQSPSRFPASSIHDETLPGGSESEATASDENREDQEEFTATSGYTQSTIEISSEPT 1128

QY 117 P---SLPPAAAVLPKLPEDDEPPARP-----PPPPAGASPLAEP-- 155  
Db 1129 PMDENSTPRDVMSTENNEETESPSQEFVNITKYESSLYSQEYKPAVASFNGLSEGSKT 1188

QY 156 -----APSTPAAPKRGSGVDLTFALPA-----ASEVIPSSAEKIMDLMEQ 200  
Db 1189 DATDGKDYNNASASTISPP-----SGNEEDKFKSALRDAYCSEKELKASAE--LDIKDV 1241

QY 201 PGNTVSSGGQEDPPSVLLETAASLPSPSLSTVSFKHGYLGNLSAVSSSEGTIETFLNEA 260  
Db 1242 SDERLS-----PAKSPSLSP-----SPSPSIEKT----- 1265

QY 261 SKELPERATNPFVNRDLAELS-----ELEYSEMGSSFKGPKGSAAILVEN--TKEEVIVR 314  
Db 1266 --PLGERSVN-----FSLTPNEIKVSAEGEARSVSPGVTOA VVEHCASPEEKTLE 1314

QY 315 SKDKEDLVCSAALHSP-QESPVGKEDRVVSPEKTMDFNEMQMSVVA-PVREYADF-- 370  
Db 1315 VVSPSOSVGTSGAGHTPYQSP-----TDEKSSHLPTVESENQAQAVPSFESEAKDE 1366

QY 371 -----PPEQAWENVKDTYEGSRDVLAAAPANVESKVDKRCLED--SLEQKSLGKDS----- 417

Search completed: June 16, 2005, 13:31:49  
Job time : 42.9713 secs

Db 1367 NERASLSPMDE--PVPDSSEPVKEVLSPLRSPPLLGSESPYEDFLSADSKVLGRSESPF 1424  
QY 418 EGRNEDASFPSTPEPVKDSRAYITCASFTSATSTTANTTLPFLLEDHTSENKT----- 470  
Db 1425 EGKNGKQGFDPRESFVSLT---STGLYQDKQBEKSTGFIPKEDFGPEKKTSDVETMS 1480  
QY 471 -----DEKKI-----EERKQIITEKTSPKTSNPFLVAVQDSEAD 505  
Db 1481 SOSALALDERKILGGVSVPTQIDVSGFKEDTKMSISEGTVSDKSATPVDSGV--AET 1538  
QY 506 YTTTDTLSKVTEAAV--SNMPEGLTPDLVQACESELNEATGKIAYETKVLVOTSEAI 563  
Db 1539 YSHMEGVA SVSTASVATSFPEPTDD-VSPSLHAEVGSPHSTVEDDLSLSVSVVQPTTF 1597  
QY 564 QBS-LYPTAQICP--SFEERAEATP-----SPVLPDIMEAPLMSLL-- 601  
Db 1598 QETEMSPSKECPRMSPSPDFSPKTA SRTPVQDHRSEQSSMSIEFGQESPEHSFAMD 1657  
QY 602 -----PSAGASVVQPSVSPLEAPPVSYD-----SIKLEPENPPPEEAMNVA 644  
Db 1658 FSRQPDHPTLGLASVHLHITEN---GPTVDVSPCDIQDSSLSHKPIPTTEEPSYTDNDLS 1714  
QY 645 LKALGTKEGKEIPESFNAAVOETEAPYISACDLIKETKLTSTEPSDFSNYSIAKFEKS 704  
Db 1715 -ELISVSQVEASPSSTSAHTPS-----QIASPLQEDTLSDVVPPREMSLYASLA---- 1762  
QY 705 VPEHAELVEDSPSEPVDLFSDDSIPEVPQTEAVML-----MKESLTVSETVAQHKE 760  
Db 1763 ----SEKVO--SLEGEKLSPKSDIS---PLTPRESSPLYSFGSDSTSAAKETAAAH-- 1810  
QY 761 ERLSASP--QELGKPY-----LESFQPNLHSTKDAASNDIPTLTKEKISLQWERFN 810  
Db 1811 -QASSPPIIDAATAEPYFGRSMLPDTQOHLALNRDLTTSSV-----EKDSGKTPGDN 1865  
QY 811 TAIYNDLLSKEDKIKESETFSDSPSIEIIDEPTFVSXKDDSPK-----LAKSYTDLE 866  
Db 1866 YAYQKPENAAGSPDEEDYDYE--SQEKTIRTHDVVRYVEKTERTIKSPCDSGSYVETIE 1923  
QY 867 VSDKSEIANIQSGADSLPCLELPCLSPKNYIPKDEHVHVSDFSENRSVSKAS----- 920  
Db 1924 KTTKTP-----EDGG-----YTCEITKTRTPEEGGYSYSEIKTTRTPEVSGYTVBK 1972  
QY 921 -----ISPSNVSALEPQTEMGSI VKSKSLTKAEAKLPSDTEKEDRS 962  
Db 1973 TERSRLDDISNGYDDTDGCHTLGDCSYVETTEKITSPESESYS 2020



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 157.778 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-2

Perfect score: 5848

Sequence: 1 MEDIDQSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5848	100.0	1163	1 RTN4 RAT	Q9Jk11 rattus norv
2	5312.5	90.8	1162	2 Q8BGM9	Q8Bgm9 mus musculu
3	5307	90.7	1163	2 Q8K3G8	Q8K3g8 mus musculu
4	4501.5	77.0	1046	2 Q8BGK7	Q8Bgk7 mus musculu
5	4403.5	75.3	1192	1 RTN4 HUMAN	Q9ncq3 homo sapien
6	3627.5	62.0	986	2 Q7TNU4	Q7Tnu4 homo sapien
7	3299.5	56.4	720	2 Q7TNU7	Q7Tnu7 mus musculu
8	2926	50.0	639	2 Q8K290	Q8K290 mus musculu
9	2610	44.6	578	2 Q8QW95	Q8Qw95 mus musculu
10	1664	28.5	658	2 Q8RSS8	Q6rs88 gallus gall
11	1620	27.7	1043	2 Q6JRV0	Q6Jrv0 xenopus lae
12	1616	27.6	1055	2 Q6JRV1	Q6Jrv1 xenopus lae
13	1596.5	27.3	1032	2 Q6JRV7	Q6Jrv7 xenopus lae
14	1586.5	27.1	1044	2 Q6JRV8	Q6Jrv8 xenopus lae
15	1554.5	26.6	1024	2 Q6JRV2	Q6Jrv2 xenopus lae
16	1539	26.3	1013	2 Q6JRV9	Q6Jrv9 xenopus lae
17	1416	24.2	375	2 Q8BHF5	Q8Bhf5 mus musculu
18	1314.5	22.5	356	2 Q8BH78	Q8bh78 mus musculu
19	1304	22.3	357	2 Q8K3G7	Q8K3g7 mus musculu
20	1283.5	21.9	392	2 Q96B16	Q96b16 homo sapien
21	1060	18.1	343	2 Q6IPN0	Q6ipn0 homo sapien
22	917	15.7	199	1 RTN4 MOUSE	Q9p972 mus musculu
23	908	15.5	199	2 Q7YRW9	Q7Yrw9 bos taurus
24	904	15.5	199	2 Q6IM70	Q6im70 sus scrofa
25	899	15.4	199	2 Q7PCJ7	Q7pcj7 macaca fasc
26	896	15.3	187	2 Q6IG15	Q6ig15 sus scrofa
27	876	15.0	199	2 Q7T224	Q7t224 gallus gall
28	850	14.5	250	2 Q6IG16	Q6ig16 sus scrofa
29	844	14.4	179	2 Q9GM33	Q9gm33 macaca fasc
30	807.5	13.8	315	2 Q6IFY4	Q6ify4 xenopus tro
31	806	13.8	1013	2 Q6T930	Q6t930 homo sapien

32	803	13.7	945	2	Q6T929	Q6t929 mus musculu
33	801	13.7	777	1	RTN1 RAT	Q64548 rattus norv
34	797.5	13.6	311	2	Q6JRV3	Q6jrv3 xenopus lae
35	797	13.6	330	2	Q6JRV4	Q6jrv4 xenopus lae
36	796.5	13.6	964	2	Q88FB4	Q88fe4 mus musculu
37	792.5	13.6	940	2	Q6RJR6	Q6rjr6 rattus norv
38	792	13.5	780	2	Q8K4S4	Q8k4s4 mus musculu
39	789.5	13.5	776	1	RTN1 HUMAN	Q16799 homo sapien
40	788	13.5	780	2	Q8K0T0	Q8k0t0 mus musculu
41	777	13.3	315	2	Q6JRW2	Q6jrw2 xenopus lae
42	774	13.2	193	2	Q6IFY5	Q6ify5 xenopus tro
43	770.5	13.2	323	2	Q6JRW1	Q6jrw1 xenopus lae
44	767.5	13.1	882	2	Q6R8K6	Q6r8k6 mus musculu
45	767	13.1	304	2	Q6JRW0	Q6jrw0 xenopus lae

#### ALIGNMENTS

RESULT 1

ID RTN4 RAT STANDARD; PRT: 1163 AA.

AC Q9Jk11; Q9Jk10; Q9ROD9; Q9WUE9; Q9WUF0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Poccen)

DE (Glut4 vesicle 20 kDa protein).

GN Name=Retn4; Synonyms=Nogo;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

[1]

RN SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.

RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;

RX MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;

RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;

RT "Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family,";

RT Biochim. Biophys. Acta 1450:68-76(1999).

[2]

RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RP MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;

RX Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,

RA Spillmann A.A., Christ F., Schwab M.E.;

RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an antigen for monoclonal antibody IN-1,";

RL Nature 403:434-439(2000).

[3]

RN SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).

RP STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;

RC Ito T., Schwartz S.M.;

RT "Cloning of a member of the reticulon gene family in rat: one of two minor splice variants,";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

[4]

RN FUNCTION.

RP MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;

RX Grandpre T., Li S., Strittmatter S.M.;

RA "Nogo-66 receptor antagonist peptide promotes axonal regeneration,";

RL Nature 417:547-551(2002).

CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By similarity).

CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Name=1; Synonyms=Nogo-A, NI-220-250;



[illegible]



Db 63 SEPVPSSAEKIMDLKEQNGNTVSSGQEDFPSPVLPETAASPLSLSTVSPFKHGYLEN 122  
Qy 243 LSAVSSSECTIETLINEASKELPERATNPFVNRDLAEFSELYSEWSSFGSKSPKGESAI 302  
Db 123 LSAVASTECTIETLINEASRELPERATNPFVNRSEAFSVLYSEWSSFGSPKGESAM 182  
Qy 303 LVENTKEEVIVRSKDKEDLVCSSAALHSPQESP-----VGKEDRVVSPSEKTMDFINEMQMS 357  
Db 183 LVENTKEEVIVRSKDKEDLVCSSAALHNPQESPATLTKVVKEDGVMSPEKTMDFINEMQMS 242  
Qy 358 VVAPVREYADPKPEQAEVWKDTYEGSRDVLAAANVESKVDKCLDESLBOKSLGKDS 417  
Db 243 VVAPVREYADPKPEQAEVWKDTYEGSRDVLAAANMESKVDKCFDESLQKGHGDS 302  
Qy 418 EGRNEDASFPSPPEPVKDSRRAYITCASFTSATESTTANPTPLLDHTSENKTKDEKTEE 477  
Db 303 ESRNENASFPPTPELVKDGSRAYITCDSFSSATESATAINFPVLEDHTSENKTKDEKTEE 362  
Qy 478 RKAQIITEKTSPTKSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA 537  
Db 363 RKAQIITEKTSPTKSNPFLVAIHDEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 422  
Qy 538 SELNEATGTKIAYETKVDLVTSEAIQESLYPTAQLCSPFEAEATPSPVLPDIWMEAPL 597  
Db 423 SELNEATGTKIAYETKVDLVTSEAIQESLYPTAQLCSPFEAEATPSPVLPDIWMEAPL 482  
Qy 598 NSLLPSAGASVVPSPVPLEAPPVSYDSIKLEPNPPPYEAMNVALKGTKEGKEP 657  
Db 483 NSLLPSTGASVAQPSASPLEVPSPVSYOGIKLEPNPPPYEAMSVALKTSDEKEIKEP 542  
Qy 658 ESFNAVQETAPYISACDLIKETKLTSTEPSDFSNYSIAKFKSPVPEHAELVEDSSP 717  
Db 543 ESFNAQAQEAAPYISACDLIKETKLTSTEPSPEFSNYSIAKFKSPVPEHCELVDSSP 602  
Qy 718 ESEPVDLFSDSDIPVPQTOBEAVMLKESITVEVSETVAQHK-BERLSASPOELGKPYLE 776  
Db 603 ESEPVDLFSDSDIPVPQTOBEAVMLKESITVEVSETVTOHKHRELSPQEVGKPYLE 662  
Qy 777 SFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLLSKKEDKIKESSTFSDS 836  
Db 663 SFQPNLHSTKDAASNEIPTLTKEKISLQMEEFNTAIYSNDDLLSKKEDKIKESSTFSDS 722  
Qy 837 SPIEIIDFPPTFVSADKSPKLAKETDLEYSKSEIANIQSGADSLPCLPCLDLSFKN 896  
Db 723 SPIEIIDFPPTFVSADKSP---KEYTDLEYSNKSSEIANVQSGANSLPCLSPCLDLSFKN 779  
Qy 897 IYPKDEVIVSEFNSRNSVSKASISPSNVSALPEPOTEMGSIKSLTKAEKLPDST 956  
Db 780 TYPKDEAHVSEFNSRNSVSKVPVLPVFNVSALPESQIEMGNIVKPKVLTKEAEKLPDST 839  
Qy 957 EKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYTAL 1016  
Db 840 EKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYTAL 899  
Qy 1017 ALLSVTISFRIYKGVIOAKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSITIKE 1076  
Db 900 ALLSVTISFRIYKGVIOAKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSITIKE 959  
Qy 1077 LRRFLVDDVLSLFAVLMVFTVVGALFNGLTLLILALISLSPVPIYERHQVQIDHY 1136  
Db 960 LRRFLVDDVLSLFAVLMVFTVVGALFNGLTLLILALISLSPVPIYERHQVQIDHY 1019  
Qy 1137 LGLANKSVKDAWAKIQAKIPGLKRAK 1163  
Db 1020 LGLANKSVKDAWAKIQAKIPGLKRAE 1046

## RESULT 5

RTN4 HUMAN

ID RTN4 HUMAN STANDARD; PRT: 1192 AA.

AC Q9NQC3; Q94962; Q9BG5; Q9H212; Q9H313; Q9Q42; Q9Y293; Q9Y2Y7;

AC Q9Y5U6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Pooen)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).  
GN Name=RTN4; Synonyms=ASV, KIAA0886, NOGO;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RP MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
Michalovich D., Simmons D.L., Walsh F.S.;  
RT "Inhibitor of neurite outgrowth in humans.";  
RL Nature 403:383-384(2000).  
RN [2]  
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RP TISSUE=Brain;  
EX MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;  
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
endoplasmic reticulum and reduces their anti-apoptotic activity.";  
RL Oncogene 19:5736-5746(2000).  
RN [3]  
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RP MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
2p14-->2p13 by radiation hybrid mapping.";  
RL Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
SEQUENCE FROM N.A. (ISOFORM 4).  
RA Jin W.-L., Ju G.;  
RT "Developmentally-regulated alternative splicing in a novel Nogo-A";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Pituitary;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [8]  
SEQUENCE FROM N.A. (ISOFORM 3).  
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
growth.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [9]  
SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
EX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,  
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding regions of unidentified human genes. XII.  
The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro.";

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RL DNA Res. 5:355-364(1998).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Ovary, Pancreas, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K.C., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettunen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Umbilical cord blood;
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
RN [12]
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
RC TISSUE=Brain;
RA Mao Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RA Sha J.H., Zhou Z.M., Li J.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [14]
RP TOPOLOGY.
RC TISSUE=Brain;
RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
RT "Identification of the Nogo inhibitor of axon regeneration as a
RT Reticulon protein.";
RL Nature 403:439-444(2000).
RN [15]
RP FUNCTION.
RC TISSUE=Brain;
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
RA Fournier A.E., Grandpre T., Strittmatter S.M.;
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration.";
RL Nature 409:341-346(2001).
RN [16]
RP REVIEW.
RX MEDLINE=2188956; PubMed=11891768; DOI=10.1002/jnr.10134;
RA Ng C.E.L., Tang B.L.;
RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT regeneration.";
RL J. Neurosci. Res. 67:559-565(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults.
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
CC This is likely consecutive to their change in subcellular

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CC location, from the mitochondria to the endoplasmic reticulum,
CC after binding and sequestration.
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum. Anchored to the membrane of the endoplasmic reticulum
CC through 2 putative transmembrane domains.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;
CC IsoId=QNQC3-1; Sequence=Displayed;
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;
CC IsoId=QNQC3-2; Sequence=VSP_005655;
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;
CC IsoId=QNQC3-3; Sequence=VSP_005652, VSP_005653;
CC Name=4;
CC IsoId=QNQC3-4; Sequence=VSP_005654;
CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC widely expressed excepted for the liver. Isoform 3 is expressed in
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC specific.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -!- CAUTION: Ref.11 sequence differs from that shown due to
CC frame shifts in positions 1149 and 1156.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ251383; CAB99248.1; -
DR EMBL; AJ251384; CAB99249.1; -
DR EMBL; AJ251385; CAB99250.1; -
DR EMBL; AB040462; BAB18927.1; -
DR EMBL; AB040463; BAB18928.1; -
DR EMBL; AF148537; AAG12176.1; -
DR EMBL; AF148538; AAG12177.1; -
DR EMBL; AF087901; AAG12205.1; -
DR EMBL; AF320999; AAG40878.1; -
DR EMBL; AF132047; AAD31021.1; -
DR EMBL; AF132048; AAD31022.1; -
DR EMBL; AB015639; BAA83712.1; -
DR EMBL; AF077050; AAD27783.1; -
DR EMBL; AF177332; AAG17976.1; -
DR EMBL; AB020693; BAA74909.2; ALT_INIT.
DR EMBL; BC001035; AAH01035.1; -
DR EMBL; BC007109; AAH07109.1; -

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Query Match 75.3%; Score 4403.5; DB 1; Length 1192;
Best Local Similarity 75.9%; Pred. NO. 2.4e-152;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

QY 1 MEDIDSSIVSSSTDSPPRPAPFKYQVTRPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60
DB 1 MEDLDQSLVSSS-DSPPRPAPFKYQVTRPEDEE-EEEEEEDEDEDELEVLK 58
QY 61 PAAGLSAAAVP--PAAAAPLDFFSDSVPPAPRGLPAAPPAAPRQPSWERSPAA--P 115
DB 59 PAAGLSAAVPTAPAAAGAPLMDFGNDFFVPAPRGLPAAPVPAERQPSWSPSVSTVP 118
QY 116 APSLPAAAVLPFSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPSTPAAPKR 166
DB 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVQAPVMTTPPAAPAPSTPAAPKR 178
QY 167 RG-SCGVDETLPALPAASEPVTPSAEKIMDLMEQNTVSSGQDFPSVLLETASLPS 225
DB 179 RGSSGVDETLPALPAASEPVTPSAAEN-MDLKEQFGNTISAGQDFPSVLLETASLPS 237
QY 226 LSPSTVTFKGHGYLGNLSAVSSSGTTEETLINEASKELPERATNPFVNRDLAEPSELEY 285

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Db 238 LSPLSAAAFKEHYEYGLNLSVLTPTGTLQENVSSEASKEVSEKAKTLLIDRLDTFSELEY 297
Qy 286 SEMGSSFKGSPKESAIIVENTKEVIVRSXDKED-LVCSAALHSPQSPVPG-----KED 339
Db 298 SEMGSSFSVSPKASAVIIVANPREBIIIVKNDEEEKVSNLILHNQQLPTALTKLVKED 357
Qy 340 RVVSPKTMIDIFNEMQSVVAPVREYADFKPFQAEWVXKDTYEGSRDVLAA-----RANV 395
Db 358 EVVSEKAKDSFNEKRVAVAPMREYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416
Qy 396 ESKVDKCLDSLEQSGKSGSEGNEDASPPSPPEPVKDSRAYITCASFT-SATESTT 454
Db 417 ESKVDKCKFADSLQETNHEKDSSESSNDTSPFTEPGIKDRSGAYITCAPFNPAATESIA 476
Qy 455 ANTPELLDHTSENKTKTEERKAQIIITEK-TSPKTSNPFVAVQDSEADYVTTDTLS 513
Db 477 TNPFLGDPITSENKTKTEERKAQIIVTEKNTSTKTSNPFVAVQDSEADYVTTDTL 536
Qy 514 KVTEAAVSNMPEGLTPDILVQACESELNEATGTKIAYETKVDLVQTSBAIQESLYPTAQL 573
Db 537 KVTEEVANMPEGLTPDILVQACESELNEVGTGKIAYETKMDLVQTSSEVQESLYPAAQL 596
Qy 574 CPSPREABATSPVLPDILVMEAPLNSLLPSGASVQVQSPVSPLEAPPVVSVDISKLEPEN 633
Db 597 CPSPRESEATSPVLPDILVMEAPLNSAVPSGASVQVQSPSSPLEA-SSVNYESIKHEPEN 655
Qy 634 PPPVEEAMNVALKAL-GTKEGIKEPESNAVAQTEAPYISIACDLIKETKLSSTEPSDF 692
Db 656 PPPVEEAMNSVLKVGKIEIKPENINAAQTEAPYISIACDLIKETKLSAEPAPDF 715
Qy 693 SNYSIAKFEKSVPEHAELVEDSPSPFVDFSDSIPPEVPTQEEAVMLMKESLSTEV 752
Db 716 SDYSEMAKVEOPVPHSELVEDSPSPFVDFSDSIPDPVQKQDETVMVLKESLTETS 775
Qy 753 -ETVAQHK-ERRLGASPOELKPYLESQPNLHSTKDA-ASNDIPTTKYKESKISLQMBEF 809
Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLNDTKOTLLPDEVSTLSKKEKIPLOMBEL 835
Qy 810 NTALYSNDLLSKKEDKIKESSETSDSPIIIEFFPTFVSAKDDSPKLAKEYTDLEVS 868
Db 836 STAVYSNDLLFISKEAQIRETETSDSPIIIEFFPTLISKTDSPSKLAREYTDLEVS 895
Qy 869 DKSIANTQSGADSLPCLPCLDSFKNIYKPK--DEVHVSDEFSENRSSVSKASISPSNV 926
Db 896 HKSIANAPDAGSLPCTELPHDLSLKNIQPKVEKISFSDFKNGSATSKVLLLPDV 955
Qy 927 SALEPQTMGSIKSVKSLTKBAEKKLPSTDEKDRSJSANVLSBELSKTSVVDLLYWRDIK 986
Db 956 SALATQABIESIVKPKVLVKEAEKKLPSTDEKDRSPSAIFSAELSKTSVVDLLYWRDIK 1015
Qy 987 KGVVFGASLFLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIOAIQKSDSGHPRA 1046
Db 1016 KGVVFGASLFLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIOAIQKSDSGHPRA 1075
Qy 1047 YLESEVAISELVQKYSNLSALGHVNSTTKELRRFLVDDLVDSLKFVLMVVFYVVGALF 1106
Db 1076 YLESEVAISELVQKYSNLSALGHVNSTTKELRRFLVDDLVDSLKFVLMVVFYVVGALF 1135
Qy 1107 NGLTLLILALISLFSIPVYERHQVQIDHYIYGLANKSVKDMAMAKIQAIPGLKRAKAD 1163
Db 1136 NGLTLLILALISLFSIPVYERHQVQIDHYIYGLANKSVKDMAMAKIQAIPGLKRAKAE 1192
RESULT 6
Q8IU4A PRELIMINARY; PRT; 986 AA.
AC Q8IU4A;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform
GN F) (RTN4 isoform G) (RTN4 isoform Aa).
Name=RTN4;
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtnd4.";
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102285; AAM64244.1; -
DR EMBL; AY123246; AAM64250.1; -
DR EMBL; AY123247; AAM64251.1; -
DR EMBL; AY123248; AAM64252.1; -
DR EMBL; AY123249; AAM64253.1; -
DR EMBL; AY123250; AAM64254.1; -
DR EMBL; AY123245; AAM64249.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon.1.
DR PROSITE; PS0845; RETICULON.1.
SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 62.0%; Score 3627.5; DB 2; Length 986;
Best Local Similarity 75.4%; Pred. No. 3.3e-124;
Matches 745; Conservative 96; Mismatches 126; Indels 21; Gaps 13;

Qy 195 MDLMEQNGNTVSSQEDFPFVLLTAASLPSTVSPKHEGYLGNLSAVSSEGTIE 254
Db 1 MDLKEQNGNTISAGQEDFPFVLLTAASLPSTVSPKHEGYLGNLSAVLTPETGLQ 60
Qy 255 ETLNEASKELPERATNPFVNRDLAEFSELEYSESGSFKGSPKGSAILVENTKEEVIVR 314
Db 61 ENTSEAKSEVSEKAKTLLIDRLDTFSELEYSESGSFSVSPKASAVIVANPREIIVK 120
Qy 315 SKKED-LVCSAALHSPQSPVPG-----KEDRVVVSPEKTMIDIFNEMQSVVAPVREYAD 368
Db 121 NKDEEEKLVSNLILHNQQLPTALTCLVKEDEVVVSSEKAKDSFNEKRVAVAPMREYAD 180
Qy 369 FKPEQAEWVXKDTYEGSRDVLAA-----RANVESKVDKCLDSLEQKSLGKDSGRNEDA 424
Db 181 FKPFERVWEVKDSKEDS-DMLAAGGKIESNLSEKVDKCKFADSLQETNHEKDSSESSNDT 239
Qy 425 SFPSTPSPVKDSSRAYITCASFT-SATESTTANTFPLEDHTSENKTKTEERKAQII 483
Db 240 SFPSTPGIKDRSGAYITCAPFNPAATESATNIFPLGDPITSENKTKTEERKAQIV 299
Qy 484 TEK-TSPKTSNPFVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDILVQACESELNE 542
Db 300 TEKNTSTKTSNPFVAVQDSEADYVTTDTLTKVTEEVANMPEGLTPDILVQACESELNE 359
Qy 543 ATGTKIAYETKVDLVQTSBAIQESLYPTAQLCPSPREABATSPVLPDILVMEAPLNSLLP 602
Db 360 VTGTKIAYETKMDLVQTSSEVQESLYPAAQLCPSPRESEATSPVLPDILVMEAPLNSAVP 419
Qy 603 SAGASVQVQSPVSPLEAPPVVSVDISKLEPENPPPYEEAMNVALKAL-GTKEGIKEPESFN 661
Db 420 SAGASVQVQSPVSPLEAPPVVSVDISKLEPENPPPYEEAMNVALKAL-GTKEGIKEPESFN 478
Qy 662 AAVQETAPYISIACDLIKETKLSSTEPSDFSNYSIAKFEKSVPEHAELVEDSPSEBP 721
Db 1
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479	AA	QTEA	PYIS	ACDL	IKET	KL	SA	PP	DF	SD	YS	EW	AK	VQ	VP	DH	SEL	VD	SS	PD	SEP	538																																				
722	VD	LF	SD	SD	SI	PE	VQ	TQ	EE	AA	VML	MK	ES	IT	VS	-	ET	VA	QHK	-	EE	RL	SA	SP	QBL	GP	LY	LE	SF	Q	779																											
539	VD	LF	SD	SD	SI	PD	VQ	TQ	EE	AA	VML	MK	ES	IT	VS	-	ET	VA	QHK	-	EE	RL	SA	SP	QBL	GP	LY	LE	SF	Q	598																											
780	PN	LH	ST	KD	A	-	AS	ND	I	PT	L	TK	E	K	I	S	Q	ME	BE	FN	T	A	I	Y	S	ND	DL	L	S	K	ED	K	I	KE	S	T	TF	SD	SS	P	838																	
599	LS	LD	NT	KD	T	LL	P	DE	V	ST	LS	KE	K	I	P	LQ	ME	BE	LS	T	AV	Y	S	ND	DL	LF	I	S	KE	AQ	I	RE	T	ET	TF	SD	SS	P	658																			
839	IE	TD	IE	PP	FP	VS	AK	DS	-	PK	L	AK	EY	TD	LE	VS	D	K	SE	T	AN	I	OS	G	AD	S	L	P	C	L	E	P	CD	L	S	PK	NI	897																				
659	IE	TD	IE	FP	TT	IS	K	T	DS	F	S	KL	AK	EY	TD	LE	V	SH	K	SE	T	AN	A	P	D	G	A	S	L	P	C	T	EL	P	D	HL	SL	LN	718																			
898	Y	P	K	-	-	DE	V	H	S	D	S	F	E	N	R	S	S	V	S	K	AS	I	S	P	S	N	V	S	A	L	E	P	O	T	E	M	G	S	I	T	K	E	A	E	K	L	P	S	D	955								
719	O	P	K	V	E	K	I	S	P	D	S	F	E	N	R	S	S	V	S	K	AS	I	S	P	S	N	V	S	A	L	E	P	O	T	E	M	G	S	I	T	K	E	A	E	K	L	P	S	D	778								
956	T	E	K	E	D	R	S	L	S	A	V	L	S	A	E	I	S	K	T	S	V	D	L	L	Y	K	R	D	I	K	T	G	V	V	F	G	A	S	L	F	L	L	L	S	L	T	V	F	S	I	V	S	V	T	A	Y	A	1015
779	T	E	K	E	D	R	S	P	S	A	I	F	S	A	E	I	S	K	T	S	V	D	L	L	Y	K	R	D	I	K	T	G	V	V	F	G	A	S	L	F	L	L	L	S	L	T	V	F	S	I	V	S	V	T	A	Y	A	838
1016	L	A	L	S	T	I	S	P	R	I	Y	K	V	I	O	A	I	O	K	S	D	E	G	H	P	P	A	I	E	S	V	A	I	S	E	E	L	V	O	K	S	I	T	K	E	A	E	K	L	P	S	D	1075					
839	L	A	L	S	T	I	S	P	R	I	Y	K	V	I	O	A	I	O	K	S	D	E	G	H	P	P	A	I	E	S	V	A	I	S	E	E	L	V	O	K	S	I	T	K	E	A	E	K	L	P	S	D	898					
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899	E	L	R	L	F	L	V	D	D	L	S	L	K	F	A	V	L	M	V	T	Y	G	A	L	F	N	G	L	I	L	I	A	L	I	S	F	S	I	P	V	I	E	R	H	O	V	I	D	H	958								
1136	Y	L	G	L	A	N	K	S	V	K	D	A	M	A	K	I	O	A	K	I	P	L	K	R	K	A	D	1163																														
959	Y	L	G	L	A	N	K	S	V	K	D	A	M	A	K	I	O	A	K	I	P	L	K	R	K	A	E	986																														

RESULT 7



OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC022192; AAH22192.1; -.  
 DR MGD; MGI:191835; Rcn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 50.0%; Score 2926; DB 2; Length 639;  
 Best Local Similarity 91.6%; Pred. No. 6.5e-99;  
 Matches 588; Conservative 20; Mismatches 30; Indels 4; Gaps 2;

Qy 523 MPEGLTPDLVQACESELENEATGKIAYETKVDLVQTSSEATQESLYPTAQICPSFEAEAA 582  
 Db 1 MPEGLTPDLVQACESELENEATGKIAYETKVDLVQTSSEATQESLYPTAQICPSFEAEAA 60

Qy 583 TPSPVLPDIVMEAPLNSLLPSAGASVQPSVPLEAPPVSDSIKLEPENPPPYEEAMN 642  
 Db 61 TPSPVLPDIVMEAPLNSLLPSAGASVQPSVPLEAPPVSDSIKLEPENPPPYEEAMN 120

Qy 643 VALKALGTKEGKEPESFNAVAQTEAPYISACDLIKETKLTSTEPSPDFSNYSIEIAKFE 702  
 Db 121 VALKTSDAKEIKEPESFNAQAQEAAPYISACDLIKETKLTSTEPSPEFSNYSIEIAKFE 180

Qy 703 KSVPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EE 761  
 Db 181 KSVPDHCLVDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHE 240

Qy 762 RLSAPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 821  
 Db 241 RLSAPQVGVKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 300

Qy 822 SKEDKIKESFTSDSSPIEIIIDEPFTFVSADKDPKLAKEYTDLVSKSEIANIQSGAD 881  
 Db 301 SKEDRMKESFTSDSSPIEIIIDEPFTFVSADKDP-KEYTDLVSKSEIANVQSGAN 357

Qy 882 SLPCLELPCDLISFKNIYKPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIKVS 941  
 Db 358 SLPCSELPCDLISFKNTYKPKDEAHVSDEFSENRSSVSKVPLLLPNVSALESQIEMGNIVKP 417

Qy 942 KSLTKEAEKKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 1001  
 Db 418 KVLTKAEAEKKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 477

Qy 1002 LTVFSIVSVTAYIALALLSVTISPRIYKGVTOAQKSDGHPFRFRAYLSEVAISELVOK 1061  
 Db 478 LTVFSIVSVTAYIALALLSVTISPRIYKGVTOAQKSDGHPFRFRAYLSEVAISELVOK 537

Qy 1062 YSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVYVGFALFNGTLTLLILALISLPS 1121  
 Db 538 YSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVYVGFALFNGTLTLLILALISLPS 597

Qy 1122 IPVIYERHQVIDHYLGLANKSVKDAKIAQIKIPGLKRAKAD 1163  
 Db 598 IPVIYERHQVIDHYLGLANKSVKDAKIAQIKIPGLKRAKAE 639

RESULT 9  
 Q80W95  
 ID Q80W95 PRELIMINARY; PRT; 578 AA.  
 AC Q80W95;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Nogo-A (Fragment)  
 GN Name=Nogo-A;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tozaki H., Hirata T.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB073672; BAC75974.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 FT NON TER 1  
 SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 44.6%; Score 2610; DB 2; Length 578;  
 Best Local Similarity 90.7%; Pred. No. 1.8e-87;  
 Matches 527; Conservative 18; Mismatches 32; Indels 4; Gaps 2;

Qy 584 PSPVLPDIVMEAPLNSLLPSAGASVQPSVPLEAPPVSDSIKLEPENPPPYEEAMN 643  
 Db 1 PSPVLPDIVMEAPLNSLLPSAGASVQPSVPLEAPPVSDSIKLEPENPPPYEEAMN 60

Qy 644 ALKALGTKEGKEPESFNAVAQTEAPYISACDLIKETKLTSTEPSPDFSNYSIEIAKFE 703  
 Db 61 ALKTSDAKEIKEPESFNAQAQEAAPYISACDLIKETKLTSTEPSPDFSNYSIEIAKFE 120

Qy 704 SVPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-BER 762  
 Db 121 SVPDHCLVDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHER 180

Qy 763 LSAPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 822  
 Db 181 LSAPQVGVKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 240

Qy 823 KEDKIKESFTSDSSPIEIIIDEPFTFVSADKDPKLAKEYTDLVSKSEIANIQSGADS 882  
 Db 241 KEDRMKESFTSDSSPIEIIIDEPFTFVSADKDP-KEYTDLVSKSEIANVQSGANS 297

Qy 883 LPCLLELPCDLISFKNIYKPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIKVS 942  
 Db 298 LPCLSELPCDLISFKNTYKPKDEAHVSDEFSENRSSVSKVPLLLPNVSALESQIEMGNIVKP 357

Qy 943 SLTKEAEKKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 1002  
 Db 358 VLTKEAEKKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 417

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QY 1003 TVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAYLESEVAISEELVQRY 1062
Db 418 TVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAYLESEVAISEELVQRY 477
QY 1063 SNSALGHVNSTIKELRRFLVDDVLSLKFVLMVFTYVGVGALFNGLTLLIILALISLSFI 1122
Db 478 SNSALGHVNSTIKELRRFLVDDVLSLKFVLMVFTYVGVGALFNGLTLLIILALISLSFI 537
QY 1123 PVIYERHOVIDHYLGLANKSVKDMAKIQAIPGLKRRAD 1163
Db 538 PVIYERHOVIDHYLGLANKSVKDMAKIQAIPGLKRRAE 578

RESULT 10
Q6RSS8
ID Q6RSS8 PRELIMINARY; PRT; 658 AA.
AC Q6RSS8;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Neurite outgrowth inhibitor NOGO-A (Fragment).
GN Name:NOGO;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Calharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;

Query Match 28.5%; Score 1664; DB 2; Length 658;
Best Local Similarity 56.7%; Pred. No. 66-53;
Matches 379; Conservative 82; Mismatches 168; Indels 40; Gaps 17;

QY 524 PGLTPDLVQEAACESEINATGTKIAYETKVLDTVOTSEAIQBSLYPTAQLCPSEFAEAT 583
Db 1 PGLTPDLVQEAACESEINATGTKIAYETKVLDTVOTSEAIQBSLYPTAQLCPSEFAEAT 60
QY 584 PGPVLPDIWEAPLSSGTAGAEASTVQLETSQLTGFTVTTASTYENVKAEKPLVQEAYN 642
Db 61 PGPVLPDIWEAPLSSGTAGAEASTVQLETSQLTGFTVTTASTYENVKAEKPLVQEAYN 120
QY 643 VAL-KALGKKEGI--KEPESFNAVQETEAAPYISACDLIKETKLTSE-PSPDFSNYSE 697
Db 121 MELTQAEAKBELTLKADRESSTSPEDLETPIYISACDLIKETKVSGESASPLTDYST 180
QY 698 IAKFE---KSVPEHAELVDDSPSEPDVDFSDDSIPEVP--QTOBEAVMLKESLTVS 752
Db 181 TPTTEHLSQDVSEHKELAELKSPQFGKCLDFSRQVMPDFGKESEDQTLILNGKSVENIE 240
QY 753 ETVAQKERRLASPOLKPKYLESFOPNLHSTKDAASN-DIPT---LTKKEKISLOWEE 808
Db 241 ---TDEQERLVDLSLAATGPKYLESFQDELSDSKIVTTQPSFTPAKIAKAKIPLWEE 297
QY 809 FNTAIVNDLLSSKEDKIKESFTSDSPIETIDFPTTFVSAKDSPKLAKETDLEVS 868
Db 298 LNALAYST-DVSVAMEPKGDSKGLSPSPVSVEDDFVMLVPKCTEFVA-EVTDRETV 355
QY 869 DKSE---IAN-IQSGADSLPCLELPCDLSPFKNIYPK--DEVH-----VSDSEFSENK 914
Db 356 HKNESKDISNEIRDEKRAPLTELPCLDSVRNVKVTEDDAHALKKSLQAIQDREVPE--- 412
QY 915 SVSKASISFNVSALEPQTEMGSIKSLITKAEKLPDTEKEDRSLSAVLSAELSKT 974

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Db 413 -VSMVSLPATGSPSTEKEIVSGKPEAFKEAERGAAAKEKE--KPTAVFSAKLNV 469
QY 975 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFISVSTAYIALALLSVTISFRIYKGVIOA 1034
Db 470 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFISVSTAYIALALLSVTISFRIYKGVIOA 529
QY 1035 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDVLSLKFV 1094
Db 530 IQKSDGHPFRAYLESDVAVSEELIQKYSVVVLGHINGTVKELRRFLVDDVLSLKFV 589
QY 1095 LMWFTYVGVGALFNGLTLLIILALISLFSPIVYERHOVIDHYLGLANKSVKDMAKIOAK 1154
Db 590 LMWFTYVGVGALFNGLTLLIILALISLFSPIVYERHOVIDHYLGLANKSVKDMAKIOAK 649
QY 1155 IPGLKRRAD 1163
Db 650 IPGLARKTE 658

RESULT 11
Q6JRV0
ID Q6JRV0 PRELIMINARY; PRT; 1043 AA.
AC Q6JRV0;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE RTN4.1-A1.
GN Name:RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RA Tissue=Wholemount embryos;
RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis";
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AY316197; AAQ82646.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1043 AA; 113994 MW; 6AF170C14DD2CB1A CRC64;

Query Match 27.7%; Score 1620; DB 2; Length 1043;
Best Local Similarity 37.2%; Pred. No. 4.4e-51;
Matches 464; Conservative 153; Mismatches 337; Indels 292; Gaps 45;

QY 5 DOSSLVSSSTDSPPPPPA-----FKYQFVTEPEDEDEEE 41
Db 3 EOSPDISSSHSGDERREPAQGERKPDLDVLDLTGAGQFQSPFGSGHPARDIEEE 62
QY 42 EDEEDEDDELELEVLERKPAAGLSAAVPPAAAAAPLLDFSDSDVPPAP----RGPLPAA 97
Db 63 EDEEERGANW-----DSLESPVSEEPGSDSI 91
QY 98 PPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDEPPAPPPPPPPAGASPLAEPAP 157
Db 92 SPVSP-----HSPAVP-----SAPMESEPP 112
QY 158 PSTPAAPKRGSGVDETLFPALPAASEPVISSAEKIMDLMEQNGTVSSGGEDRPSVLL 217
Db 113 PAPCTAP-----SGVDENLFTLPAASAHLMHASDKIM-----EPYSTVSTGQEEFASVLL 164
QY 218 ETAASLPSLPSLSTVSFKHEGYLGNLSAVSSSEGTIEETLNFEASKELPERATNPFVNRDL 277
Db 165 QSTASLSSLSLSTLSDSSKEH-----AETVAFPTGLAATEALQEPDNDM----- 208

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QY 278 AEFSELEYSEMSSFKGSPKGSAILVENTKEVIVRSKDKEDLVCSAALHSP--QESPV 335
DB 209 -----SVSRITSHLPLSDNLESKAL-DQVKEVIFSEK-----GYVDHPTSQQETI 254
QY 336 GKEDRVVPEKTMDFNEMQMSVAP-----VREEYADPKFP-----EQAWEVK 380
DB 255 SEEHAKLYSQSAKEMFSGMLQSVAPPHEEFTDIKEVYDVPYDFKPFMSKSGDVGVEYSD 314
QY 381 TYEGSRDVLAAANVESKVDKCLDSLEOKSLGKDSGRNEDASFPPTPEVKDSSRAY 440
DB 315 VAE-KFQVDVGRNLNESAOKHE-----EKSSEMEIDSISDDIS-PLTPELLPD----- 361
QY 441 ITCASGTSATESTANTPFLLED-----HTSENKTKDEKKIEERKAQIITEKTS--- 488
DB 362 -----STDYDMFATVEQNIPIFSFGGHVAGNKTDEKKIEDIEAQ-----KTSVGF 406
QY 489 ---PKTSNPFL-VAVQDSEADYTTDTLSKVTEAASNMPGLTDPDLVQACESELNAT 544
DB 407 GLKVATVNPFFYNESAQESB--YVTTTHVATH-----VSTKEGPTPDIVQEAVERSEAYDTG 459
QY 545 GTKIAYETKVDLVOT-SEAIQESLYPTAQLCPSPFEAEATPSVLPDIMEAPLNSLLPS 603
DB 460 IPKQYESNIDLVTQAANSVQEKVSPTAQAPARLEETDSVSPVLPDIMEAPLASALET 519
QY 604 AGASVQPSVSPLEAPPVSVYSIKLEPENPPPYEEAMNVALK-----AL-GTKEGIKE 656
DB 520 V---ALKPDISVGIKPARVEKTKAEPEKPPSYEEATEVLQNDLAAALGSGKQ--- 573
QY 657 PESFNAVQETBAPYISACDLIKETKLTSTEPSDFSNYSIEAKPEKSPVPHAEIATEDSS 716
DB 574 ----AVVEETETPVISACDLIKGTESVAGTFEFSLKQ-NBPESQFMPS---DESS 624
QY 717 PESEPVDLFSDSDIIEVQ-----TOEAVMLKESLTVESVTAQHK-----EERLSASP 767
DB 625 PDSE-----CSEPSYQWDSVEVQKEAFSIKTESVNAQSIIPPEQKQVFDQKSEESSP 677
QY 768 QELGKPYLESFOPNI---HSTKDAASNDIPTLTKEKISLOWEBENTAIYNSDDLLSSKE 824
DB 678 ---SKYLDSTQPEICVSKATSDLFAGLITLLQEK--PLOMEELDEGL-SLEKIPCTKY 731
QY 825 DKIKESFTSDSSPIEIIIEFPTFVSADKSPKAKYETDLEVSQKSIANIQSGADSLP 884
DB 732 SPVSES---PEPRSPVPEDLSSKLGDIQKEVLIQAKPEDKVKQRNLDFFPENIEFTP 788
QY 885 CLELPDCLSPKNIYPKDEVHVSDEFSENRSVSKASISPSNVSALEPOTENGSIY----- 939
DB 789 AVQKPPDD-----SGKAVSDTF-----GGLDTTITKGSVAHVYKV 822
QY 940 -KSKSLTKEAB-KKLPSTDEKEDRSLSAVLSAELSSTSVVDLLYWRDILKKTGVVFGASLF 997
DB 823 DKPKPESKEDDGSKUP-----KESKASTVSSSDF-MNSVVDLITYWRDILKRSVWFGASLF 877
QY 998 LLLSLTVFSIVSVTAIALALLSVTISFRYKGVIAQIKSDGEGHPFRAYLESEVAISEE 1057
DB 878 LLLSLSVFSIVSVLAVIALALLSVTISLRYKGIILQAIQKSEGHPPFSILESNLAVED 937
QY 1058 LVQKYSNAGLHVNSITIELRLFLVDDLVDSLKFAVLMWVFTYVGLFNGLITLLIALI 1117
DB 938 LVQKYNALVHNVCTVKELRHLFLVEDLVDSLKFAVLMWVFTYVGLFNGLITLLIALI 997
QY 1118 SLFSPVLYERHVOVDHYGLANKSVKDMAKIOAKIPGLKRRK 1163
DB 998 SLFSPVLYERHVOVDHYGLANKSVKDSLTSLILSKVPGLKRRKAE 1043

RESULT 12
Q6JRV1
ID Q6JRV1 PRELIMINARY; PRT; 1055 AA.
AC Q6JRV1;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
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DE RTN4.1-A2.
OS Name=RTN4;
GN Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus;
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=wholemount embryos;
RX PubMed=1501938; DOI=10.1016/j.mcn.2003.09.021;
RA Klingner M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrasch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis";
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AY316196; AAQ82645.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1055 AA; 115426 MW; F583A19F9BA51EDF CRC64;

Query Match 27.6%; Score 1616; DB 2; Length 1055;
Best Local Similarity 37.4%; Pred. No. 6.2e-51;
Matches 467; Conservative 153; Mismatches 345; Indels 282; Gaps 46;

QY 5 DQSLVSSSTDSPPRPPA-----FKYQVTEPEDEDEEEE 41
DB 3 EQSPDISSSHSGDRREPAQFGERKPMDDLDVLDLTGGAGQFSQFSGSHPARDIBEE 62
QY 42 EDEEDD---BDLSEVLERKPAAGLSAAVPPAAAPLDDFSSDSVPP-APRGP-LPA 96
DB 63 EDEEERGAKWKSLEPSPVEEPP-----SIDSLSPVSPHSPAVPS 103
QY 97 APPAAPQRQSPWERSAPAPSLPAAAVLPSKLPEDDPPPPPPPPAGASPLAEPAA 156
DB 104 APMEEPERPPA-----PCTAPSGSVAFTFLARLPEE----- 135
QY 157 PPSTPAAPKRGSGSVDETLFALPAASEPVPSSABKIMDLMEQPGNTVSSGOEDFPVSL 216
DB 136 -----DENLFTLPAASAHLMHASDKIM----BPYSTVSTGQEEFASVL 175
QY 217 LETASLSPLSTVSKRHGYLNLGNSAVSSSGTIBETLNEASKELPERATNPFVNRD 276
DB 176 LQSTASLSLSPSLSTDSKEH-----ATVAPPTGLAATEALQEBTDNMY----- 220
QY 277 LAEFSELEYSEMSSFKGSPKGSAILVENTKEVIVRSKDKEDLVCSAALHSP--QESP 334
DB 221 -----SVSRITSHLPLSDNLESKAL-DQVKEVIFSEK-----GYVDHPTSQQET 265
QY 335 VGKEDRVVPEKTMDFNEMQMSVAP-----VREEYADPKFP-----EQAWEVK 379
DB 266 ISEEHAKLYSQSAKEMFSGMLQSVAPPHEEFTDIKEVYDVPYDFKPFMSKSGDVGVEVS 325
QY 380 DTYESGRDVLAAANVESKVDKCLDSLEOKSLGKDSGRNEDASFPPTPEVKDSSRA 439
DB 326 DVAE-KFQVDVGRNLNESAOKHE-----EKSSEMEIDSISDDIS-PLTPELLPD----- 373
QY 440 YITCASGTSATESTANTPFLLED-----HTSENKTKDEKKIEERKAQIITEKTS--- 488
DB 374 -----STDYDMFATVEQNIPIFSFGGHVAGNKTDEKKIEDIEAQ-----KTSVGF 417
QY 489 ---PKTSNPFL-VAVQDSEADYTTDTLSKVTEAASNMPGLTDPDLVQACESELNAT 543
DB 418 FGLKVATVNPFFYNESAQESB--YVTTTHVATH-----VSTKEGPTPDIVQEAVERSEAYDT 470
QY 544 GTKIAYETKVDLVOT-SEAIQESLYPTAQLCPSPFEAEATPSVLPDIMEAPLNSLLP 602
DB 471 GIPKQKYESNIDLVTQAANSVQEKVSPTAQAPARLEETDSVSPVLPDIMEAPLASALE 530
QY 603 SAGASVQPSVSPLEAPPVSVYSIKLEPENPPPYEEAMNVALK-----AL-GTKEGIK 655
DB 603 SAGASVQPSVSPLEAPPVSVYSIKLEPENPPPYEEAMNVALK-----AL-GTKEGIK 655
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Db 531 TV---ALKPDIPVGIKPARVEKTKAEPEKPPSYEEAVTEVLQNDLAAALGGSKQG-- 585

QY 656 EPESFNAVOETAPYISACDLIKETKLTSTEPSDFSNYSIEIAKEKSVPEHAEIIVDS 715

Db 586 -----AVVEETETPYISACDLIKGTESVAGFTFESKLQ-NEPESQFMEPS---DES 635

QY 716 SPSESEPVDFSDSIPEVQ-----TOEAVMLMKESLTVSETVAHK-----EERLSAS 766

Db 636 SPDSE-----CSEPSYKQWDEVVOKAEFSIKTESVNAQSIITPEQKQVDFQKSEES 688

QY 767 POELGKPYLESFOPNI---HSTKDAASNDIPTLTKEKISLOWEENTAIYNSNDLLSSK 823

Db 689 P---SKSYLDSQPEICVSKATSDLFAKGLTTLQEK--PLQWEELDEGL-SLEKIPCTK 742

QY 824 EKIKESETFSOSSPIEIIIDEPFTFVSAKDDSPKLAKYTDLEVSKSIANIQSGADSL 883

Db 743 YSPVSES---PEPRPSVPVEDLSKGLDIQKEVLIAKPEDKVKQKRSNLDVFPENIET 799

QY 884 PCLELPCDLSFKNIYPKDEHVHVSDEFSENRSVSKASISPSNVSALEPOTEMGSIV--- 939

Db 800 PAVQKPPD-----SGKAVSDTF-----GGIDTTTKGSAVHEVK 833

QY 940 --KSKSLTKAE-KKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVFGASL 996

Db 834 VDKPKPSKEDDGSKL-----KESKASTVSSDF-MNSVVDLLIYWRDIKRSQVFGASL 888

QY 997 FLLSLTVSVSVTYAIYALALLSVTISPIRYKGVIOAIQKSDGHPFRAYLESEVAISE 1056

Db 889 FLLSLSVFSIVSLAYIALALLSVTISLRIYKGILOAIQKSEGHPPFRSILESNAVPE 948

QY 1057 ELVOKYSNAGLHVNSTIKELRFLVDDLVDSLKEAVLMWVFTYVYGALPNGLTLLILAL 1116

Db 949 DLVQKVCNVALHNVCTVKELRHLFLVEDLVSLKFAVLMWVFTYIYALPNGLTLLILAL 1008

QY 1117 ISLFSPIVIERHQVIDHYLGLANKSVKDAKIAKIPGLKRAK 1163

Db 1009 ISLFSPIVIERHQVDHYLALVNLKASTDLILSKVPLGKRAE 1055

RESULT 13

Q6JRV7 PRELIMINARY; PRT; 1032 AA.

AC O6JRV7; ID

DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DE RTN4.2-A1

GN Names=RTN4;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Wholount embryos;

RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;

RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von Hanwehr S.,

RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;

RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A

RT expression in Xenopus laevis.";

RL Mol. Cell. Neurosci. 25:205-216(2004).

RL EMBL; AY316190; AK82639.1; --

DR GO; GO:0005783; C:endoplasmic reticulum; IEA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 1032 AA; 113594 MW; 3C20F57B5A104E9F CRC64;

Query Match 27.3%; Score 1596.5; DB 2; Length 1032;  
 Best Local Similarity 37.5%; Pred. No. 3.1e-50;  
 Matches 465; Conservative 170; Mismatches 311; Indels 295; Gaps 54;

QY 6 QSSLYSSSDTSPPRP-----PAFKYQFVTEPEDEDEDEDEDED 47

Db 4 QSSDISSSHEPBDTKPWEDLDVLTGAGACGFTFPVSPAR-HMEEKSENEDEDED 62

QY 48 DEDLEE-LEVLERKPAAGLSAAAAPIILDFSSDSSVPPAPRGPLPAAPAPERPQ 106

Db 63 EKSWKESLE-----ASPYLE----- 77

QY 107 SWERSPAAPAPSLPAAAVLPSKLPEDEPPARPPPPPPAGASPLAEPAPSTPAAPKR 166

Db 78 ----DPGSTSGSSP-----TPHSPPSPAPSTPEERPPATCTAP-- 112

QY 167 RCGSGVDFTLPAAPSEBPVIPSAAEKIMDLMEQNGNTVSSQOEPPPSVLLTAASLPSL 226

Db 113 --SSSLDENLFLPAPASAHMLHSADKIM---EPSSTVSTQGEQFASVLLQSTASLSSL 166

QY 227 SPLSTVSKFEKGYLGNLSAVSSSEGTIBETLNEASKELPERATNPF-VNRDLAEFSELY 285

Db 167 PSLSS---KEH-----VQTVAFSTGL-----AANEALQEPDNTYSASRSLDITLTK- 211

QY 286 SEMSGSKGSPKGESAILVENTKEEVIKVRKDKEDLVCSAALHSP--QESPVKEDRVVS 343

Db 212 -----ALDQFKEEVIFSDK-----GYVVEHPTSQOETISEEHAKLY 247

QY 344 PEKTDWIDFNEQMOWVAVPVR-----EVADEKPF-----EQAMVEVKDITYEGSRDV 388

Db 248 SOSAKEMFSGMLQSVAPPHBEFTDIKEVDYQVDFKPFISSNSRDIGYEVKDVAE---KL 304

QY 389 LAARANVSKVDKRCLEDSLEQKSLGKDSSEGNEDASFPSTPEPVKDSRAYITCASFTS 448

Db 305 HVGRNLNLESTAKHE--EKSSBEKEM-----DISDDIS-PLTPEVLSDSTDYEMF----- 350

QY 449 ATRESTANTFP--LLEDHTSENKTDKIEERKAQIIIEKTS-----PKTSNPL-VAV 499

Db 351 ---ATVEHSYPSFSLGSRVAGNKTDEKKIEDFAQ---KTSVGFGLKVATVYPPYDESA 403

QY 500 QDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQACESELNEATGTCLAYETKVDLVOT 559

Db 404 QESE--YVTTG---ATRVQVSTKAGPTPDIVQAYEASEAYDTGISKLNYEPNDLVOT 457

QY 560 -SEAIQESLYPTAQLCPSEAEATPSVLPDIVMEAPLNSLLPSAGASVWQPSVPLRA 618

Db 458 AATSMQEKVSPTAQV-PALLE-DSVSSPVLDPVMEAPLASTL-CLETMALPKDISPVRI 514

QY 619 PPVSYDSIKLEPENPPPPPEEAMNVALKALG-----TKEGIKEPESFNAAQETEA 669

Db 515 EPPARDEKTKAEPEKPPSYEEAVTEVLQDQGPAAADLGDSKQG-----AVKKEAEA 566

QY 670 ----PVISIACDLIKETKLTSTEPSDFSNYSIEIAKEKSV--PEHAELVEDSPSESPVD 723

Db 567 PYISPIYIACDLIKGTQSA-----SDTFEFSKQHEFDSQWPESDSSPDSE--- 617

QY 724 LFSDDSIPEVPQTOBEAVNLMKESLTVSET-----VAQKKEERLSASPOE 769

Db 618 -----LSEPSYKQWDEVVOKAEFSIKTESVNAQSIITPEQKQVDFQKSE--SSP-- 666

QY 770 LQKPYLESFOPNLHSTK--DAASNDIPT-LTKKEKISLOWEENTAIYNSNDLLSKEDK 826

Db 667 -SKPYLASFPQPIYYSKATDLFAKGLDTEISIPQRHLHMEFDEGLYSS-KLPQSKYSP 724

QY 827 IKESETFSDSDSPIEII---DEPPTFVSAKDDSPKLAKYTDLEVSKSIANIQSGADSL 883

Db 725 VSESEPEFR-LSPPELTSKHEELQTHI-AGHPEDKLOXN-----KDKLDF----- 766

QY 884 PCLELPCDLSFKNIYPKDEHVHVSDEFSENRSVSKASISPSNVSALEPOTEMGSIVSKS 943

Db 767 ---LPENIEFTPIVQK-----ADDFGK-AASATHGGVDTTAKGASEVHEE--KVTKEPP 814

QY 944 LTKEAE-KKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSL 1002

Db 815 PSKDKDEVSKLP---KKESKAPSTVPFSSDFRNSVVDLIYWRDIKRSVGVFGASLFLLSL 871

QY 1003 TVFSIVSVTYAIYALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKY 1062

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Db 872 SVFVSIVSLAYIALALLSVTISFRIYKGLVLAQKSEEGHPSRILESIALPDEWVQKH 931
Qy 1063 SNSALGHVNSTIKELRRLFLVDLVDLSKFAVLMVFTVVGALFNLGLTLLIALLISLPSI 1122
Db 932 CTVALNQVNRVTAELRRLFLVDLVDLSKFAVLMVFTVVGALFNLGLTLLIALLISLPSI 991
Qy 1123 PVIYERHQVQIDHYLGLANKSVKDMAKIQAIPGLKRXAD 1163
Db 992 PVIYERHQVQVHYLALINKNLKNTSDLLAKVPLGKRKSE 1032

RESULT 14
Q6JRV8 PRELIMINARY; PRT; 1044 AA.
AC Q6JRV8;
DT 05-JUL-2004 (TREMREL. 27, Created)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DT 05-JUL-2004 (TREMREL. 27, Last annotation update)
DE RTN4.2-A2.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Wholemount embryos;
RX PubMed15019938; DOI=10.1016/j.j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis";
RL Mol. Cell. Neurosci. 25:205-216 (2004).
DR EMBL; AY316189; AAQ82638.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon.1.
DR PROSITE; PS50845; RETICULON.1.
SQ SEQUENCE 1044 AA; 115088 MW; 34FB48351A6C9888 CRC64;

Query Match 27.1%; Score 1586.5; DB 2; Length 1044;
Best Local Similarity 37.4%; Pred. No. 7.3e-50;
Matches 465; Conservative 171; Mismatches 320; Indels 287; Gaps 54;

Qy 6 QSSVSSSTDSPPRP-----PAFYQVFT-----EPEDDEDEEERDE 44
Db 4 QSSDISSHEPGDTKPWEDDDVLDLTGGAGQFSPTFPVSPARHMEKEEENEDEE 63
Qy 45 EDDDELELEVLKPAAGLSAAVPPAAAPLDDFSSDVPAPRGLPAPAPAPER 104
Db 64 KSWKESLASPVLE-----DQGST-----GSSPTPHSP--PEFSAPTEEP 104
Qy 105 QPSWERSPAAPAPLPPAAAVLPSKLPDDEPPARPPPPPPAGASPLAEPAPSTPAAP 164
Db 105 PPA-----TCTAPSSSLATVYLAQLRKE----- 128
Qy 165 KRGGSGVDETLFALPAASEVPVPSAEEKINDLMEQONTVSSQGDPPSVLLETAASLP 224
Db 129 -----DENLFLPAASAHMLHLSADKIM-----EPSSTVSTGQEDFASVLLQSTASLS 176
Qy 225 SLSPLSVTSFKHGHYGLNLSAVSSSEGTIEETLNEASKELPERATNPF--VNRDLAEFSEL 283
Db 177 SLPLSSS---KEH-----VQVAFSTGL-----AANEALQPTDNTYTSRSLDTLET 222
Qy 284 EYSEMGSSFGKSPKGESAILVENTKERVIVRSKOKEDLVCSAALHSP--QESPVGKEDRV 341
Db 223 K-----ALDQFKEEIVFSDK-----GVVHEHPTSQETISEEHAK 257
Qy 342 VSPKTMDFINEMQMSVAVPRE-----EYADFPP-----EQAMVVKDTYEGSR 386
Db 258 LYSQSAKEMFSGMLQSVAPPHEEFTDIKEVDYQYVDFKPFISNSRDIIGYEVKDAE--- 314
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Qy 387 DVLAARANVESKVRKCLLEDLSLEOKSLGKDSGRNEDASFSTPEPVKDSRAYITCASFP 446
Db 315 KLHVRGLMDESTAKHE--EKSEEEKEM-----DISDIS--PLTPEVLSOSTDYEMP----- 362
Qy 447 TSATSTTANTPP--LLEDHTSENKTDKKEKKAQIITEKTS-----PKTSPPFL-V 497
Db 363 -----ATVESHSPYFSLGSRVAGNKTDEKKTIEDPEAQ-----KTSVGFGLKVATVNPFFYDE 413
Qy 498 AVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEBACESELNATGKIAYETKVDIV 557
Db 414 SAQSESE--YVTTG-----ATRVQVSTKAEQTPDIVQEAYESAYDTGISKLYEPNIDIV 467
Qy 558 QT-SEAIQESLVPQAOLCPSFEERATPSVLPDITVMEAPLNSLPSAGASVQVQSVSPL 616
Db 468 QTAATSMQEKVSPTAQV--PALLE--DSVSSPVLDPVMEAPLASTL--CLETMALKEPDISV 524
Qy 617 EAPPVSVYSIKLEPPNPPPYEEAMNVALKALG-----TKEGIKEPESFNAVQBT 667
Db 525 RIEPPARDEKTKARPEKPPSYEEAVTEVLQDQGPAAADLGDGSKQ-----AVVKEA 576
Qy 668 EA-----PVISACDLIKETKLTSTPSPDFSNYSYSEIAKFEKV--PEHAELVEDSSPESP 721
Db 577 EAPVISPYSIACDLIKGTQAAA-----SDTFEFSKFEQHEFDSQFMEPSDESSPDS- 629
Qy 722 VDLFSDDSIPVVPQTOBEAVMLKESLTVSET-----VAQHKERLSASP 767
Db 630 -----LSEPSYKQWDSVVRKETFTIKTESMAQSFVPEQKPGIDQKSE--SSP 678
Qy 768 QELGKPYLESQPNLHSTK--DAASNDIPT--LTKKEKISLOWEEFNATYISNDLLSSKE 824
Db 679 --SKPYLASFOPEIYVSKATDLFAKGLDTEISIPQERHLHMERFDEGLYSS--KLPGSKY 734
Qy 825 DKIKESETFSSSPEIIEI---DEPFTFVSAKODSPKLAKEYTDLDEVSKSEIANIQSGAD 881
Db 735 SPVSESEPEFR--LSPEELTSKHEEIQTHI--AKHPEDKLQKN-----KDKLDP----- 778
Qy 882 SLPCLELPCLDLSFKNIYPKDBVHVHSDPESENRSKVASISPSNVSALEPOTEMGSIKVS 941
Db 779 -----LPENIEFTPIVQK-----ADDPGK--AASATHGGVDTTAKGASEVHEE--KVTKP 824
Qy 942 KSLTKAEAF--KKLPSTDEKEDSLSAVLSAELSKTSVVDLLYWRDIKTKTGVVFGASLFLLL 1000
Db 825 EPPSKDESKVSKLP--KKESKAPSTVPSSDFRNSVDLIYWRDIKRSVGVFGASLFLLL 881
Qy 1001 SLTVFSIVSVTAYIALALLSVTISFRIYKGLVLAQKSEEGHPSRILESIALPDEWVQ 1060
Db 882 SLVSFISVSLAYIALALLSVTISFRIYKGLVLAQKSEEGHPSRILESIALPDEWVQ 941
Qy 1061 KYSNSALGHVNSTIKELRRLFLVDLVDLSKFAVLMVFTVVGALFNLGLTLLIALLISLIF 1120
Db 942 KHCTVALNQVNRVTAELRRLFLVDLVDLSKFAVLMVFTVVGALFNLGLTLLIALLISLIF 1120
Qy 1121 SIPVYERHQVQIDHYLGLANKSVKDMAKIQAIPGLKRXAD 1163
Db 1002 SIPVYERHQVQVHYLALINKNLKNTSDLLAKVPLGKRKSE 1044

RESULT 15
Q6JRV2 PRELIMINARY; PRT; 1024 AA.
AC Q6JRV2;
DT 05-JUL-2004 (TREMREL. 27, Created)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DT 05-JUL-2004 (TREMREL. 27, Last annotation update)
DE RTN4.1-A3.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 5.68322 Seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKREKAD 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	679	73.4	208	2 I60904	neuroendocrine-spe
2	679	73.4	776	2 A46583	neuroendocrine-spe
3	665	71.9	267	2 A60021	tropomyosin-relate
4	321	34.7	2484	2 T26216	hypothetical prote
5	321	34.7	2607	2 T26215	hypothetical prote
6	320	34.6	222	2 T26213	hypothetical prote
7	194	21.0	255	2 B84899	hypothetical prote
8	182	19.7	271	2 T13013	hypothetical prote
9	163	17.6	275	2 T05595	hypothetical prote
10	142	15.4	393	2 S67763	probable membrane
11	135.5	14.6	242	2 B85016	hypothetical prote
12	134	14.5	183	2 A84527	hypothetical prote
13	131.5	14.2	295	2 S59439	probable membrane
14	123	13.3	206	2 T01153	probable seed matu
15	109.5	11.8	264	2 T47948	hypothetical prote
16	107.5	11.6	203	2 T47571	hypothetical prote
17	94	10.2	288	2 B90043	conserved hypothet
18	93.5	10.1	457	2 H85095	hypothetical prote
19	92.5	10.0	458	2 A72258	hypothetical prote
20	92.5	10.0	677	2 F95232	immunity protein,
21	92.5	10.0	680	2 H98096	conserved hypothet
22	91	9.8	160	2 T28422	hypothetical prote
23	90.5	9.8	442	2 C75057	hypothetical prote
24	89	9.6	224	2 D71915	hydrogenase, cytoc
25	89	9.6	468	2 A38223	nicotinic acetylch
26	87	9.4	1065	2 E89795	acriflavin resista
27	86	9.3	589	2 F84201	transport ATP-bind
28	86	9.3	1055	2 H90023	hypothetical prote
29	85.5	9.2	296	2 S46018	probable membrane

30	85.5	9.2	299	2 B69155	hypothetical prote
31	85	9.2	299	2 C64397	hypothetical prote
32	85	9.2	459	2 G86264	F3F19 hypothetical
33	85	9.2	689	2 T09007	ABC-transporter ho
34	84.5	9.1	151	2 G96705	unknown protein, 7
35	83.5	9.0	445	2 A02358	glucosyltransferas
36	83.5	9.0	570	2 S52765	secB protein - Str
37	83.5	9.0	823	2 H83724	hypothetical prote
38	83	9.0	180	2 E97200	probable phosphata
39	83	9.0	252	2 G97886	hypothetical prote
40	83	9.0	388	1 D70006	conserved hypothet
41	82.5	8.9	410	2 A95044	conserved hypothet
42	82.5	8.9	502	2 F70316	conserved hypothet
43	82.5	8.9	675	2 T50332	STC1 homolog SPBC1
44	82.5	8.9	937	2 T41400	probable peroxisom
45	82	8.9	224	1 A64599	hydrogenase (EC 1.

ALIGNMENTS

RESULT 1

I60904

neuroendocrine-specific protein C - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: I60904

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: I60904

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-208 <RES>

A:Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 73.4%; Score 679; DB 2; Length 208;

Best Local Similarity 67.9%; Pred. No. 3.6e-52;

Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

Qy	3	VDLLYWRDIKKTGVVFCASLFLLLSLTVFSTVSVTAVIALLLSVTISFRYKGVQIAIQ	62
Db	22	IDLLYWRDIKQTGIVFGSFLLLSFLTQFVSVVAYLALAAALSATISFRYKSVLQAVQ	81
Qy	63	KSDGHPFRAYLSEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDLVDLSLKFAVLM	122
Db	82	KTDSGHPFKAYLEILEITLSQEQIQKYDCLQFYVNSTLKELRRLFLVDLVDLSLKFAVLM	141
Qy	123	WVFYVGALENGLLTLLILALISLPSIPVYERHQVDHYGLANKSVKDMAKIQAKIP	182
Db	142	WLLTYVGALENGLLTLLMAVSMETLPVYVYHQVDQYGLVTRTHNAVVAQIKAKIP	201
Qy	183	GLKREKAD	189
Db	202	GAKRHAE	208

RESULT 2

A46583

neuroendocrine-specific protein, splice form A - human

N:Contains: neuroendocrine-specific protein, splice form B

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762







RESULT 7  
 E84899  
 hypothetical protein At2g46170 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: E84899  
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shes, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: E84899  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-255 <STO>  
 A:Cross-references: UNIPROT:O82352; GB:AE002093; NID:G3702332; PIDN:AAC62889.1; GSPDB:GN  
 C:Genetics:  
 A:Gene: At2g46170  
 A:Map position: 2  
 Query Match 21.0%; Score 194; DB 2; Length 255;  
 Best Local Similarity 27.6%; Pred. No. 1.2e-09;

A;Map position: 4  
A;Introns: 89/1; 149/2; 196/3; 220/1  
A;Note: F9D16.100



Search completed: June 16, 2005, 13:31:51  
Job time : 7.68322 secs.

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 27.2927 Seconds  
(without alignments)  
2678.292 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKTKGVVFGA.....VKDAMAKIQAKIPGLKRRAD 189.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	925	100.0	361	3	AAY71385	Aay71385 Alternati
2	925	100.0	1163	3	AAY71310	Aay71310 Rat neuro
3	925	100.0	1163	3	AAY71384	Aay71384 Alternati
4	925	100.0	1163	5	ABB81074	Abb81074 Rat neuro
5	925	100.0	1163	8	ADO26399	Ado26399 Rat trunc
6	925	100.0	1163	8	ADP45572	Adp45572 Rat NogoA
7	922	99.7	379	7	ADB85283	Adb85283 Rat foocoe
8	921	99.6	199	5	ABB81077	Abb81077 Rat neuro
9	921	99.6	360	3	AAY71383	Aay71383 Rat neuro
10	921	99.6	360	5	ABB81076	Abb81076 Rat neuro
11	921	99.6	522	3	AAY71312	Aay71312 Rat neuro
12	919	99.4	199	3	AAY71559	Aay71559 Rat Nogo
13	919	99.4	359	3	AAY71558	Aay71558 Rat Nogo
14	919	99.4	403	3	AAY71563	Aay71563 Rat Nogo
15	919	99.4	1162	3	AAY71557	Aay71557 Rat Nogo
16	917	99.1	1162	8	ADT89537	Adt89537 Mus muscu
17	908	98.2	893	3	AAY95012	Aay95012 Human sec
18	908	98.2	983	6	ABU11573	Abu11573 Human MDD
19	908	98.2	1178	3	AAY71311	Aay71311 Human neu-
20	908	98.2	1192	3	AAY56967	Aay56967 Human MAG
21	908	98.2	1192	4	ABB82349	Abb82349 Human NOG
22	908	98.2	1192	4	AAU04591	Aau04591 Human NOG
23	908	98.2	1192	5	ABG30938	Abg30938 Human Nog
24	908	98.2	1192	5	ABP68600	Abp68600 Human pan
25	908	98.2	1192	5	ABB81078	Abb81078 Human neu

#### ALIGNMENTS

##### RESULT 1

AAY71385  
ID AAY71385 standard; protein; 361 AA.

XX AC AAY71385;

DT 02-NOV-2000 (first entry)

DE Alternative version of rat neurite growth inhibitor Nogo B.

XX Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.

XX Rattus sp.

PH Key Location/Qualifiers

FT Region 1. .172

FT /note= "Corresponds to amino acids 1-172 of Nogo A  
protein shown in AAY71310"

FT Inhibitory-site 1. .171

FT /note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30

FT /note= "Casein kinase II site"

FT Region 31. .58

FT /note= "Acidic region"

FT Region 173. .361

FT /note= "Corresponds to amino acids 975-1163 of Nogo A  
protein (AAY71310)"

FT Region 174. .361

FT /note= "This region is common to Nogo A, B and C  
isoforms"

FT Domain 186. .221

FT /label= Transmembrane domain

FT /note= "C-terminal hydrophobic region"

FT Modified-site 222

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 269. .271

FT /note= "Asn is N-glycosylated"

FT Modified-site 271

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 287

FT /note= "Protein kinase C (PKC) site"

FT Domain 288. .323

26	908	98.2	1192	6	ABR59667	AbR59667 Human Nog
27	908	98.2	1192	8	ADO08103	Ado08103 Human pol
28	908	98.2	1192	8	ADO26400	Ado26400 Human tru
29	908	98.2	1192	8	ADP45551	Adp45551 Human Nog
30	908	98.2	1192	8	ADP67234	Adp67234 Human Nog
31	908	98.2	1192	8	ADR13966	Adr13966 Human NOG
32	906.5	98.0	1163	8	ADO08105	Ado08105 Mouse pol
33	905	97.8	200	4	AAAB64514	Aab64514 Human sec
34	904	97.7	199	2	AAW53947	Aaw53947 Human NSP
35	904	97.7	199	2	AAW78313	Aaw78313 Fragment
36	904	97.7	199	3	AAAB12805	Aab12805 Human NSP
37	904	97.7	199	4	AAAB82348	Aab82348 Human NOG
38	904	97.7	199	5	ABB81080	Abb81080 Human neu
39	904	97.7	199	8	ADP67236	Adp67236 Human NOG
40	904	97.7	373	3	AAV53624	Aay53624 A bone ma
41	904	97.7	373	3	AAV56969	Aay56969 Human MAG
42	904	97.7	373	3	AAAB24242	Aab24242 Human NOG
43	904	97.7	373	4	AAAB82350	Aab82350 Human NOG
44	904	97.7	373	5	AAAM47954	Aam47954 Human RTN
45	904	97.7	373	5	ABG30937	Abg30937 Human Nog

FT FT /label= Transmembrane domain  
 FT FT /note= "C-terminal hydrophobic region"  
 FT FT 339..341  
 FT FT Modified-site  
 FT FT /note= "Asn is N-glycosylated"  
 FT FT 341  
 FT FT Modified-site  
 FT FT /note= "Protein kinase C (PKC) site"  
 FT FT  
 XX WO2000312335-A2.  
 PN  
 XX  
 XX 02-JUN-2000.  
 XX  
 XX 05-NOV-1999; 99WO-US026160.  
 XX  
 XX 06-NOV-1998; 98US-0107446P.  
 PR  
 XX  
 XX (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 PA  
 XX  
 XX Schwab ME, Chen MS;  
 PI  
 XX WPI; 2000-400052/34.  
 XX  
 XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 XX of the central nervous system and inducing regeneration of neurons.  
 PT  
 PT  
 XX  
 PS Claim 4; Page; 122pp; English.  
 XX  
 CC The present sequence is an alternative version of rat Nogo B protein  
 CC which is a potent neural cell growth inhibitor and is free of all central  
 CC nervous system (CNS) myelin material with which it is native  
 CC associated. The Nogo B transcript arises as a result of alternative  
 CC splicing of Nogo gene. Nogo proteins and fragments displaying neurite  
 CC growth inhibitory activity are used in the treatment of neoplastic  
 CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,  
 CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic  
 CC neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma  
 CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's  
 CC diseases. Therapeutics which promote Nogo activity can be used to treat  
 CC or prevent hyperproliferative or benign dysproliferative disorders e.g.  
 CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic  
 CC acids can be used to inhibit production of Nogo protein to induce  
 CC regeneration of neurons or to promote structural plasticity of the CNS in  
 CC disorders where neurite growth, regeneration or maintenance are deficient  
 CC or desired. The animal models can be used in diagnostic and screening  
 CC methods for predisposition to disorders and to screen for or test  
 CC molecules which can treat or prevent disorders or diseases of the CNS.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from Nogo A protein sequence (AAV71310) and corresponds to  
 CC residues 1-172 fused to 975-1163 of Nogo A. This sequence is an  
 CC alternative version of the Nogo B sequence (see AAV71383) described in  
 CC the specification as being residues 1-172 fused to C-terminal 188 amino  
 CC acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in  
 CC claim 32 and SEQ ID NO: 29 in disclosure of the specification. However  
 CC the specification does not include sequences for these SEQ ID numbers  
 XX  
 SQ Sequence 361 AA;  
 Query Match 100.0%; Score 925; DB 3; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-90;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTIFRIYKGVIOA 60  
 DB 173 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTIFRIYKGVIOA 232  
 QY 61 IOKSDSGHPFRAYLESEVAISELVOKYSNALSALGHVNSTIKELRRFLVDLVDLSLKFAV 120  
 DB 233 IOKSDSGHPFRAYLESEVAISELVOKYSNALSALGHVNSTIKELRRFLVDLVDLSLKFAV 292  
 QY 121 LMWFTYVVGALFNGLLTLLIALISLFSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 180  
 DB 293 LMWFTYVVGALFNGLLTLLIALISLFSIPVIYERHQVQIDHYGLANKSVKDMAKIOAK 352

QY 181 IFGLKRRKAD 189  
 DB 353 IFGLKRRKAD 361  
 RESULT 2  
 AAY71310  
 ID AAY71310 standard; protein; 1163 AA.  
 XX  
 XX AAY71310;  
 AC  
 XX 02-NOV-2000 (first entry)  
 DT  
 XX Rat neurite growth inhibitor Nogo A.  
 DE  
 XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening.  
 XX  
 XX Rattus sp.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Inhibitory-site 1..171  
 FT /note= "Inhibits NIH 3T3 fibroblast spreading"  
 FT Modified-site 30  
 FT /note= "Casein kinase II site"  
 FT Region 31..58  
 FT /note= "Acidic region"  
 FT Region 31..57  
 FT /note= "Region specifically described in claim 16"  
 FT Region 172..259  
 FT /note= "This region is not essential for inhibitory activity"  
 FT Modified-site 233  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 242..244  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 291  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 295  
 FT /note= "Protein kinase C (PKC) site"  
 FT Misc-difference 404  
 FT /note= "Encoded by TTC"  
 FT Modified-site 436  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 468..470  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 484  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 488  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 502  
 FT /note= "Casein kinase II site"  
 FT Inhibitory-site 542..722  
 FT Modified-site 576  
 FT /note= "Casein kinase II site"  
 FT Peptide 623..640  
 FT /note= "used as immunogen to generate antibody AS 472"  
 FT Modified-site 626  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 694..696  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 715  
 FT /note= "Casein kinase II site"  
 FT Peptide 762..1163  
 FT /note= "used as immunogen to generate antibody AS Bruna"  
 FT Modified-site 784  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 821

FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 850  
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 FT 855  
 FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 863  
 FT Modified-site /note= "Casein kinase II site"  
 FT 868  
 FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 893  
 FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 912. .914  
 FT Modified-site /note= "Asn is N-glycosylated"  
 FT 925. .927  
 FT Modified-site /note= "Asn is N-glycosylated"  
 FT 954  
 FT Modified-site /note= "PKC and casein kinase II sites"  
 FT 956  
 FT Modified-site /note= "PKC and casein kinase II sites"  
 FT 975. .1162  
 FT Region /note= "This region is not essential for inhibitory activity"  
 FT 976. .1163  
 FT Region /note= "C-terminal common region found in Nogo A, B and C isoforms"  
 FT 988. .1023  
 FT Domain /label= Transmembrane domain  
 FT /note= "C-terminal hydrophobic region specifically described in claim 16"  
 FT 1024  
 FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 1071. .1073  
 FT Modified-site /note= "Asn is N-glycosylated"  
 FT 1073  
 FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 1089  
 FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 1090. .1125  
 FT Domain /label= Transmembrane domain  
 FT /note= "C-terminal hydrophobic region specifically described in claim 16"  
 FT 1141. .1143  
 FT Modified-site /note= "Asn is N-glycosylated"  
 FT 1143  
 FT Modified-site /note= "Protein kinase C (PKC) site"  
 FT 1143  
 FT PN WO200031235-A2.  
 FT XX  
 FT PD 02-JUN-2000.  
 FT XX  
 FT PF 05-NOV-1999; 99WO-US026160.  
 FT XX  
 FT PR 06-NOV-1998; 98US-0107446P.  
 FT XX  
 FT PA (SCHW/) SCHWAB M E.  
 FT (CHEN/) CHEN M S.  
 FT PA  
 FT PI Schwab ME, Chen MS;  
 FT XX  
 FT DR WPI; 2000-400052/34.  
 FT N-PSDB; AAD01173.  
 FT XX  
 FT PT Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.  
 FT XX  
 FT PS Claim 3; Fig 2A; 122pp; English.  
 FT XX  
 FT CC The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The protein was derived from a cDNA generated by fusing ROI8U37-3, R1-3U21 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins

CC and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence designated as SEQ ID NO: 2 is stated to be the same as the sequence shown in Fig. 13 (see AAY71384) of the specification. However, this sequence does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers  
 XX Sequence 1163 AA;  
 SQ  
 Query Match 100.0%; Score 925; DB 3; Length 1163;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-89;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SVDLLYWRDIKKTGVVFGASLFLLLSLTVPSIVSVTAYIALALLSVTISPIYKGVIOA 60  
 Db 975 SVDLLYWRDIKKTGVVFGASLFLLLSLTVPSIVSVTAYIALALLSVTISPIYKGVIOA 1034  
 Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDDLVSLKFAV 120  
 Db 1035 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDDLVSLKFAV 1094  
 Qy 121 LMWVFTYVGFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
 Db 1095 LMWVFTYVGFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1154  
 Qy 181 IPGLKRRKAD 189  
 Db 1155 IPGLKRRKAD 1163  
 RESULT 3  
 AAY71384  
 ID AAY71384 standard; protein; 1163 AA.  
 XX  
 AC AAY71384;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Alternative version of rat neurite growth inhibitor Nogo A.  
 XX  
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Inhibitory-site 1. .171  
 FT /note= "Inhibits NIH 3T3 fibroblast spreading"  
 FT Modified-site 30  
 FT /note= "Casein kinase II site"  
 FT Region 31. .58  
 FT /note= "Acidic region"  
 FT Region 172. .259





QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 DB 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034  
 QY 61 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAV 120  
 DB 1035 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAV 1094  
 QY 121 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYVLGLANKSVKDAMAKIOAK 180  
 DB 1095 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYVLGLANKSVKDAMAKIOAK 1154  
 QY 181 IPGLKRRKAD 189  
 DB 1155 IPGLKRRKAD 1163

RESULT 4  
 ID ABB81074 standard; protein; 1163 AA.  
 AC ABB81074;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Rat neurotransmitter receptor protein Nogo-A.  
 XX  
 KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnerability; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW neotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN US2002072493-A1.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 28-JUN-2001; 2001US-00893348.  
 XX  
 PR 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI Moalem G;  
 XX  
 XX WPI; 2002-607255/65.  
 DR N-PSDB; ABN86600.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX  
 PS Example 5; Page 44-47; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative

CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-artetitic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC to uraemia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polynuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen  
 XX  
 SQ Sequence 1163 AA;

Query Match 100.0%; Score 925; DB 5; Length 1163;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-89;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 DB 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034  
 QY 61 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAV 120  
 DB 1035 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAV 1094  
 QY 121 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYVLGLANKSVKDAMAKIOAK 180  
 DB 1095 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYVLGLANKSVKDAMAKIOAK 1154  
 QY 181 IPGLKRRKAD 189  
 DB 1155 IPGLKRRKAD 1163

RESULT 5  
 ADO26399  
 ID ADO26399 standard; protein; 1163 AA.  
 XX  
 AC ADO26399;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Rat truncated Nogo-A protein.  
 XX  
 XX rat; human; Nogo-A; truncated; affinity; membrane-bound protein.  
 XX Rattus sp.  
 OS  
 XX WO2004039836-A1.  
 PN  
 XX 13-MAY-2004.  
 PD  
 XX 31-OCT-2002; 2002WO-EP012210.  
 PF  
 XX 31-OCT-2002; 2002WO-EP012210.  
 PR  
 XX (PIER-) PIERIS PROTEOLAB AG.  
 PA  
 XX Skerra A, Fiedler M;  
 PI  
 XX WPI; 2004-376159/35.  
 DR  
 XX New isolated truncated Nogo-A polypeptide that corresponds to a truncated  
 PT form of the Nogo-A protein, useful for identifying a compound having  
 PT detectable affinity to a Nogo-A protein.

XX Claim 1; Fig 6A; 80pp; English.

XX The present invention relates to an isolated truncated Nogo-A polypeptide that corresponds to a truncated form of the Nogo-A protein from the rat and from the human. The truncated polypeptide is useful for identifying a compound having detectable affinity to a Nogo-A protein. The present sequence is a Nogo-A polypeptide of the invention.

XX Sequence 1163 AA;

Query Match 100.0%; Score 925; DB 8; Length 1163;  
Best Local Similarity 100.0%; Pred. No. 4.4e-89;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034

QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 1035 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

QY 121 LMWVFTYVGALFNLTLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAMAKIOAK 180  
Db 1095 LMWVFTYVGALFNLTLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAMAKIOAK 1154

QY 181 IPGLKREKAD 189  
Db 1155 IPGLKREKAD 1163

RESULT 6  
ADP45572  
ID ADP45572 standard; protein; 1163 AA.

XX ADP45572;

XX 09-SEP-2004 (first entry)

XX Rat NogoA protein SEQ ID NO:26.

XX binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;  
XX nerve repair; neuroprotective; gene therapy;  
XX central nervous system injury; CNS injury; neurodegenerative disorder;  
XX rat.

XX Rattus norvegicus.

XX WO2004052932-A2.

XX 24-JUN-2004.

XX 09-DEC-2003; 2003WO-EP013960.

XX 10-DEC-2002; 2002GB-00028832.

XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS PHARMA GMBH.  
XX (UYZU-) UNIV ZUERICH.

XX Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;  
XX Zurini M;

XX WPI; 2004-468818/44.  
XX N-PSDB; ADP45571.

XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.

XX Example 1; SEQ ID NO 26; 121pp; English.

CC The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents rat NogoA, which is used in the exemplification of the present invention.

XX Sequence 1163 AA;

Query Match 100.0%; Score 925; DB 8; Length 1163;  
Best Local Similarity 100.0%; Pred. No. 4.4e-89;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034

QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 1035 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

QY 121 LMWVFTYVGALFNLTLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAMAKIOAK 180  
Db 1095 LMWVFTYVGALFNLTLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDAMAKIOAK 1154

QY 181 IPGLKREKAD 189  
Db 1155 IPGLKREKAD 1163

RESULT 7  
ADB85283  
ID ADB85283 standard; protein; 379 AA.

XX ADB85283;

XX 04-DEC-2003 (first entry)

XX Rat foocen-m2 reticulon SEQ ID NO:164.

XX rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
XX transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
XX protease; enzyme; analgesic; gene therapy; pain; diabetes.

XX Rattus norvegicus.

XX EP1284297-A2.

XX 19-FEB-2003.

XX 26-JUL-2002; 2002EP-00255228.

XX 27-JUL-2001; 2001GB-00018354.  
XX 07-FEB-2002; 2002GB-00002880.

XX (WARN ) WARNER LAMBERT CO.

XX Brooksbank RA, Dixon AK, Lee K, Pincock RD;  
XX WPI; 2003-364994/35.  
XX N-PSDB; ADB85284.

XX Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.

XX Disclosure; Page 239-240; 256pp; English.

XX The invention relates to a novel isolated gene sequence that is down-  
 CC regulated in the spinal cord in response to streptozocin-induced  
 CC diabetes, or comprising, hybridising or having at least 80% sequence  
 CC identity to a sequence whose expression products are kinases,  
 CC phosphatases, ion channel proteins, receptors, transporters, G-protein  
 CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
 CC given in the specification. A gene of the invention has analgesic  
 CC activity, and may have a use in gene therapy. The gene sequences, vector,  
 CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a protein encoded by a gene of the  
 CC invention.

XX SQ Sequence 379 AA;

Query Match 99.7%; Score 922; DB 7; Length 379;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-89;  
 Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOA 60  
 Db :|||||  
 191 AVVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOA 250

Qy 61 IQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKPAV 120  
 Db :|||||  
 251 IQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKPAV 310

Qy 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHOVQIDHYLGLANKSVKDMAKIOAK 180  
 Db :|||||  
 311 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHOVQIDHYLGLANKSVKDMAKIOAK 370

Qy 181 IPGLKRRKAD 189  
 Db :|||||  
 371 IPGLKRRKAD 379

# RESULT 8

ABB81077  
 ID ABB81077 standard; protein; 199 AA.

XX AC ABB81077;

XX DT 05-NOV-2002 (first entry)

XX DE Rat neurotransmitter receptor protein Nogo-C.

XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnerability; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW neotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.

XX OS Rattus norvegicus.

XX FN US2002072493-A1.

XX PD 13-JUN-2002.

XX PF 28-JUN-2001; 2001US-00893348.

XX PR 19-MAY-1998; 98IL-00124500.

XX PR 21-JUL-1998; 98WO-US014715.

XX PR 22-DEC-1998; 98US-00218277.

XX PR 19-MAY-1999; 99US-00314161.

XX PA (YEDA ) YEDA RES & DEV CO LTD.

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR N-PSDB; ABN86600.

XX Promoting nerve regeneration and preventing neuronal degeneration in the  
 PS central/peripheral nervous system from injury/disease, comprises  
 CC administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.

XX Example 5; Page 48-49; 93pp; English.

XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or  
 CC damage caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia -  
 CC telangiectasia, Friedreich's ataxia, amyloid polynuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-C, an example of NS-specific  
 CC antigen

XX SQ Sequence 199 AA;

Query Match 99.6%; Score 921; DB 5; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.2e-89;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOAI 61  
 Db :|||||  
 12 VVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOAI 71

Qy 62 QKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKPAVL 121  
 Db :|||||  
 72 QKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKPAVL 131

Qy 122 MWFTYVYGALFNGLTLLILALISLFSIPVIYERHOVQIDHYLGLANKSVKDMAKIOAKI 181  
 Db :|||||  
 132 MWFTYVYGALFNGLTLLILALISLFSIPVIYERHOVQIDHYLGLANKSVKDMAKIOAKI 191

Qy 182 PGLKRRKAD 189  
 Db :|||||  
 192 PGLKRRKAD 199

# RESULT 9

AAAY71383

ID AAAY71383 standard; protein; 360 AA.

XX AC AAAY71383;

XX DT 02-NOV-2000 (first entry)



PA (YEDA ) YEDA RES & DEV CO LTD.  
XX PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
XX PI Moalem G;  
XX DR WPI; 2002-607255/65.  
XX DR N-P5DB; ABN86600.  
XX PT Promoting nerve regeneration and preventing neuronal degeneration in the  
XX PT central/peripheral nervous system from injury/disease, comprises  
XX PT administering nervous system-specific activated T cells/antigen, or  
XX PT analogs/peptides.  
XX PS Example 5; Page 47-48; 93pp; English.  
XX CC The invention relates to promoting nerve regeneration or conferring  
XX CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
XX CC central/peripheral nervous system (NS). The method involves administering  
XX CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
XX CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
XX CC combinations. The method is useful for promoting nerve regeneration and  
XX CC preventing neuronal degeneration in central/peripheral nervous system  
XX CC from injury/disease, where the injury is spinal cord injury, blunt  
XX CC trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or  
XX CC damages caused by surgery such as tumour excision. The disease is not an  
XX CC autoimmune disease or neoplasm. The disease results in a degenerative  
XX CC process occurring in either gray or white matter or both. The disease is  
XX CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
XX CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
XX CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
XX CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
XX CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
XX CC neuropathies associated with various diseases, including but not limited  
XX CC to uremia, porphyria, hypocalcemia, Sjogren Larsson syndrome, acute  
XX CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
XX CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
XX CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
XX CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
XX CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
XX CC telangiectasia, Friedreich's ataxia, amyloid polynuropathies,  
XX CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
XX CC disease, or lipoproteinemia. The present sequence represents the rat  
XX CC neurotransmitter receptor protein Nogo-B, an example of NS-specific  
XX CC antigen  
XX SQ Sequence 360 AA;  
Query Match 99.6%; Score 921; DB 5; Length 360;  
Best Local Similarity 100.0%; Pred. No. 2.6e-89;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAI 61  
Db 173 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAI 232  
QY 62 QKSDGHPFRAYLESEVAISELVOKYSNLSALGHVNSTIKELRRLFLVDDLVDLSLKPAVL 121  
Db 233 QKSDGHPFRAYLESEVAISELVOKYSNLSALGHVNSTIKELRRLFLVDDLVDLSLKPAVL 292  
QY 122 MWVFTYVGLFNGLLTLLALISLFSIPVIERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
Db 293 MWVFTYVGLFNGLLTLLALISLFSIPVIERHQVQIDHYLGLANKSVKDMAKIOAKI 352  
QY 182 PGLKPKAD 189  
Db 353 PGLKPKAD 360  
RESULT 11  
AA71312  
ID AA71312 standard; protein; 522 AA.  
XX AC  
XX AA71312;

XX 02-NOV-2000 (first entry)  
DT Rat neurite growth inhibitor Nogo C.  
DE  
XX Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.  
XX Rattus sp.  
XX OS  
XX FH Key Location/Qualifiers  
XX FT Region 1..39 /note= "Sequence upstream to the N-terminus of Nogo C  
XX FT protein"  
XX FT Misc-difference 3 /note= "Encoded by TAG"  
XX FT Region 11..191 /note= "Region specifically described in claim 16"  
XX FT Misc-difference 29 /note= "Encoded by TAA"  
XX FT Protein 40..238 /label= Nogo\_C\_protein  
XX FT Region 51..238 /note= "C-terminal common region found in Nogo A, B and C  
XX FT isoforms"  
XX FT Region 239..522 /note= "Sequence downstream to the C-terminus of Nogo C  
XX FT protein"  
XX FT Misc-difference 239 /note= "Encoded by TGA"  
XX FT Misc-difference 263 /note= "Encoded by TGA"  
XX FT Misc-difference 276 /note= "Encoded by TAG"  
XX FT Misc-difference 281 /note= "Encoded by TGA"  
XX FT Misc-difference 295 /note= "Encoded by TAA"  
XX FT Misc-difference 298 /note= "Encoded by TAA"  
XX FT Misc-difference 314 /note= "Encoded by TGA"  
XX FT Misc-difference 318 /note= "Encoded by TGA"  
XX FT Misc-difference 335 /note= "Encoded by TAG"  
XX FT Misc-difference 371 /note= "Encoded by TGA"  
XX FT Misc-difference 374 /note= "Encoded by TAG"  
XX FT Misc-difference 380 /note= "Encoded by TAA"  
XX FT Misc-difference 406 /note= "Encoded by TAA"  
XX FT Misc-difference 408 /note= "Encoded by TAG"  
XX FT Misc-difference 410 /note= "Encoded by TAA"  
XX FT Misc-difference 422 /note= "Encoded by TAA"  
XX FT Misc-difference 433 /note= "Encoded by TGA"  
XX FT Misc-difference 440 /note= "Encoded by TAG"  
XX FT Misc-difference 453 /note= "Encoded by TAG"  
XX FT Misc-difference 465 /note= "Encoded by TAG"  
XX FT



CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.  
 CC However, the specification does not include sequences for these SEQ ID  
 CC numbers  
 XX  
 SQ Sequence 199 AA;  
 Query Match 99.4%; Score 919; DB 3; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-89;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVVDLLYWRDIKKTGVFGASLFLLSLTFTVSIVSTAYIALLSVTISFRIYKGVIOA 60  
 DB 12 SVVDLLYWRDIKKTGVFGASLFLLSLTFTVSIVSTAYIALLSVTISFRIYKGVIOA 71  
 QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 120  
 DB 72 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 131  
 QY 121 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
 DB 132 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 191  
 QY 181 IPGLKRKA 188  
 DB 192 IPGLKRKA 199  
 RESULT 13  
 AAY71558  
 ID AAY71558 standard; protein; 359 AA.  
 XX  
 AC AAY71558;  
 XX  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat Nogo A protein fragment used in the construction of mutant Nogo-B.  
 XX  
 DE Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.  
 XX  
 OS Rattus sp.  
 XX  
 Key Location/Qualifiers  
 FH 1..171  
 FT Region /note= "Corresponds to residues 1-171 of rat Nogo A  
 FT protein shown in AAY71310"  
 FT Region 172..359  
 FT /note= "Corresponds to residues 975-1162 of rat Nogo A  
 FT protein shown in AAY71310"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PF 06-NOV-1998; 98US-0107446P.  
 XX  
 XX (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX WPI; 2000-400052/34.  
 DR  
 XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX

PS Example; Page; 122pp; English.  
 XX  
 CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is derived by fusing two fragments of rat Nogo A protein shown in  
 CC AAY71310. The fragment is used in the construction of mutant Nogo-B. The  
 CC mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +  
 CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory  
 CC sites of Nogo protein. Major inhibitory region was identified in the Nogo  
 CC A sequence from amino acids 172-974, particularly amino acids 542-722. In  
 CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3  
 CC fibroblast spreading. Note: The present sequence is not given in the  
 CC specification but is derived from rat Nogo A sequence shown in AAY71310.  
 CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in  
 CC disclosure of the specification. However, the specification does not  
 CC include sequences for these SEQ ID numbers  
 XX  
 SQ Sequence 359 AA;  
 Query Match 99.4%; Score 919; DB 3; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-89;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 172 SVVDLLYWRDIKKTGVFGASLFLLSLTFTVSIVSTAYIALLSVTISFRIYKGVIOA 231  
 QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 120  
 DB 232 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 291  
 QY 121 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
 DB 292 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 351  
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 DB 352 IPGLKRKA 359  
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 ID AAY71563 standard; protein; 403 AA.  
 XX  
 AC AAY71563;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat Nogo A protein fragment used in the construction of mutant EST.  
 XX  
 DE Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.  
 XX



```

OS Rattus sp.
XX WO200031235-A2.
XX 02-JUN-2000.
XX 05-NOV-1999; 99WO-US026160.
XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX Example; Page; 122pp; English.
XX The patent relates to neurite growth inhibitor Nogo which is free of all
XX central nervous system (CNS) myelin material with which it is native
XX associated. Nogo proteins and fragments displaying neurite growth
XX inhibitory activity are used in the treatment of neoplastic disease of
XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
XX ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
XX degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
XX Therapeutics which promote Nogo activity can be used to treat or prevent
XX hyperproliferative or benign dysproliferative disorders e.g. psoriasis
XX and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
XX used to inhibit production of Nogo protein to induce regeneration of
XX neurons or to promote structural plasticity of the CNS in disorders where
XX neurite growth, regeneration or maintenance are deficient or desired. The
XX animal models can be used in diagnostic and screening methods for
XX predisposition to disorders and to screen for or test molecules which can
XX treat or prevent disorders or diseases of the CNS. The present sequence
XX is a fragment of rat Nogo A protein shown in AAY71310, which is used in
XX the construction of mutant EST. The mutant is composed of His-tag/TT-
XX tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for
XX mapping the inhibitory sites of Nogo protein. Major inhibitory region was
XX identified in the Nogo A sequence from amino acids 172-974, particularly
XX amino acids 542-722. In addition, N-terminal region 1-171 was found to be
XX inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is
XX not given in the specification but is derived from rat Nogo A sequence
XX shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ
XX ID NO: 29 in disclosure of the specification. However, the specification
XX does not include sequences for these SEQ ID numbers
XX Sequence 403 AA;
XX
XX Query Match 99.4%; Score 919; DB 3; Length 403;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-89;
XX Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SVVDLLYWRDIIKKTGVVFGASLFLLSLTFTSVSTVATYIALALLSVTISFRIYKGVIOA 60
DB 216 SVVDLLYWRDIIKKTGVVFGASLFLLSLTFTSVSTVATYIALALLSVTISFRIYKGVIOA 275
QY 61 IQKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 120
DB 276 IQKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 335
QY 121 LMMVFTYVGFALFNLGLTLLIALLSLFSIPVIYERHQVQIDHYGLANKSVKQAMAKIOAK 180
DB 336 LMMVFTYVGFALFNLGLTLLIALLSLFSIPVIYERHQVQIDHYGLANKSVKQAMAKIOAK 395
QY 181 IGPLKRA 188
DB 396 IGPLKRA 403

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RESULT 15  
 AAY71557  
 ID AAY71557 standard; protein; 1162 AA.  
 XX  
 AC AAY71557;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.  
 XX  
 KW Rat: neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Example; Page; 122pp; English.  
 XX  
 CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is native  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in  
 CC the construction of mutant EST. The mutant is composed of His-tag/TT-  
 CC tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for  
 CC mapping the inhibitory sites of Nogo protein. Major inhibitory region was  
 CC identified in the Nogo A sequence from amino acids 172-974, particularly  
 CC amino acids 542-722. In addition, N-terminal region 1-171 was found to be  
 CC inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is  
 CC not given in the specification but is derived from rat Nogo A sequence  
 CC shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ  
 CC ID NO: 29 in disclosure of the specification. However, the specification  
 CC does not include sequences for these SEQ ID numbers  
 XX  
 SQ Sequence 1162 AA;  
 XX  
 SQ



Query Match 99.4%; Score 919; DB 3; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 1.9e-88;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
DB 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034  
QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKPAV 120  
DB 1035 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKPAV 1094  
QY 121 LMWFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIOAK 180  
DB 1095 LMWFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIOAK 1154  
QY 181 IPGLKRKA 188  
DB 1155 IPGLKRKA 1162

Search completed: June 16, 2005, 13:11:00  
Job time : 28.2927 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 7.13706 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVWFGA.....VKDAMAKIQAKIPGLKRRAD 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	904	97.7	199	2	US-08-700-607-1
2	904	97.7	201	4	US-09-949-016-9124
3	679	73.4	208	2	US-08-700-607-7
4	679	73.4	356	2	US-08-700-607-6
5	679	73.4	439	4	US-09-949-016-9180
6	679	73.4	776	2	US-08-700-607-5
7	679	73.4	776	4	US-09-949-016-6998
8	665	71.9	267	2	US-08-700-607-8
9	625.5	67.6	192	4	US-09-949-016-8859
10	539.5	58.3	168	4	US-09-149-476-563
11	518	56.0	219	4	US-09-270-767-45132
12	516	55.8	241	2	US-08-700-607-3
13	475	51.4	588	4	US-09-949-016-7290
14	286	30.9	92	4	US-09-149-476-411
15	246	26.6	114	4	US-09-513-999C-7861
16	142	15.4	374	4	US-09-248-796A-16008
17	100	10.8	80	3	US-08-905-223-411
18	95	10.3	468	4	US-08-487-596-8
19	95	10.3	468	4	US-08-660-451A-8
20	94	10.2	382	4	US-09-949-016-11596
21	88.5	9.6	1278	4	US-09-462-136-2
22	88.5	9.6	1318	4	US-09-949-016-10152
23	86.5	9.4	592	4	US-09-134-000C-5477
24	86	9.3	414	4	US-08-956-171E-5246
25	86	9.3	414	4	US-08-781-986A-5246
26	85.5	9.2	1051	3	US-09-134-001C-5005
27	84.5	9.1	593	4	US-09-328-352-4866

Sequence 302, App  
Sequence 3963, Ap  
Sequence 5202, Ap  
Sequence 2858, Ap  
Sequence 6175, Ap  
Sequence 14833, A  
Sequence 1, Appli  
Sequence 3, Appli  
Sequence 4880, Ap  
Sequence 4818, Ap  
Sequence 53, Appl  
Sequence 2019, Ap  
Sequence 27968, A  
Sequence 8, Appli  
Sequence 19, Appl  
Sequence 52, Appl  
Sequence 419, App  
Sequence 3805, Ap

ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
US-08-700-607-1

Query Match 97.7%; Score 904; DB 2; Length 199;  
Best Local Similarity 97.3%; Pred. No. 7.9e-89;  
Matches 183; Conservative 3; Mismatches 0; Gaps 0;

Oy 2 VVDLLYWRDIKKTGVWFGASIFLLLSLTVFSIVSVAYIALALLSVTISFRIYKGVIOAI 61

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Db 12 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAYL 121
Db 72 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 131
QY 122 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181
Db 132 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 191
QY 182 PGLKRRAD 189
Db 192 PGLKRAE 199

RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

Query Match 97.7%; Score 904; DB 4; Length 201;
Best Local Similarity 97.3%; Pred. No. 8e-89; 2; Indels 0; Gaps 0;
Matches 183; Conservative 3; Mismatches 2;

QY 2 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 14 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 73
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAYL 121
Db 74 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 133
QY 122 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181
Db 134 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 193
QY 182 PGLKRRAD 189
Db 194 PGLKRAE 201

RESULT 3
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

Query Match 73.4%; Score 679; DB 2; Length 208;
Best Local Similarity 67.9%; Pred. No. 1e-64; 29; Indels 0; Gaps 0;
Matches 127; Conservative 31; Mismatches 29;

QY 3 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 62
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QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAYL 122
Db 82 KTDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 141
QY 123 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 182
Db 142 WLYTVGFALFNGLTLLMAVSMFTLPVVYVVKHQADQYLGIVRTHINAVVAKIOAKI 201
QY 183 GLKRRAD 189
Db 202 GAKRAE 208

RESULT 4
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307309
US-08-700-607-6

Query Match 73.4%; Score 679; DB 2; Length 356;
Best Local Similarity 67.9%; Pred. No. 2.2e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFISVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
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QY 63 KSDGHPFRAYLESEVASELVQKYSNSALGHVNSTIKELRRLFLVDDVDSLKFAVLM 122
DB 230 KTDGHPFRAYLELEITLSQEQIKYTDCLQFYVNSTUKELRRLFLVQDVLDSLKFAVLM 289

QY 123 WVFTYVGALFNGLTLLILALSLFSPVIYERHQVIDHYLGLANKSVKDMAKIOAKIP 182
DB 290 WLLTYVGALFNGLTLLLMVAVSMFTLPVYVYKHOAQIDQYLGVLVTRTHNAVVAKIOAKIP 349

QY 183 GLKRAKD 189
DB 350 GAKRHAE 356

RESULT 5
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180
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Query Match 73.4%; Score 679; DB 4; Length 439;
Best Local Similarity 67.9%; Pred. No. 2.9e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFISVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
DB 253 IDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYIALAALSATISFRIYKSVLQAVQ 312

QY 63 KSDGHPFRAYLESEVASELVQKYSNSALGHVNSTIKELRRLFLVDDVDSLKFAVLM 122
DB 313 KTDGHPFRAYLELEITLSQEQIKYTDCLQFYVNSTUKELRRLFLVQDVLDSLKFAVLM 372

QY 123 WVFTYVGALFNGLTLLILALSLFSPVIYERHQVIDHYLGLANKSVKDMAKIOAKIP 182
DB 373 WLLTYVGALFNGLTLLLMVAVSMFTLPVYVYKHOAQIDQYLGVLVTRTHNAVVAKIOAKIP 432

QY 183 GLKRAKD 189
DB 433 GAKRHAE 439

RESULT 6
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
; US-08-700-607-5

Query Match 73.4%; Score 679; DB 2; Length 776;
Best Local Similarity 67.9%; Pred. No. 6.5e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFISVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
DB 590 IDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYIALAALSATISFRIYKSVLQAVQ 649
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QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDVSLKFAVL 122  
DB 650 KTDGHPFRAYLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVQDLVSLKFAVL 709  
QY 123 WFTYVYGALFNGLTLLILALISLFSPIYERHQQVQIDYGLVRLTHINAVAKIOAKIP 182  
DB 710 WLLTYVYGALFNGLTLLILALISLFSPIYERHQQVQIDYGLVRLTHINAVAKIOAKIP 769  
QY 183 GLKRAK 189  
DB 770 GAKRAE 776

RESULT 7  
US-09-949-016-6998  
; Sequence 6998, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6998  
; LENGTH: 776  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6998

Query Match 73.4%; Score 679; DB 4; Length 776;  
Best Local Similarity 67.9%; Pred. No. 6.5e-64;  
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;  
QY 3 VDLRYRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQ 62  
DB 590 IDLLYRDIKQTGIVFGSFLLLSLTVFSIVSVVAYLALAAALSATISPRIYKSVLQAVQ 649  
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDVSLKFAVL 122  
DB 650 KTDGHPFRAYLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVQDLVSLKFAVL 709  
QY 123 WFTYVYGALFNGLTLLILALISLFSPIYERHQQVQIDYGLVRLTHINAVAKIOAKIP 182  
DB 710 WLLTYVYGALFNGLTLLILALISLFSPIYERHQQVQIDYGLVRLTHINAVAKIOAKIP 769  
QY 183 GLKRAK 189  
DB 770 GAKRAE 776

RESULT 8  
US-08-700-607-8  
; Sequence 8, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 281046  
US-08-700-607-8

Query Match 71.9%; Score 665; DB 2; Length 267;  
Best Local Similarity 67.2%; Pred. No. 4.6e-63;  
Matches 123; Conservative 32; Mismatches 28; Indels 0; Gaps 0;  
QY 3 VDLRYRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQ 62  
DB 13 IDLLYRDIKQTGIVFGSFLLLSLTVFSIVSVVAYLALAAALSATISPRIYKSVLQAVQ 72  
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDVSLKFAVL 122  
DB 73 KTDGHPFRAYLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVQDLVSLKFAVL 132  
QY 123 WFTYVYGALFNGLTLLILALISLFSPIYERHQQVQIDYGLVRLTHINAVAKIOAKIP 182  
DB 133 WLLTYVYGALFNGLTLLILALISLFSPIYERHQQVQIDYGLVRLTHINAVAKIOAKIP 192  
QY 183 GLK 185  
DB 193 GAR 195

RESULT 9  
US-09-949-016-8859  
; Sequence 8859, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8859

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; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match      67.6%; Score 625.5; DB 4; Length 192;
Best Local Similarity 60.0%; Pred. No. 5e-59;
Matches 114; Conservative 40; Mismatches 35; Indels 1; Gaps 1;

QY 1 SVVDLLYWRDIKKTGVFGASFLALLSLTVFISVTAIALALLSVTISPRIYKGVIOA 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 SVHDLIFWRDVKKTGVFGFTTLMLLSLAASFVISVWSYLIALLSVTISPRIYKSVIOA 62
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 IQKSDGHPFRAYLSEVAISEBELVQKYSNSALGHVNSTIKELRFLVDDLVDLSLKFV 120
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VQKSEGHFFKAYLDVDTLSSEAFHYNNAAMVHINRAKLIIIRFLVEDLVDLSKLAV 122
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 LMWVTYVYCALPNGTLLILALISLFSPIVYERHQQVQIDHYGLANKSVKDMAKIOAK 180
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 FFWLMTYVCAVNGITLLILAEILLFSPVYVEKYKTQIDHYVGIARDQTKSIVEKIOAK 182
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 IPGL-KRKAD 189
Db 183 LPGIARKKAE 192

RESULT 10
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      58.3%; Score 539.5; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 6.7e-50;
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

QY 24 LLLSVTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSEVAISEE 83
Db 1 MLLSLAASFVISWSYLIALLSVTISFRIYKSVIQAVQKSEGHFKAYLDVDTLSSE 60

QY 84 LVQKYSNLSALGHVNSTIKELRELFLVDLVDLSKFAVLMMVFTYVYVGFNGTLTLIALI 143
Db 61 AFHNYNMAAMVHINRALKIIRLFLVEDLVDLSKLAVFWMVLMVYVGVAFNGITLLILAE 120

QY 144 SLFSPVIYERHOVQIDHYGLANKSVKDAMAKIOAKIPGL-KRKAD 189
Db 121 LIFSVPVYVEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKAE 167

RESULT 11
US-09-270-767-45132
; Sequence 45132, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45132
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45132

Query Match      56.0%; Score 518; DB 4; Length 219;
Best Local Similarity 52.2%; Pred. No. 1.9e-47;
Matches 93; Conservative 41; Mismatches 44; Indels 0; Gaps 0;

QY 5 LLYWRDIKKTGVVFGASLFLLLSVTSFVSIVSVTAYIALALLSVTISFRIYKGVIOAIQKS 64
Db 26 LIYWRDVKKSGIVFGAGLITLAAISFSVISFAYLSLTLTFTGTVAFRIYKSVTQAVQKT 85

QY 65 DEGHFPFRAYLSEVAISELVOKYSNLSALGHVNSTIKELRRLFLVDLVDLSKFAVLMMV 124
Db 86 NEGHPFKDYLEDLTLISHEKVQNIAGVAHNGFISELRRLFLVEDIIDSIKFGVILMV 145

QY 125 FTYVGFALFNGTLTLIALISLFSIPVIYERHOVQIDHYGLANKSVKDAMAKIOAKIP 182
Db 146 FTYVGFAGFNGMTLVILAFVSLFPLPKVYNNKQSIDTHLDLVRSKLTETDKIRVAIP 203

RESULT 12
US-08-700-607-3
; Sequence 3, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hallman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
```



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
;; STREET: 3174 Porter Drive  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: U.S.  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 1.5  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/700,607  
;; FILING DATE: Filed Herewith  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PP-0114 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-855-0555  
;; TELEFAX: 415-845-4166  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 241 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; IMMEDIATE SOURCE:  
;; LIBRARY: THPINOB01  
;; CLONE: 31870  
US-08-700-607-3

Query Match 55.8%; Score 516; DB 2; Length 241;  
Best Local Similarity 59.9%; Pred. No. 3.6e-47;  
Matches 94; Conservative 33; Mismatches 30; Indels 0; Gaps 0;  
  
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Db 47 AVHDLIXWRDVKTGFVGTTLMLSLAAFSVSVSLIALLSVTISFRIYKSVIOA 106  
  
Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAV 120  
Db 107 VQKSEEGHPFRAYLDVDTLTSSEAFHNYMNAAMVHINRAKLIIRLFLVEDLVDSLKLV 166  
  
Qy 121 LMWFTYVGALENGLTLLILALISLFSIPVIYERHQQV 157  
Db 167 FMWLTYYGAVFNGITLLILAEILLXSVPIVYXKYKV 203

RESULT 13  
US-09-949-016-7290  
; Sequence 7290, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7290  
; LENGTH: 588  
; TYPE: PRT

;; ORGANISM: Human  
US-09-949-016-7290  
  
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Best Local Similarity 50.5%; Pred. No. 3.1e-42;  
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Db 388 VADLLYWKDTRTSGVFTGLVSLCLLHFFSVVAHLALLLCGTISLRVYKVLQAV 447  
  
Qy 62 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAVL 121  
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; Sequence 411, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
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; EARLIER FILING DATE: 1997-03-07  
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19	EARLIER APPLICATION NUMBER: 60/056,892
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21	EARLIER APPLICATION NUMBER: 60/057,761
22	EARLIER FILING DATE: 1997-08-22
23	EARLIER APPLICATION NUMBER: 60/047,595
24	EARLIER FILING DATE: 1997-05-23
25	EARLIER APPLICATION NUMBER: 60/047,599
26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/047,588
28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/047,585
30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/047,586
32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/047,590
34	EARLIER FILING DATE: 1997-05-23
35	EARLIER APPLICATION NUMBER: 60/047,594
36	EARLIER FILING DATE: 1997-05-23
37	EARLIER APPLICATION NUMBER: 60/047,589
38	EARLIER FILING DATE: 1997-05-23
39	EARLIER APPLICATION NUMBER: 60/047,593
40	EARLIER FILING DATE: 1997-05-23
41	EARLIER APPLICATION NUMBER: 60/047,614
42	EARLIER FILING DATE: 1997-05-23
43	EARLIER APPLICATION NUMBER: 60/043,578
44	EARLIER FILING DATE: 1997-04-11
45	EARLIER APPLICATION NUMBER: 60/043,576
46	EARLIER FILING DATE: 1997-04-11
47	EARLIER APPLICATION NUMBER: 60/047,501
48	EARLIER FILING DATE: 1997-05-23
49	EARLIER APPLICATION NUMBER: 60/043,670
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51	EARLIER APPLICATION NUMBER: 60/056,632
52	EARLIER FILING DATE: 1997-08-22
53	EARLIER APPLICATION NUMBER: 60/056,664
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59	EARLIER APPLICATION NUMBER: 60/056,909
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61	EARLIER APPLICATION NUMBER: 60/056,875
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65	EARLIER APPLICATION NUMBER: 60/056,887
66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/056,908
68	EARLIER FILING DATE: 1997-08-22
69	EARLIER APPLICATION NUMBER: 60/048,964
70	EARLIER FILING DATE: 1997-06-06
71	EARLIER APPLICATION NUMBER: 60/057,650
72	EARLIER FILING DATE: 1997-09-05
73	EARLIER APPLICATION NUMBER: 60/056,884



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:29:05 ; Search time 24.5171 Seconds  
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2960.058 Million cell updates/sec

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	925	100.0	1163	9	US-09-893-348-18
2	925	100.0	1163	16	US-10-810-653-18
3	922	99.7	379	14	US-10-205-194-164
4	921	99.6	199	9	US-09-893-348-21
5	921	99.6	199	16	US-10-810-653-21
6	921	99.6	360	9	US-09-893-348-20
7	921	99.6	360	16	US-10-810-653-20
8	917	99.1	1162	16	US-10-633-423-10
9	917	99.1	1162	16	US-10-427-741-10
10	908	98.2	1192	9	US-09-789-386-2
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12	908	98.2	1192	9	US-09-893-348-23	Sequence 23, Appl
13	908	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appl
14	908	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
15	908	98.2	1192	15	US-10-267-502-429	Sequence 429, App
16	908	98.2	1192	16	US-10-327-213-9	Sequence 9, Appl
17	908	98.2	1192	16	US-10-466-258-9	Sequence 23, Appl
18	908	98.2	1192	16	US-10-810-653-23	Sequence 431, App
19	906.5	98.0	1163	15	US-10-267-502-431	Sequence 25, Appl
20	904	97.7	199	9	US-09-893-348-25	Sequence 1, Appl
21	904	97.7	199	15	US-10-660-946-1	Sequence 1, Appl
22	904	97.7	199	16	US-10-810-653-25	Sequence 25, Appl
23	904	97.7	373	9	US-09-789-386-6	Sequence 6, Appl
24	904	97.7	373	9	US-09-765-205-6	Sequence 24, Appl
25	904	97.7	373	9	US-09-893-348-24	Sequence 72, Appl
26	904	97.7	373	14	US-10-060-036-72	Sequence 8, Appl
27	904	97.7	373	15	US-10-408-967-8	Sequence 4, Appl
28	904	97.7	373	16	US-10-466-258-4	Sequence 24, Appl
29	904	97.7	373	16	US-10-810-653-24	Sequence 6, Appl
30	904	97.7	373	17	US-10-347-669-6	Sequence 7, Appl
31	901	97.4	1192	15	US-10-408-967-7	Sequence 9, Appl
32	897	97.0	199	15	US-10-408-967-9	Sequence 9, Appl
33	895	96.8	199	11	US-09-978-360A-467	Sequence 467, App
34	864	93.4	199	16	US-10-466-258-11	Sequence 11, Appl
35	679	73.4	208	15	US-10-660-946-7	Sequence 7, Appl
36	679	73.4	356	15	US-10-660-946-6	Sequence 5, Appl
37	679	73.4	776	15	US-10-660-946-5	Sequence 430, App
38	679	73.4	776	15	US-10-267-502-430	Sequence 1481, Ap
39	679	73.4	776	16	US-10-723-860-1481	Sequence 93, Appl
40	678	73.3	777	14	US-10-205-219-93	Sequence 432, App
41	678	73.3	780	15	US-10-267-502-432	Sequence 127, App
42	665	71.9	267	14	US-10-205-194-127	Sequence 8, Appl
43	665	71.9	267	15	US-10-660-946-8	Sequence 20, Appl
44	622.5	67.3	236	9	US-09-729-674-20	Sequence 26, Appl
45	622.5	67.3	236	9	US-09-765-205-26	

ALIGNMENTS

RESULT 1  
US-09-893-348-18  
; Sequence 18, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-893-348-18

Query Match 100.0%; Score 925; DB 9; Length 1163;  
Best Local Similarity 100.0%; Pred. No. 4e-81;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
 US-10-810-653-18  
 ; Sequence 18, Application US/10810653  
 ; Publication No. US20040253218A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal  
 ; APPLICANT: COHEN, Irun R.  
 ; APPLICANT: BESERMAN, Pierre  
 ; APPLICANT: MOSONEGO, Alon  
 ; APPLICANT: MOALEN, Gila  
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
 ; FILE REFERENCE: EIS-SCHWARTZ=2A  
 ; CURRENT APPLICATION NUMBER: US/10/810,653  
 ; CURRENT FILING DATE: 2004-03-29  
 ; PRIOR APPLICATION NUMBER: US/09/893,348  
 ; PRIOR FILING DATE: 2001-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/314,161  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: US 09/218,277  
 ; PRIOR FILING DATE: 1998-12-22  
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715  
 ; PRIOR FILING DATE: 1998-07-21  
 ; PRIOR APPLICATION NUMBER: IL 124500  
 ; PRIOR FILING DATE: 1998-05-19  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 18  
 ; LENGTH: 1163  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 ; US-10-810-653-18

Query Match	100.0%;	Score 925;	DB 16;	Length 1163;
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; Sequence 164, Application US/10205194

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; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
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; ORGANISM: Rattus norvegicus
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; OTHER INFORMATION: Foccen-m2 reticulon
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QY 181 IPLGKRRKAD 189
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RESULT 4
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; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-21

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Query Match 99.6%; Score 921; DB 9; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

QY 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 121  
DB 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 131

QY 122 MWVFTYVGFALFNGLLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
DB 132 MWVFTYVGFALFNGLLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 191

QY 182 PGLKPKAD 189  
DB 192 PGLKPKAD 199

RESULT 5

US-10-810-653-21  
; Sequence 21, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus

US-10-810-653-21

Query Match 99.6%; Score 921; DB 16; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

QY 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 121  
DB 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 131

QY 122 MWVFTYVGFALFNGLLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
DB 132 MWVFTYVGFALFNGLLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 191

QY 182 PGLKPKAD 189  
DB 192 PGLKPKAD 199

RESULT 6

US-09-893-348-20  
; Sequence 20, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus

Query Match 99.6%; Score 921; DB 9; Length 360;

Best Local Similarity 100.0%; Pred. No. 2.2e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 232

QY 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 121  
DB 233 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 292

QY 122 MWVFTYVGFALFNGLLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
DB 293 MWVFTYVGFALFNGLLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 352

QY 182 PGLKPKAD 189  
DB 353 PGLKPKAD 360

RESULT 7

US-10-810-653-20  
; Sequence 20, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-810-653-20

Query Match 99.6%; Score 921; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 2.2e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 232  
QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121  
DB 233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 292  
QY 122 MMVFTYVYGALFNGLTLLILALISLFSIPVIYERHQVIDHYGLANKSVKDMAKIOAKI 181  
DB 293 MMVFTYVYGALFNGLTLLILALISLFSIPVIYERHQVIDHYGLANKSVKDMAKIOAKI 352  
QY 182 PGLKRRKAD 189  
DB 353 PGLKRRKAD 360

RESULT 8  
US-10-633-423-10  
; Sequence 10, Application US/10633423  
; Publication No. US20040191240A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023 US00  
; CURRENT APPLICATION NUMBER: US/10/633,423  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: US 10/427,741  
; PRIOR FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 1162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-633-423-10

Query Match 99.1%; Score 917; DB 16; Length 1162;  
Best Local Similarity 98.9%; Pred. No. 2.4e-80;  
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
DB 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1033  
QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
DB 1034 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1093  
QY 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVIDHYGLANKSVKDMAKIOAK 180  
DB 1094 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVIDHYGLANKSVKDMAKIOAK 1153  
QY 181 IPGLKRRKAD 189

DB 1154 IPGLKRRKAE 1162  
RESULT 9  
US-10-427-741-10  
; Sequence 10, Application US/10427741  
; Publication No. US20040191291A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; APPLICANT: Yamashita, Toshihide  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023  
; CURRENT APPLICATION NUMBER: US/10/427,741  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 1162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-427-741-10

Query Match 99.1%; Score 917; DB 16; Length 1162;  
Best Local Similarity 98.9%; Pred. No. 2.4e-80;  
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
DB 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1033  
QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
DB 1034 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1093  
QY 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVIDHYGLANKSVKDMAKIOAK 180  
DB 1094 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVIDHYGLANKSVKDMAKIOAK 1153  
QY 181 IPGLKRRKAD 189  
DB 1154 IPGLKRRKAE 1162

RESULT 10  
US-09-789-386-2  
; Sequence 2, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2  
Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 1.9e-79;



Matches	184;	Conservative	3;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	SVVDLLIWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA	60						
Db	1004	SVVDLLIWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA	1063						
Qy	61	IQKSDGEGHPRAYLESEVAISEELVQKYSNSALCHVNNSTIKELRRFLVDDLDVDSLKFV	120						
Db	1064	IQKSDGEGHPRAYLESEVAISEELVQKYSNSALCHVNNCTTIKELRRFLVDDLDVDSLKFV	1123						
Qy	121	LMWFTYVVGALFNGLTLLIILALISLSPVPIYERHQVQIDHYILGLANKSVKIDAMAKIQAK	180						
Db	1124	LMWFTYVVGALFNGLTLLIILALISLSPVPIYERHQVQIDHYILGLANKSVKIDAMAKIQAK	1183						
Qy	181	IPGLKRRKAD	189						
Db	1184	IPGLKRRKAE	1192						

RESULT 11  
 US-09-758-140-6  
 ; Sequence 6, Application US/09758140  
 ; Patent No. US20020012965A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Strittmatter, Stephen M.  
 ; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth  
 ; FILE REFERENCE: 44574-5073-US  
 ; CURRENT APPLICATION NUMBER: US/09/758,140  
 ; CURRENT FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: US 60/175,707  
 ; PRIOR FILING DATE: 2000-01-12  
 ; PRIOR APPLICATION NUMBER: US 60/207,366  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 60/236,378  
 ; PRIOR FILING DATE: 2000-09-29  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-758-140-6

Query Match	98.2%;	Score 908;	DB 9;	Length 1192;
Best Local Similarity	97.4%;	Pred. No. 1.9e-79;		
Matches 184;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	SVDLLIWRDIKKTGVVFGASLFLLSLTVFISVSTAYIALALLSVTISFRIYKGVIQA	60	
Db	1004	SVDLLIWRDIKKTGVVFGASLFLLSLTVFISVSTAYIALALLSVTISFRIYKGVIQA	1063	
QY	61	IQSDSGHPPRAYLESEVAISEELVKQYSNSALGHVNNTIKELRRFLVLDLVDSLUKFV	120	
Db	1064	IQSDSGHPPRAYLESEVAISEELVKQYSNSALGHVNCTIKELRRFLVLDLVDSLUKFV	1123	
QY	121	LMMVFTVVGALFNGLTLIIILALSIFSPVPIYERHQVIDHYLGANKSVKDAMAKIOAK	180	
Db	1124	LMMVFTVVGALFNGLTLIIILALSIFSPVPIYERHQIQIDHYLGANKVNDAMAKIOAK	1183	
QY	181	IPGLKKRAD	189	
Db	1184	IPGLKKRAE	1192	

RESULT 12  
US-09-893-348-23  
; Sequence 23, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michael  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, pierre  
; APPLICANT: MOSONEGO, Alon

```

; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
; FILE REFERENCE: EIS-SWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-893-348-23

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Query Match	98.2%;	Score 908;	DB 9;	Length 1192;							
Best Local Similarity	97.4%;	Pred. No. 1.9e-79;									
Matches 184;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;							
QY	1	SVVDLLYWRD	IKKTGVVFCAS	FLLLSLTVF	SVSVTA	YIALALIS	VTTSF	FRYIKG	VIQA	60	
DB	1004	SVVDLLYWRD	IKKTGVVFCAS	FLLLSLTVF	SVSVTA	YIALALIS	VTTSF	FRYIKG	VIQA	1063	
QY	61	IOKSDGEGH	FPFRAYLSE	VAISBELVQ	KYSNSAL	GHVNSTI	KBLRRL	FLVD	LDLSL	KFAV	120
DB	1064	IOKSDGEGH	FPFRAYLSE	VAISBELVQ	KYSNSAL	GHVNSTI	KBLRRL	FLVD	LDLSL	KFAV	1123
QY	121	LWMVFTYU	GALFNG	LTLLIL	ALISLFS	IPVIERHQ	VDIDHYL	GLANKS	VKDMAK	IQAK	180
DB	1124	LWMVFTYU	GALFNG	LTLLIL	ALISLFS	VPVIERHQ	VDIDHYL	GLANKS	VKDMAK	IQAK	1183
QY	181	IPGLKRX	KAD	189							
DB	1184	IPGLKRX	KAE	1192							

```

RESULT 13
US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US2002007295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

```

Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 1.9e-79;  
Matches 184: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAV 120
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAV 1123
QY 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 1124 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183
QY 181 IPGLKRRKAD 189
Db 1184 IPGLKRRKAE 1192
```

## RESULT 14

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yugu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 71

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-036-71

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Query Match 98.2%; Score 908; DB 14; Length 1192;
Best Local Similarity 97.4%; Pred. No. 1.9e-79;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAV 120
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAV 1123
QY 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 1124 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183
QY 181 IPGLKRRKAD 189
Db 1184 IPGLKRRKAE 1192
```

## RESULT 15

US-10-267-502-429

; Sequence 429, Application US/10267502

; Publication No. US20040071700A1

; GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob

; APPLICANT: Galant, Ron

; TITLE OF INVENTION: Obesity Linked Genes

; FILE REFERENCE: LSD-07416

; CURRENT APPLICATION NUMBER: US/10/267,502

; CURRENT FILING DATE: 2003-01-27

; NUMBER OF SEQ ID NOS: 439

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 429

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-267-502-429

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Query Match 98.2%; Score 908; DB 15; Length 1192;
Best Local Similarity 97.4%; Pred. No. 1.9e-79;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAV 120
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAV 1123
QY 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 1124 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183
QY 181 IPGLKRRKAD 189
Db 1184 IPGLKRRKAE 1192
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Search completed: June 16, 2005, 13:03:58

Job time : 24.5171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 25.6406 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRKAD 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	1163	1 RTN4 RAT	Q9jk11 rattus norv
2	917	99.1	578	2 Q80W95	Q80w95 mus musculu
3	917	99.1	639	2 Q8K290	Q8k290 mus musculu
4	917	99.1	1046	2 Q8BGK7	Q8bgk7 mus musculu
5	917	99.1	1162	2 Q8BGM9	Q8bgm9 mus musculu
6	914	98.8	375	2 Q8BHf5	Q8bhf5 mus musculu
7	913	98.7	199	1 RTN4 MOUSE	Q99p72 mus musculu
8	913	98.7	356	2 Q8BH78	Q8bh78 mus musculu
9	908	98.2	986	2 Q8IU04	Q8iua4 homo sapien
10	908	98.2	1192	1 RTN4 HUMAN	Q9nqc3 homo sapien
11	906.5	98.0	1163	2 Q8K3G8	Q8k3g8 mus musculu
12	905	97.8	392	2 Q96B16	Q96b16 homo sapien
13	904	97.7	199	2 Q7YRW9	Q7yrw9 bos taurus
14	904	97.7	343	2 Q6IPN0	Q6ipn0 homo sapien
15	902.5	97.6	357	2 Q8K3G7	Q8k3g7 mus musculu
16	900	97.3	199	2 Q6IM70	Q6im70 sus scrofa
17	896	96.9	187	2 Q6IG15	Q6ig15 sus scrofa
18	895	96.8	199	2 Q7PCJ7	Q7pcj7 macaca fasc
19	879	95.0	658	2 Q6RS58	Q6rsa8 gallus gall
20	872	94.3	199	2 Q7T224	Q7t224 gallus gall
21	844	91.2	179	2 Q9GM33	Q9gm33 macaca fasc
22	773	83.6	193	2 Q6IFY5	Q6ify5 xenopus tro
23	772	83.5	315	2 Q6IFV4	Q6ifv4 xenopus tro
24	764	82.6	1024	2 Q6JRV2	Q6jrv2 xenopus lae
25	764	82.6	1043	2 Q6JRV0	Q6jrv0 xenopus lae
26	764	82.6	1055	2 Q6JRV1	Q6jrv1 xenopus lae
27	761	82.3	193	2 Q6JRV6	Q6jrv6 xenopus lae
28	761	82.3	330	2 Q6JRV4	Q6jrv4 xenopus lae
29	760	82.2	199	2 Q6PB23	Q6pb23 xenopus lae
30	760	82.2	311	2 Q6JRV3	Q6jrv3 xenopus lae
31	747	80.8	1013	2 Q6JRV9	Q6jrv9 xenopus lae

32	747	80.8	1032	2 Q6JRV7	Q6jrv7 xenopus lae
33	747	80.8	1044	2 Q6JRV8	Q6jrv8 xenopus lae
34	744	80.4	193	2 Q6JRW4	Q6jrw4 xenopus lae
35	744	80.4	323	2 Q6JRW1	Q6jrw1 xenopus lae
36	743	80.3	199	2 Q6JRW3	Q6jrw3 xenopus lae
37	743	80.3	304	2 Q6JRW0	Q6jrw0 xenopus lae
38	743	80.3	316	2 Q6JRW2	Q6jrw2 xenopus lae
39	733	79.2	214	2 Q7T222	Q7t222 carassius a
40	719	77.7	196	2 Q6IRI6	Q6ie16 cyprinus ca
41	711	76.9	193	2 Q6IEB4	Q6ie16 fugu rubrip
42	705	76.2	197	2 Q6EHZ3	Q6ehz3 brachydanio
43	697.5	75.4	209	2 Q6IEJ1	Q6ie11 oncorhynch
44	683	73.8	208	2 Q6IAX4	Q6iax4 homo sapien
45	679	73.4	199	2 Q9BQ59	Q9bq59 homo sapien

## ALIGNMENTS

RESULT 1  
RTN4 RAT  
ID RTN4 RAT STANDARD; PRT; 1163 AA.  
AC Q9UK11; Q9JK10; Q9ROD9; Q9WUE9; Q9WUFO;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)  
DE (Glut4 vesicle 20 kDa protein).  
GN Name=Rtn4; Synonyms=Nogo;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
RX MEDLINE=9249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;  
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:  
a new member of the reticulon family.";  
RL Blochim. Biophys. Acta 1450:68-76(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;  
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
RA Spillmann A.A., Christ F., Schwab M.E.;  
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
antigen for monoclonal antibody IN-1.";  
RL Nature 403:434-439(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in rat: one of two  
minor splice variants.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP FUNCTION.  
RX MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;  
RA GrandPre T., Li S., Strittmatter S.M.;  
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
RL Nature 417:547-551(2002).  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
block the regeneration of the nervous central system in adults (By  
similarity).  
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By  
similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
membrane of the endoplasmic reticulum through 2 putative  
transmembrane domains (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=4;  
Name=1; Synonyms=Nogo-A, NI-220-250;

```
CC      IsoId=Q9JK11-1; Sequence=Displayed;
CC      Name=2; Synonyms=Nogo-B, Foccen-M1;
CC      IsoId=Q9JK11-2; Sequence=VSP_005658;
CC      Name=3; Synonyms=Nogo-C, VP20;
CC      IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
CC      Name=4; Synonyms=Foccen-M2;
CC      IsoId=Q9JK11-4; Sequence=VSP_005659;
CC      -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
CC      nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
CC      present in dorsal root ganglion, sciatic nerve and PC12 cells
CC      after longer exposure. Isoforms 2 and 3 are detected in kidney,
CC      cartilage, skin, lung and spleen. Isoform 3 is expressed at high
CC      level in skeletal muscle. In adult animals isoform 1 is expressed
CC      mainly in the nervous system.
CC      -!- SIMILARITY: Contains 1 reticulin domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AF051335; AAF01564.1; -
CC      EMBL; AJ242961; CAB71027.1; -
CC      EMBL; AJ242962; CAB71028.1; -
CC      EMBL; AJ242963; CAB71029.1; -
CC      EMBL; AF132045; AAD31019.1; -
CC      EMBL; AF132046; AAD31020.1; -
CC      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
CC      GO; GO:0005635; C:nuclear membrane; ISS.
CC      GO; GO:0005515; F:protein binding; ISS.
CC      GO; GO:0019987; P:negative regulation of axon extension; ISS.
CC      GO; GO:0030517; P:negative regulation of anti-apoptosis; ISS.
CC      InterPro; IPR003388; Reticulon.
CC      Pfam; PF02453; Reticulon; 1.
CC      PROSITE; PS50845; RETICULON; 1.
CC      Alternative splicing; Direct protein sequencing;
CC      Endoplasmic reticulum; Transmembrane.
CC      DOMAIN 1 989 Cytoplasmic (Potential).
CC      TRANSMEM 990 1010 Potential.
CC      DOMAIN 1011 1104 Luminal (Potential).
CC      TRANSMEM 1105 1125 Potential.
CC      DOMAIN 1126 1163 Cytoplasmic (Potential).
CC      DOMAIN 976 1163 Reticulon.
CC      DOMAIN 33 46 Poly-Glu.
CC      DOMAIN 73 76 Poly-Ala.
CC      DOMAIN 140 145 Poly-Pro.
CC      VARSPLIC 1 564 Missing (in isoform 3).
CC      VARSPLIC 965 975 /FTID=VSP_005656.
CC      AVLSAELSKTS -> MDGQKHKWKD (in isoform
CC      3).
CC      /FTID=VSP_005657.
CC      VARSPLIC 173 975 Missing (in isoform 2).
CC      /FTID=VSP_005658.
CC      VARSPLIC 192 975 Missing (in isoform 4).
CC      /FTID=VSP_005659.
CC      CONFLICT 1130 1131 Missing (in Ref. 3; AAD31020).
CC      SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;
Query Match 100.0%; Score 925; DB 1; Length 1163;
Best Local Similarity 100.0%; Pred. No. 3.le-68;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALSVTSFRIYKGVIOA 60
Db      |||||
Db      975 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALSVTSFRIYKGVIOA 1034
Qy      61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPFAV 120
Db      |||||
Db      1035 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPFAV 1094
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Qy      121 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db      |||||
Db      1095 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1154
Qy      181 IPGLKRRKAD 189
Db      |||||
Db      1155 IPGLKRRKAD 1163
RESULT 2
Q80W95 PRELIMINARY; PRT; 578 AA.
ID Q80W95;
AC Q80W95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER 1
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
Query Match 99.1%; Score 917; DB 2; Length 578;
Best Local Similarity 98.9%; Pred. No. 7e-68;
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      1 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALSVTSFRIYKGVIOA 60
Db      |||||
Db      390 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALSVTSFRIYKGVIOA 449
Qy      61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPFAV 120
Db      |||||
Db      450 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPFAV 509
Qy      121 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db      |||||
Db      510 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 569
Qy      181 IPGLKRRKAD 189
Db      |||||
Db      570 IPGLKRRKAE 578
RESULT 3
Q8K290 PRELIMINARY; PRT; 639 AA.
ID Q8K290;
AC Q8K290;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Frange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC032192; AAH32192.1; -;  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS00845; RETICULON; 1.  
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 99.1%; Score 917; DB 2; Length 639;  
 Best Local Similarity 98.9%; Pred. No. 7.8e-68;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 451 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 510

Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVSLKFAV 120  
 Db 511 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVSLKFAV 570

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 180  
 Db 571 LMWVFTYVGALFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 630

Qy 181 IPGLKRRKAD 189  
 Db 631 IPGLKRRKAE 639

RESULT 4  
 Q8BGK7 PRELIMINARY; PRT; 1046 AA.  
 AC Q8BGK7  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RTN4.  
 GN Name=Rtn4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
 RT "Genomic structure and functional characterisation of the promoters of  
 human and mouse nogo/rtn4.";

RL J. Mol. Biol. 325:299-323 (2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;  
 RA Van der Putten H., Mir A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY102280; AA073502.1; -;  
 DR MGD; AY102286; AA073507.1; -;  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0001525; P:angiogenesis; IMP.  
 DR GO; GO:0007399; P:angiogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS00845; RETICULON; 1.  
 SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 99.1%; Score 917; DB 2; Length 1046;  
 Best Local Similarity 98.9%; Pred. No. 1.3e-67;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 858 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 917

Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVSLKFAV 120  
 Db 918 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVSLKFAV 977

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 180  
 Db 978 LMWVFTYVGALFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 1037

Qy 181 IPGLKRRKAD 189  
 Db 1038 IPGLKRRKAE 1046

RESULT 5  
 Q8BGK9 PRELIMINARY; PRT; 1162 AA.  
 AC Q8BGK9  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RTN4.  
 GN Name=Rtn4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
 RT "Genomic structure and functional characterisation of the promoters of  
 human and mouse nogo/rtn4.";  
 RL J. Mol. Biol. 325:299-323 (2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;

RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AY102284; AAM73506.1; -;  
DR EMBL; AY102286; AAM73511.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PSS0845; Reticulon; 1.  
SQ SEQUENCE 1162 AA; 126612 MW; 855697FPBEE11781F CRC64;  
  
Query Match 99.1%; Score 917; DB 2; Length 1162;  
Best Local Similarity 98.1%; Pred. No. 1.4e-67;  
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
DB 974 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1033  
  
QY 61 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRLFLVDDLVDSLKFAV 120  
DB 1034 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRLFLVDDLVDSLKFAV 1093  
  
QY 121 LMWFTYVYVGAFLNGTLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDMAKIOAK 180  
DB 1094 LMWFTYVYVGAFLNGTLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDMAKIOAK 1153  
  
QY 181 IPLKRRKAD 189  
DB 1154 IPLKRRKAE 1162  
  
RESULT 6  
QBHF5 PRELIMINARY; PRT; 375 AA.  
ID QBHF5;  
AC QBHF5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE RTN4.  
GN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of  
human and mouse nogo/rtn4.";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RX STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvcJ7;  
RX STRAIN=129SvcJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AY102282; AAM73504.1; -;  
DR EMBL; AY102286; AAM73509.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PSS0845; Reticulon; 1.  
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;  
  
Query Match 98.8%; Score 914; DB 2; Length 375;  
Best Local Similarity 98.4%; Pred. No. 8e-68;  
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
DB 187 AVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 246  
  
QY 61 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRLFLVDDLVDSLKFAV 120  
DB 247 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRLFLVDDLVDSLKFAV 306  
  
QY 121 LMWFTYVYVGAFLNGTLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDMAKIOAK 180  
DB 307 LMWFTYVYVGAFLNGTLTLLILALISLFSIPVIYERHVOQIDHYLGLANKSVKDMAKIOAK 366  
  
QY 181 IPLKRRKAD 189  
DB 367 IPLKRRKAE 375  
  
RESULT 7  
RTN4 MOUSE  
ID RTN4 MOUSE STANDARD; PRT; 199 AA.  
AC Q99P72; OSCTE3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).  
GN Name=Rtn4; Synonyms=NOCO;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3T3-L1; TISSUE=Adipocyte;  
RA Coulson A.C., Craggs P.D., Morris N.J.;  
RT "Mouse vp20/RTN4C cDNA.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
RP SEQUENCE OF 170-199 FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (By  
CC similarity).  
CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
CC membrane of the endoplasmic reticulum through 2 putative  
CC transmembrane domains (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=1;  
CC Comment=A number of isoforms may be produced;  
CC Name=s1;  
CC IsoId=Q99P72-1; Sequence=Displayed;  
CC -1- SIMILARITY: Contains 1 reticulon domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC ENBL; AFJ26337; AAK08076.1; -;  
CC EMBL; AK003859; -; NOT ANNOTATED\_CDS.  
CC MGD; MGI:1915835; Rtn4.  
CC GO; GO:0005783; C:endoplasmic reticulum; IDA.  
CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.  
CC GO; GO:0005635; C:nuclear membrane; ISS.  
CC GO; GO:0005515; F:protein binding; IPI.  
CC GO; GO:0019887; P:negative regulation of anti-apoptosis; ISS.  
CC GO; GO:0030517; P:negative regulation of axon extension; ISS.  
CC GO; GO:0007399; P:neurogenesis; IDA.  
CC InterPro; IPR003388; Reticulon.  
CC Pfam; PF02453; Reticulon; 1.  
CC PROSITE; PS50845; RETICULON; 1.  
CC KW Alternative splicing; Endoplasmic reticulum; Transmembrane.  
CC FT DOMAIN 1 25 Cytoplasmic (Potential).  
CC FT TRANSMEM 26 50 Potential.  
CC FT DOMAIN 51 137 Luminal (Potential).  
CC FT TRANSMEM 138 162 Potential.  
CC FT DOMAIN 163 199 Cytoplasmic (Potential).  
CC FT DOMAIN 12 199 Reticulon.  
CC SQ SEQUENCE 199 AA; 22466 MW; 07BESD580059ED9C CRC64;  
  
Query Match 98.78; Score 913; DB 1; Length 199;  
Best Local Similarity 98.94; Pred. No. 5.1e-68;  
Matches 186; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 61  
Db 12 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 71  
  
Qy 62 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAVL 121  
Db 72 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAVL 131  
  
Qy 122 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
Db 132 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 191  
  
Qy 182 PGLKRRAD 189  
Db 192 PGLKRAE 199  
  
RESULT 8  
Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.  
AC Q8BH78;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE RTN4.  
GN Names=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of  
RT human and mouse nogo/rtn4.";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvvcJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102281; AAM73503.1; -;  
DR EMBL; AY102286; AAM73508.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0005525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
DR SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;  
  
Query Match 98.78; Score 913; DB 2; Length 356;  
Best Local Similarity 98.94; Pred. No. 9.2e-68;  
Matches 186; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 61  
Db 169 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 228  
  
Qy 62 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAVL 121  
Db 229 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKPAVL 288  
  
Qy 122 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
Db 289 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 348  
  
Qy 182 PGLKRRAD 189  
Db 349 PGLKRAE 356  
  
RESULT 9  
Q8IU04  
ID Q8IU04 PRELIMINARY; PRT; 986 AA.  
AC Q8IU04;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE RNT4 (RTN4 isoform AB) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform  
DE F) (RTN4 isoform G) (RTN4 isoform Aa).  
GN Names=Rtn4;  
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4";
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=restis;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102285; AAM64244.1; -
DR EMBL; AY123246; AAM64250.1; -
DR EMBL; AY123247; AAM64251.1; -
DR EMBL; AY123248; AAM64252.1; -
DR EMBL; AY123249; AAM64253.1; -
DR EMBL; AY123250; AAM64254.1; -
DR EMBL; AY123245; AAM64249.1; -
DR GO; GO:0005783; C:endooplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
DR SEQUENCE 986 AA; 108449 MW; 0CDE8F6470364415A CRC64;

Query Match          98.2%; Score 908; DB 2; Length 986;
Best Local Similarity 97.4%; Pred. No. 6.8e-67;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVVLLLYWRDVKKTGVFGASLFLLLSLTVFSIVSVTAIYALSLVTSFRIYKGVIOA 60
DB 798 SVVLLLYWRDVKKTGVFGASLFLLLSLTVFSIVSVTAIYALSLVTSFRIYKGVIOA 857

QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRFLVLDVLSKPAV 120
DB 858 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVLDVLSKPAV 917

QY 121 LMWFTYVYGALFNGLLTLLILALISLFSIPVIYERHQVVIDHYLGLANKSVKDMAKIOAK 180
DB 918 LMWFTYVYGALFNGLLTLLILALISLFSIPVIYERHQVVIDHYLGLANKSVKDMAKIOAK 977

QY 181 IPGLKRRKAD 189
DB 978 IPGLKRRKAE 986

RESULT 10
RTN4 HUMAN
ID RTN4 HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; Q9A962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9Y293; Q9Y2Y7;
DC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
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RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans.";
RL Nature 403:383-384(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
RT 2p14-->2p13 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 88:101-102(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RT "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
RA Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22389237; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., FAhey J., Helton E., Kettman M., Madan A., Rodriguez S., Rodriguez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Makra M.A., RT "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.", RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[11] SEQUENCE FROM N.A. (ISOFORM 3).

RP TISSUE=Umbilical cord blood;

RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;

RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.; RT "Cloning and functional analysis of cDNAs with open reading frames for RT 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.", RL Genome Res. 10:1546-1560(2000).

[12] SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).

RP TISSUE=Brain;

RX Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

RA Mao Y.M., Xie Y., Zheng Z.H.; [13] SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).

RX TISSUE=Testis;

RA Sha J.H., Zhou Z.M., Li J.M.; [14] Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN TOPOLOGY.

RP TISSUE=Brain;

RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;

RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.; RT "Identification of the Nogo inhibitor of axon regeneration as a RT Reticulon protein.", RL Nature 403:439-444(2000).

[15] FUNCTION.

RP TISSUE=Brain;

RX MEDLINE=21089055; PubMed=1201742; DOI=10.1038/35053072;

RA Fournier A.E., GrandPre T., Strittmatter S.M.; RT "Identification of a receptor mediating Nogo-66 inhibition of axonal RT regeneration.", RL Nature 409:341-346(2001).

[16] REVIEW.

RP MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134;

RA Ng C.B.L., Tang B.L.; RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron RT regeneration.", RL J. Neurosci. Res. 67:559-565(2002).

CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help CC block the regeneration of the nervous central system in adults. CC Isoform 2 reduces the anti-apoptotic activity of Bcl-x1 and Bcl-2. CC This is likely consecutive to their change in subcellular CC location, from the mitochondria to the endoplasmic reticulum, CC after binding and sequestration.

CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic CC reticulum. Anchored to the membrane of the endoplasmic reticulum CC through 2 putative transmembrane domains.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;

CC IsoId=Q9NQC3-1; Sequence=Displayed;

CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foocon-M;

CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;

CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocon-S;

CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;

CC Name=4;

CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;

CC -1- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain CC and testis and weakly in heart and skeletal muscle. Isoform 2 is CC widely expressed excepted for the liver. Isoform 3 is expressed in CC brain, skeletal muscle and adipocytes. Isoform 4 is testis- CC specific.

CC -1- SIMILARITY: Contains 1 reticulon domain.

CC -1- CAUTION: Ref.11 sequence differs from that shown due to CC frameshifts in positions 1149 and 1156.

CC -----

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CC -----

CC EMBL; AJ251383; CAB99248.1; -

CC EMBL; AJ251384; CAB99249.1; -

CC EMBL; AJ251385; CAB99250.1; -

CC EMBL; AB040462; BAB18927.1; -

CC EMBL; AB040463; BAB18928.1; -

CC EMBL; AF148517; AAG12176.1; -

CC EMBL; AF148538; AAG12177.1; -

CC EMBL; AF087901; AAG12205.1; -

CC EMBL; AF320999; AAG40878.1; -

CC EMBL; AF132047; AAD31021.1; -

CC EMBL; AF132048; AAD31022.1; -

CC EMBL; AB015639; BAA83712.1; -

CC EMBL; AF077050; AAD27783.1; -

CC EMBL; AF177332; AAG17976.1; -

CC EMBL; AB020693; BAA74909.2; ALT\_INIT.

CC EMBL; BC001035; AAH01035.1; -

CC EMBL; BC007109; AAH07109.1; -

Query Match 98.2%; Score 908; DB 1; Length 1192;

Best Local Similarity 97.4%; Pred. No. 8.3e-67; Indels 0; Gaps 0;

Matches 184; Conservative 3; Mismatches 2;

Qy 1 SVVDLLYWRDKTKTGVVFGASLFLSLTVFSVSVTAYIALALLSVTFRIYKGVIOA 60

Db 1004 SVVDLLYWRDKTKTGVVFGASLFLSLTVFSVSVTAYIALALLSVTFRIYKGVIOA 1063

Qy 61 IQKSDGHPFRAYLESEVAISELQKYSNLSALGHVNSTIKELRRLFLVDLVDLSLKFV 120

Db 1064 IQKSDGHPFRAYLESEVAISELQKYSNLSALGHVNSTIKELRRLFLVDLVDLSLKFV 1123

Qy 121 LMMVFTYVGNLFNGLTLILALISLPSIPVYERHVOIDHYLGLANKSVKDAWAKIOAK 180

Db 1124 LMMVFTYVGNLFNGLTLILALISLPSIPVYERHVOIDHYLGLANKSVKDAWAKIOAK 1183

Qy 181 IPGLKRRKAD 189

Db 1184 IPGLKRRKAE 1192

RESULT 11

Q8K3G8 PRELIMINARY; PRT; 1163 AA.

AC Q8K3G8; 01-OCT-2002 (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Nogo-A.

GN Name=RTn4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

```

RN RC SEQUENCE FROM N.A.
RP STRAIN=BA1B/c;
RA Jin W., Long M., Li R., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114152; AAM77068.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;

Query Match 98.0%; Score 906.5; DB 2; Length 1163;
Best Local Similarity 98.4%; Pred. No. 1.1e-66;
Matches 187; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 59
Db 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 1033
QY 60 AIQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLKPFA 119
Db 1034 AIQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLKPFA 1093
QY 120 VLMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQOA 179
Db 1094 VLMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQOA 1153
QY 180 KIPGLKRRKAD 189
Db 1154 KIPGLKRRKAE 1163

RESULT 12
Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Reticulon 4, isoform D (RTN4 isoform B2).
GN Name=RTN4;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2238257; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323 (2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016165; AAH16165.1; -.
DR EMBL; AY102278; AAM64247.1; -.
DR EMBL; AY102285; AAM64242.1; -.
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 97.8%; Score 905; DB 2; Length 392;
Best Local Similarity 96.8%; Pred. No. 4.7e-67;
Matches 183; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 60
Db 204 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 263
QY 61 IQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLKPFAV 120
Db 264 IQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLKPFAV 323
QY 121 LMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQOA 180
Db 324 LMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQOA 383
QY 181 IPGLKRRKAD 189
Db 384 IPGLKRRKAE 392

RESULT 13
Q7YRW9 PRELIMINARY; PRT; 199 AA.
AC Q7YRW9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB RTN4-C.
GN Name=RTN4;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family."
RL FASEB J. 17:1238-1247 (2003).
DR EMBL; AY164744; AAP47319.2; -.
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;

Query Match 97.7%; Score 904; DB 2; Length 199;

```

Best Local Similarity 97.3%; Pred. No. 2.8e-67;  
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

Qy 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121  
Db 72 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131

Qy 122 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOVDHYLGLANKSVKDMAKIOAKI 181  
Db 132 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOVDHYLGLANKSVKDMAKIOAKI 191

Qy 182 PGLKRRAD 189  
Db 192 PGLKRRAD 199

## RESULT 14

Q6IPNO PRELIMINARY; PRT; 343 AA.

AC Q6IPNO  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE RIN4 protein.  
GN Name=RIN4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC071848; AAH71848.1; -;  
DR GO: GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro: IPR003388; Reticulon.  
DR Pfam: PF02453; Reticulon; 1.  
DR PROSITE: PS50845; RETICULON; 1.  
SQ SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;

Query Match 97.7%; Score 904; DB 2; Length 343;  
Best Local Similarity 97.3%; Pred. No. 5e-67;  
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 156 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 215

Qy 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121  
Db 216 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 275

Qy 122 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOVDHYLGLANKSVKDMAKIOAKI 181  
Db 276 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOVDHYLGLANKSVKDMAKIOAKI 335

Qy 182 PGLKRRAD 189  
Db 336 PGLKRRAD 343

## RESULT 15

Q8K3G7 PRELIMINARY; PRT; 357 AA.

AC Q8K3G7  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Nogo-B.  
GN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Jin W., Li R., Long M., Shen J., Ju G.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY114153; AAM77069.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO: GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro: IPR003388; Reticulon.  
DR Pfam: PF02453; Reticulon; 1.  
DR PROSITE: PS50845; RETICULON; 1.  
SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFBDF15 CRC64;

Query Match 97.6%; Score 902.5; DB 2; Length 357;  
Best Local Similarity 98.4%; Pred. No. 6.9e-67;  
Matches 186; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 169 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 228

Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 229 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 288

Qy 121 LMVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOVDHYLGLANKSVKDMAKIOAK 180  
Db 289 LMVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOVDHYLGLANKSVKDMAKIOAK 348

Qy 181 IPGLKRRAD 189  
Db 349 IPGLKRRAD 357

Search completed: June 16, 2005, 13:17:34  
Job time : 26.6406 secs

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GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 05:38:22 ; Search time 2737.5 Seconds  
(without alignments)  
3345.401 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDKTKGVFGA.....VKDAMAKIQAKIPGLKRRAD 189

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -MODEL=frame; -p2n.model -DEV=xlp

-Q/cn2\_1/USPTO.spool\_p/US09830972/runat\_16062005\_153944\_19011/app.query.fasta\_1.654  
-DB=GenEmbl -QFMT=fastcap -SUFFIX=rg -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL  
-OUTFMT=ptlo -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*

1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sv.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	3489	6	AX766046 Sequence
2	925	100.0	3492	6	CQ829507 Sequence
3	925	100.0	4684	10	RNO242961 Rattus no
4	922	99.7	2782	6	AX700396 Sequence

5	922	99.7	2782	10	AX164741	AY164741 Rattus no
6	922	99.7	2782	10	AF132045	AF132045 Rattus no
7	921	99.6	764	10	AF051335	AF051335 Rattus no
8	921	99.6	1568	10	RNO242963	AJ242963 Rattus no
9	921	99.6	2156	10	AY164740	AY164740 Rattus no
10	921	99.6	2156	10	RNO242962	AJ242962 Rattus no
11	921	99.6	2410	10	BC070879	BC070879 Rattus no
12	917	99.1	1738	10	AB073672	AB073672 Mus muscu
13	917	99.1	2958	10	BC032192	BC032192 Mus muscu
14	917	99.1	3815	10	BC032272	BC032272 Mus muscu
15	917	99.1	4063	10	AY102280	AY102280 Mus muscu
16	917	99.1	4518	10	BC056373	BC056373 Mus muscu
17	917	99.1	4627	10	AY102284	AY102284 Mus muscu
18	914	98.8	2266	10	AY102282	AY102282 Mus muscu
19	913	98.7	734	10	AF326337	AF326337 Mus muscu
20	913	98.7	1769	10	AY102283	AY102283 Mus muscu
21	913	98.7	2209	10	AY102281	AY102281 Mus muscu
22	908	98.2	2481	9	AF063601	AF063601 Homo sapi
23	908	98.2	2883	9	AF320999	AF320999 Homo sapi
24	908	98.2	3491	9	AF333336	AF333336 Homo sapi
25	908	98.2	3576	6	AX766050	AX766050 Sequence
26	908	98.2	3579	6	BD249446	BD249446 Protein s
27	908	98.2	3579	9	HA251383	AJ251383 Homo sapi
28	908	98.2	3919	6	CQ829486	CQ829486 Sequence
29	908	98.2	4053	6	AX195249	AX195249 Sequence
30	908	98.2	4053	9	AB020693	AB020693 Homo sapi
31	908	98.2	4060	9	AY123250	AY123250 Homo sapi
32	908	98.2	4070	9	AY123249	AY123249 Homo sapi
33	908	98.2	4093	6	BD270070	BD270070 Secreted
34	908	98.2	4102	9	AY123245	AY123245 Homo sapi
35	908	98.2	4109	9	AY123248	AY123248 Homo sapi
36	908	98.2	4123	9	AY123247	AY123247 Homo sapi
37	908	98.2	4160	9	AY123246	AY123246 Homo sapi
38	908	98.2	4166	9	AB040462	AB040462 Homo sapi
39	908	98.2	4632	9	AF148537	AF148537 Homo sapi
40	908	98.2	4789	6	CQ874017	CQ874017 Sequence
41	908	98.2	4789	9	AY102279	AY102279 Homo sapi
42	908	98.2	4822	6	AR220865	AR220865 Sequence
43	905.5	98.0	3821	10	AY114152	AY114152 Mus muscu
44	905	97.8	1784	9	BC016165	BC016165 Homo sapi
45	905	97.8	2389	9	AY102278	AY102278 Homo sapi

ALIGNMENTS

RESULT 1	AX766046	Sequence 1 from Patent WO03002602.	3489 bp	DNA	linear	PAT 25-JUN-2003
LOCUS	AX766046	AX766046.1	GI:32260128			
DEFINITION	AX766046	Rattus norvegicus (Norway rat)				
ACCESSION	AX766046	Rattus norvegicus				
VERSION	AX766046.1	Rattus norvegicus				
KEYWORDS		Nogo and nogo receptor derived peptides for t-cell mediated neuroprotection				
SOURCE		Eisenbach-Schwartz,M. and Hauben,E.				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE		1				
AUTHORS		Eisenbach-Schwartz,M. and Hauben,E.				
TITLE		Nogo and nogo receptor derived peptides for t-cell mediated neuroprotection				
JOURNAL		Patent: WO 03002602-A 1 09-JAN-2003;				
FEATURES		YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)				
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ORIGIN						
Alignment Scores:			2.82e-85	Length:		3489
Pred. No.:						

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Score: 925.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AX766046 (1-3489)

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QY 21 SerLeuPheLeuLeuSerLeuThyValPheSerIleValSerValThrAlaTyrIle 40
DB 2983 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGCAATGTTCAGTGTAAACGGCTACAT 3042
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3043 GCCTTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGT 3102
QY 61 IleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3103 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATAATTAGAATCTCAAGTTGCTATA 3162
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlnLeuThrLeuLeuLeu 140
DB 3283 TTGATGGGGTGTACTTATGTTGGTGGCTTGTTCATGGTCTGACACTACTGATTTTA 3342
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
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QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3403 CATTATCTAGGACTTGCAACACAGAGTGTTAGGATGCCATGCCAATAATCCAGCAAA 3462
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3463 ATCCCTGGATTGAAGCCCAAGCAGAT 3489

RESULT 2
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LOCUS CQ829507 3492 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 25 from Patent WO2004052932.
ACCESSION CQ829507
VERSION CQ829507.1 GI:49732820
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1. Barske, C., Mir, A.K., Oertle, T., Schnell, L., Schwab, M.E., Vitaliti, A. and Zurini, M.
AUTHORS Nogo a binding molecules and pharmaceutical use thereof
TITLE Nogo a binding molecules and pharmaceutical use thereof
JOURNAL Patent: WO 2004052932-A 25 24-JUN-2004;
Novartis AG (CH)
FEATURES
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ORIGIN

Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CQ829507 (1-3492)

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QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

DB 3043 GCCTTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGT 3102

QY 61 IleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIle 80

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DB 3163 TCAGAGGAATGGTTCAGAAATACAGTAATTCGTCTTTGGTGTGTAACGACCAATA 3222

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

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QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlnLeuThrLeuLeuLeu 140

DB 3283 TTGATGGGGTGTACTTATGTTGGTGGCTTGTTCATGGTCTGACACTACTGATTTTA 3342

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160

DB 3343 GCTCTGATCTCACTCTCTCAGTATTCCTGTTATTTAAGACGGCATCAGGTGAGATAGAT 3402

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

DB 3403 CATTATCTAGGACTTGCAACACAGAGTGTTAGGATGCCATGCCAATAATCCAGCAAA 3462

QY 181 IleProGlyLeuLysArgLysAlaAsp 189

DB 3463 ATCCCTGGATTGAAGCCCAAGCAGAT 3489

Alignment scores:		
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Score:	922.00	Matches: 188

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Query Match: 99.68% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AX700396 (1-2782)

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 1331 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGATTTAGAAATCTGAAGTTCACAT 1390

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 1391 GCCTTGGCCCTGCTCTCGGTGACATACAGTTCCTGCTCTGCTGCTGCTGCTGCTG 1450

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80
Db 1451 ATCCAGAAATCAGATGAAGCCCAATTCAGGGCATATTTAGAAATCTGAAGTTCGATA 1510

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 1511 TCAGAGAAATGCTTCTGAGAAATACAGTAATTCCTGCTCTGCTGCTGCTGCTGCTG 1570

QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 1571 AAAGAACTGAGCGGCTTCTTCTAGTGTATGATTTAGTTCCTGAGTTCGAGTGC 1630

QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 1631 TTGATGTGGGTGTTACTTATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1690

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 1691 GCTCTGATCTCACTCTCAGTATTCCTGTTATTAAGACGGCATCAGGTGAGATAGAT 1750

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 1751 CATATCTAGGACTTCGAAACAGAGTGTTAAGATGCCATGCCCAAAATCCAAAGCAAA 1810

QY 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 1811 ATCCCTGGATTGAAGCGCAAGCAGAT 1837

RESULT 5
LOCUS AY164741 2782 bp mRNA linear ROD 30-JUN-2003
DEFINITION Rattus norvegicus RTN4-B2 (Rtn4) mRNA, complete cds; alternatively spliced.
ACCESSION AY164741
VERSION AY164741.1 GI:32331282
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 2782)
AUTHORS Oertle,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
TITLE A reticular rhapsody: phylogenetic evolution and nomenclature of the RTN/Nogo gene family
JOURNAL PNAS 97: 1238-1247 (2000)
PUBMED 12832288
REFERENCE 2 (bases 1 to 2782)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department of Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Zurich 8057, Switzerland
FEATURES Location/Qualifiers
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Db      1811 ATCCCTGGATTGAAGCGCAAGCAGAT 1837
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DEFINITION complete cds.
ACCESSION AF132045
VERSION AF132045.1 GI:4838512
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2782)
AUTHORS Ito,T. and Schwartz,S.M.
TITLE Cloning of a member of the reticulon gene family in rat: One of two
JOURNAL minor splice variants
AUTHORS Unpublished
REFERENCE 2 (bases 1 to 2782)
AUTHORS Ito,T. and Schwartz,S.M.
JOURNAL Direct Submission
TITLE Submitted (27-FEB-1999) Pathology, University of Washington, 1959
JOURNAL Pacific NE, Seattle, WA 98195, USA
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Alignment Scores:
Pred. No.: 4,318-85 Length: 2782
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Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.47% Mismatches: 0
Query Match: 99.68% Indels: 0
DB: 10 Gaps: 0
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Qy      41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Db      1391 GCCTTTGGCCCTCTCTCGTGACTATCAGCTTTAGGATATATAAGGGCGGTATCCAGGCT 1450
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Db      1451 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTAGATCTGAAGTTGCTATA 1510
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Qy      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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Db      1511 TCAGAGGAATTTGGTTTCAGAAATACAGTAATTTCTGCTCTTGGTTCATGTGAACACCAATA 1570
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Qy      101 LysGluLeuAraGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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Qy      161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Qy      181 IleProGlyLeuLysArgLysAlaAsp 189
Db      1811 ATCCCTGGATTGAAGCGCAAGCAGAT 1837
|||||
RESULT 7
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LOCUS      Rattus norvegicus GLUT4 vesicle 20kDa protein mRNA, complete cds.
DEFINITION
ACCESSION AF051335
VERSION AF051335.1 GI:6016998
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 764)
AUTHORS Morris,N.J., Ross,S.A., Neveu,J.M., Lane,W.S. and Lienhard,G.E.
TITLE Cloning and characterization of a 22 kDa protein from rat
JOURNAL adipocytes: a new member of the reticulon family
MEDLINE Biochim. Biophys. Acta 1450 (1), 68-76 (1999)
PUBMED 9249816
REFERENCE 2 (bases 1 to 764)
AUTHORS Morris,N.J.
JOURNAL Direct Submission
TITLE Submitted (26-FEB-1998) Biochemistry, Dartmouth Medical School,
Hannover, NH 03755, USA
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Pred. No.: 921.00 Matches: 188
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 99.57% Indels: 0
Query Match: 10 Gaps: 0
DB: 10

US-09-830-972-2_COPY_975_1163 (1-189) x AF051335 (1-764)

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QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 150 TTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATTGCC 209
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 210 TTGGCCCTGCTCTCGGTGACTATTCAGCTTTAGGATATATAAGGGCGGTGATCCAGGCTATC 269
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
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QY 162 TyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 570 TATCTAGGACTTCGAACCAAGAGTGTAAAGGATGCCCAATCCAAAGCAAAATC 629
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 630 CCTGGATTGAAGCGCAAGCAGAT 653

RESULT 8
RNO242963
LOCUS Rattus norvegicus mRNA for Nogo-C protein. linear ROD 28-JAN-2000
DEFINITION Rattus norvegicus mRNA for Nogo-C protein.
ACCESSION AJ242963
VERSION AJ242963.1 GI:6822250
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Db      391 GAGGAATGGTTCAGAAATACAGTAATTCCTGCTCTGGTCATGTGAACAGCACATAAAAA 450
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Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
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Qy      142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      631 TATCTAGACTTGCACCAAGAGTGTTAAGGATGCGCATGCGCCCAAAATCCAGCAAAAATC 690
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      691 CCTGGATTGAAGCGCAAGCAGAT 714

RESULT 9
AY164740      2156 bp mRNA linear ROD 30-JUN-2003
LOCUS        Rattus norvegicus RTN4-B1 (Rtn4) mRNA, complete cds; alternatively
DEFINITION   spliced.
ACCESSION   AY164740
VERSION     AY164740.1 GI:32331280
KEYWORDS    Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE   1 (bases 1 to 2156)
AUTHORS    Oertle,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
TITLE      A reticular rhapodry: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family
JOURNAL    FASEB J. 17 (10), 1238-1247 (2003)
PUBMED    12832288
REFERENCE   2 (bases 1 to 2156)
AUTHORS    Oertle,T. and Schwab,M.E.
TITLE      Direct Submission
JOURNAL    Submitted (16-OCT-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
FEATURES    Location/Qualifiers
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3' UTR
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US-09-830-972-2_COPY_975_1163 (1-189) x AY164740 (1-2156)

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Qy      142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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LOCUS        Rattus norvegicus mRNA for Nogo-B protein.
DEFINITION   Rattus norvegicus mRNA for Nogo-B protein.
ACCESSION   AJ242962
VERSION     AJ242962.1 GI:6822248
KEYWORDS    Nogo-B protein.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE   1
AUTHORS    Chen,M.S., Huber,A.B., van der Haar,M.E., Frank,M., Schnell,L.,
Spillmann,A.A., Christ,F. and Schwab,M.E.
TITLE      Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1
JOURNAL    Nature 403 (5768), 434-439 (2000)
PUBMED    20129258
PUBMED    10667796
REFERENCE   2 (bases 1 to 2156)
AUTHORS    Van der Haar,M.E.

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**TITLE**  
**JOURNAL**  
**COMMENT**  
**FEATURES**  
 source  
 Direct Submission  
 Submitted (14-JUN-1999) Van der Haar M.E., Department of  
 Neuromorphology, Brain Research Institute, University of Zurich,  
 Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND  
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 Alignment Scores:  
 Pred. No.: 3,94e-85 Length: 2156  
 Score: 921.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
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 Db 1245 CTGTGATTGAAGCGCAAGCAGAT 1268  
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 complete cds.  
 ACCESSION BC070879  
 VERSION BC070879.1 GI:47477874  
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 Rattus.  
 1 (bases 1 to 2410)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
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 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
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 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
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 Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalley, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 2410)  
 Strausberg, R.  
 Direct Submission  
 Submitted (17-MAY-2004) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
 Tissue Procurement: Howard Jacobs  
 cDNA Library Preparation: Express Genomics  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@nigri.nih.gov](mailto:nisc_mgc@nigri.nih.gov)  
 Akher, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
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 Young, A., Zhang, L.-H. and Green, E.D.  
 Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 175 Row: a Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929187  
This clone has the following problem: The cds is short compared to the longest cds in the locus.

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## ORIGIN

Alignment Scores:  
Pred. No.: 4,54e-85 Length: 2410  
Score: 921.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
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DEFINITION Mus musculus mRNA for Nogo-A, partial cds.  
ACCESSION AB073672  
VERSION AB073672.1 GI:30268592  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Tozaki, H. and Hirata, T.  
TITLE The partial sequence of mouse nogo-A cDNA clone#4109  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1738)  
AUTHORS Tozaki, H. and Hirata, T.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2001) Hirokazu Tozaki, Division of Brain  
Function, National Institute of Genetice; Yata 1111, Miehima,  
Shizuoka 411-8540, Japan [E-mail:htozaki@lab.nig.ac.jp],  
URL: http://www.nig.ac.jp/home-j.html, Tel: 81-55-981-6721 (ex. 6721),  
Fax: 81-55-981-6722)  
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## ORIGIN

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Score: 917.00 Matches: 187  
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Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 99.14% Indels: 0  
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ORGANISM Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2958)
AUTHORS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
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AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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## RESULT 14

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## LOCUS

BC032272 Mus musculus reticulon 4, mRNA (cdna clone IMAGE:5366860), partial cds.

## DEFINITION

BC032272.1 GI:22749634

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

1 (bases 1 to 3815)  
Strausberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L., Statileton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Udén,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Pahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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2 (bases 1 to 3815)  
Strausberg,R.  
Direct Submission  
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nih.gov](mailto:nisc_mgc@nih.gov)  
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakeley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Madu,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

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Percent Similarity: 99.47% Conservatives: 1  
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TITLE Genomic Structure and Functional Characterisation of the Promoters of Human and Mouse nogo/rtn4	
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)	
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AUTHORS Oertle,T. and Schwab,M.E.	
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JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland	
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Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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2 (bases 1 to 4518)
Strausberg,R.
Direct Submission
Submitted (11-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
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Clone distribution: MGC clone distribution information can be found
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TESTAANI FVLEDSHTSEKDEKKI BERKAOI ITERSPTKSNPFLVAIHDSADIY
TTNLSKVTEAVATMPGLDVLQAESELENEATGTAKIAYTKVDLVQTSIAQIE
SIYPTALCPSFEAEATPSPVLPDI VMEAPLNLSTGASVQSPSLVLEPSPVS
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ORIGIN
Alignment Scores:
Pred. No.:      2.63e-84      Length:      4518
Score:          917.00      Matches:      187
Percent Similarity: 99.47%      Conservative: 1
Best Local Similarity: 98.94%      Mismatches: 1
Query Match:     99.14%      Indels:      0
DB:              10          Gaps:         0
US-09-830-972-2_COPY_975_1163 (1-189) x BC056373 (1-4518)
Qy      1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db      3039 TCAGTTGTGACCTCCTCTGCTACCTGGAGAGACATTAAAGACTGGAGTGGTGTGTCGCC 3098
Qy      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      3099 AGCTTATTCCTGCTGCTGCTCTCTGACAGTGTTCAGCATTGTTCAGTGAACGGCTACATT 3158
Qy      41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db      3159 GCCTTGGCCCTGCTCTCTGCTACCTATCAGCTTTAGGATATATAAGGGTGTGATCCAAAGCT 3218
Qy      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      3219 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAAATCTGAAGTTGCCATA 3278
Qy      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db      3279 TCAGAGGAATTTGGTTTCAGAAATATAGTAAATTTCTGCTCTTGTTCATGTGACAGCACAATA 3338
Qy      101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db      3339 AAAGAATTGAGGCGTCTCTTCTTAGTGATGATTTAGTTGATTCCTCGAAGTTGCACGTG 3398
Qy      121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db      3399 TTGATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTGTTGACACTACTGATTTTA 3458

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US-09-830-972-2\_COPY\_975\_1163 (1-189) x AF326337 (1-734)

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Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      160 TTATTCCTGCTGCTCTGCTGAGAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATTCGC 219

Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      220 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 279

Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      280 CAGAAATCAGATGAGCGCCACCCATTGAGGCATATTTGGAATCTGAAGTTGCCATATCA 339

Qy      82 GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIleLys 101
Db      340 GAGGAATGGTTTCAGAAATATAGTAATCTGCTCTTGGTTCATGTGAACAGCACCAATAAAA 399

Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      400 GAATTCAGCGGCTCTCTCTGATGATTTAGTTGATTTAGTTGATTTCCCTGAGTTTCAGTGTG 459

Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db      460 ATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATAGTTTGGACACTACTGATTTTAGCC 519

Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      520 CTGATCTCACTCTTCAGTATTTCTGTTATATATGAACGGCATCAGCGGCAGATAGATCAT 579

Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      580 TATCTAGGACTTGCACCAACAGAGTGTTAAGATGCCATGCGCCAAATCCAGCAAAATC 639

Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      640 CCTGGATTGAGCGCAAGCAGAA 663

RESULT 20
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LOCUS Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.
DEFINITION AY102283
ACCESSION AY102283.1 GI:23379814
VERSION AY102283.1
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1769)
AUTHORS Certle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 1769)
AUTHORS Certle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
REFERENCE 3 (bases 1 to 1769)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
FEATURES
source 1..1769

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280..879
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880..1769
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3' UTR

ORIGIN
Alignment Scores:
Pred. No.: 2,048-84 Length: 1769
Score: 913.00 Matches: 186
Percent Similarity: 99.47% Conservative: 1
Best Local Similarity: 98.94% Mismatches: 1
Query Match: 98.70% Indels: 0
DB: 10 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AY102283 (1-1769)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      313 GTTGTGACCTCTCTGCTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 372

Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      373 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATTCGC 432

Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      433 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 492

Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      493 CAGAAATCAGATGAGCGCCACCCATTGAGGCATATTTGGAATCTGAAGTTGCCATATCA 552

Qy      82 GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIleLys 101
Db      553 GAGGAATGGTTTCAGAAATATAGTAATCTGCTCTTGGTTCATGTGAACAGCACCAATAAAA 612

Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      613 GAATTCAGCGGCTCTCTCTGATGATTTAGTTGATTTCCCTGAGTTTCAGTGTGTTG 672

Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db      673 ATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATAGTTTGGACACTACTGATTTTAGCT 732

Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      733 CTGATCTCACTCTTCAGTATTTCTGTTATATATGAACGGCATCAGCGGCAGATAGATCAT 792

Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      793 TATCTAGGACTTGCACCAACAGAGCGTTAAGATGCCATGCGCCAAATCCAGCAAAATC 852

Qy      182 ProGlyLeuLysArgLysAlaAsp 189

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## ORIGIN

Alignment Scores:  
Pred. No.: 1,03e-83 Length: 2481  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AF063601 (1-2481)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 1568 TCAGTGTGTCACCTCTGCTGACGAGACATTAAGACAGCTGAGTGTGTTGGTGC 1627  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 1628 AGCTATTCCTGCTGCTTTCATGACAGTATTCAGCATTTGAGCGCTAACAGCTTACAT 1687  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 1688 GCCTTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 1747  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 1748 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGCAATCTGAAGTTGCTATA 1807  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 1808 TCTGAGGAGTGTGTTGAGAGTACAGTAATCTGCTCTGCTGCTGATGACCTGACGATA 1867  
QY 101 LysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 1868 AAGGAACCTCAGCGCCCTCTCTTAGTGTATGATTTAGTTGATCTCTGAAGTTGCGAGTG 1927  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
DB 1928 TTGATGTGGTATTTACCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1987  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 1988 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGACGGCNCACGACAGATAGAT 2047  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 2048 CATTAICTAGGACTTCGAAATAGATGTTAAAGATGCTATGCTAAATCCAAAGCAAA 2107  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 2108 ATCCCTGGATGAAGCGCAAGCTGAA 2134

## RESULT 23

AF320999  
LOCUS 2883 bp mRNA linear PRI 18-DEC-2000  
DEFINITION Homo sapiens Nogo-A protein short form mRNA, complete cds,  
alternatively spliced.

## ACCESSION

AF320999

## VERSION

AF320999.1 GI:11878277

## KEYWORDS

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## SOURCE

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 2883)

## AUTHORS

Jin, W.-L. and Ju, G.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Unpublished  
2 (bases 1 to 2883)  
Jin, W.-L. and Ju, G.  
Direct Submission  
Submitted (12-NOV-2000) Institute of Neurosciences, No. 17 Chang Le  
West Road, Xian, Shannxi 710032, China  
Location/Qualifiers  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1,25e-83 Length: 2883  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AF320999 (1-2883)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 2314 TCAGTGTGTCACCTCTGCTGACGAGACATTAAGACAGCTGAGTGTGTTGGTGC 2373  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 2374 AGCTATTCCTGCTGCTTTCATGACAGTATTCAGCATTTGAGCGCTAACAGCTTACAT 2433  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 2434 GCCTTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 2493  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 2494 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGCAATCTGAAGTTGCTATA 2553  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 2554 TCTGAGGAGTGTGTTGAGAGTACAGTAATTCCTGCTCTTGGTTCATGTCAGTGAACGACGATA 2613  
QY 101 LysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 2614 AAGGAACCTCAGCGCCCTCTCTTAGTGTATGATTTAGTTGATCTCTGAAGTTGCGAGTG 2673  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140

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Db 2674 TTGATGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTTG 2733
Qy 141 AlaleuileSerLeuPheSerileProValilleTyrgluArgHisGlnValGlnleileasp 160
Db 2734 GCTCTCATTTTCACTCTTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT 2793
Qy 161 HistyLeuGlyLeuAlaAsnLysSerVallyAspAlaMetAlaLysileGlnAlalys 180
Db 2794 CATTATCTAGGACTTGCAATAAAGAAATGTTAAAGATGCTATGGCTAAATAACCAAGCAAAA 2853

Qy 181 IleProGlyLeuLysArgLysAlaasp 189
Db 2854 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2880

RESULT 24
AF333336 3491 bp mRNA linear PRI 27-MAY-2003
LOCUS Homo sapiens testis specific reticulon 5 protein mRNA, complete
DEFINITION
cds.
ACCESSION AF333336
VERSION AF333336.1 GI:13377627
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3491)
AUTHORS Zhou, Z.M., Sha, J.H., Li, J.M., Lin, M., Zhu, H., Zhou, Y.D., Wang, L.R.,
Zhu, H., Wang, Y.Q. and Zhou, K.Y.
TITLE Expression of a novel reticulon-like gene in human testis
JOURNAL Reproduction 123 (2), 227-234 (2002)
MEDLINE 21857060
PUBMED 11866689
REFERENCE 2 (bases 1 to 3491)
AUTHORS Sha, J.H., Zhou, Z.M. and Li, J.M.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2001) Key Lab of Reproductive Medicine, Nanjing
Medical University, Han Zhong Road 140, Nanjing, Jiangsu 210029,
China
FEATURES
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ORIGIN

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Alignment Scores:
Pred. No.: 1.6e-83 Length: 3491
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AF333336 (1-3491)

Qy 1 SerValValAspLeuLeuTyrrPArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 2570 TCAGTTGTGTGACCTCTCTGTCTGAGAGACATTAAGAAAGCTGGAGTGGTGTGTGGTGGC 2629

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrile 40
Db 2630 AGCTATTTCCTGCTGCTTCATTGACAGTATTGACATTTGAGCGTGAACGCCATACATT 2689

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAla 60
Db 2690 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCT 2749

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIle 80
Db 2750 ATCCAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATA 2809

Qy 81 SerGluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100
Db 2810 TCTGAGGAGTTGGTTGAGAGTACAGTAAATCTGCTCTTGTGTCATGTGAAGTGCAGATA 2869

Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 2870 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 2929

Qy 121 LeuMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu 140
Db 2930 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTATGCTGCTGACACTACTGATTTTG 2989

Qy 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrrGluArgHisGlnValGlnIleAsp 160
Db 2990 GCTCTCATTTCTCTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT 3049

Qy 161 HistyLeuGlyLeuAlaAsnLysSerVallyAspAlaMetAlaLysileGlnAlalys 180
Db 3050 CATTATCTAGGACTTGCAATAAAGAAATGTTAAAGATGCTATGGCTAAATAACCAAGCAAAA 3109

Qy 181 IleProGlyLeuLysArgLysAlaasp 189
Db 3110 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3136

RESULT 25
AX766050 3576 bp DNA linear PAT 25-JUN-2003
LOCUS Sequence 5 from Patent WO03002602.
DEFINITION
ACCESSION AX766050
VERSION AX766050.1 GI:32260129
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eisenbach-Schwartz, M. and Hauben, E.
TITLE Nogo and nogo receptor derived peptides for t-cell mediated
neuroprotection
JOURNAL Patent: WO 03002602-A 5 09-JAN-2003;
YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL)
FEATURES
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1..3576
/organism="Homo sapiens"
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exon

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## ORIGIN

## Alignment Scores:

Pred. No.: 1.65e-83 Length: 3576  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: Gaps: 6

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AX766050 (1-3576)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 3010 TCAGTTGTTGACCTCTCTGACGAGACATTAAGAACACTGGAGTGGTGTGGTGC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3070 AGCCTATTCTGCTGCTTTTCATTGACAGATTTACAGATTTGAGCGTAACAGCTACAT 3129  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60  
DB 3130 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuSerGluValAlaIle 80  
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3250 TCTGAGGAGTTGGTTCAGAGATACAGTAATTCCTCTTGGTTCATGTCAGCCAGATA 3309  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3310 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTGCGAGT 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3370 TTGATGGGTATTTACCTATGTTGGTGGCTTTGTTAAATGGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGATCAGCGCAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3490 CATTATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

## RESULT 26

BD249446 3579 bp DNA linear PAT 17-JUL-2003  
LOCUS Protein similar to neuroendocrine-specific protein, and encoding  
CDNA.

## ACCESSION

BD249446  
VERSION BD249446.1 GI:33059216  
KEYWORDS JP 2002522016-A/1  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 3579)

## AUTHORS

Michalovich, D. and Prinjha, R. K.

## TITLE

Protein similar to neuroendocrine-specific protein, and encoding

## JOURNAL

Patent: JP 2002522016-A 1 23-JUL-2002;

## COMMENT

SMITHKLINE BEECHAM PLC  
OS Homo sapiens (human)  
PN JP 2002522016-A/1  
PD 23-JUL-2002  
PF 21-JUL-1999 JP 2000561310

PR 22-JUL-1998 GB 9816024.5, 19-JUL-1999 GB 9916898.1 PI  
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA  
PC  
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/53, PC  
G01N33/566//  
PC C12P21/08, C12N15/00, C12N5/00  
PC C12P21/08, C12N15/00, C12N5/00  
CC Protein similar to neuroendocrine-specific protein, and CC  
encoding cDNA

FH Key Location/Qualifiers

FT source 1..3579

FT /organism="Homo sapiens (human)".

## FEATURES

## source

1..3579

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.65e-83 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: Gaps: 6

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BD249446 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 3010 TCAGTTGTTGACCTCTCTGACGAGACATTAAGAACACTGGAGTGGTGTGGTGC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3070 AGCCTATTCTGCTGCTTTTCATTGACAGATTTACAGATTTGAGCGTAACAGCTACAT 3129  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60  
DB 3130 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuSerGluValAlaIle 80  
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3250 TCTGAGGAGTTGGTTCAGAGATACAGTAATTCCTCTTGGTTCATGTCAGCCAGATA 3309  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3310 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTGCGAGT 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3370 TTGATGGGTATTTACCTATGTTGGTGGCTTTGTTAAATGGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGATCAGCGCAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3490 CATTATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

## RESULT 27

HSA251383

LOCUS

HSA251383 3579 bp mRNA linear PRI 22-JUL-2000



DEFINITION Homo sapiens mRNA for Nogo-A protein (Nogo gene).

ACCESSION AJ251383

VERSION AJ251383.1 GI:9408095

KEYWORDS Nogo gene; Nogo-A protein.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS

Prinjha, R., Moore, S. E., Vinson, M., Blake, S., Morrow, R.,

Christie, G., Michalovich, D., Simmons, D. L. and Walsh, P. S.

Inhibitor of neurite outgrowth in humans

Nature 403 (6768), 383-384 (2000)

20129242

PUBMED 10667780

REFERENCE 2 (bases 1 to 3579)

AUTHORS Michalovich, D.

Direct Submission

Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline

Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND

HERZEGOVINA

FEATURES

source

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/gene="Nogo"

1..3579

/gene="Nogo"

/codon\_start=1

/evidence="experimental"

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AGQEDFPVLETAASPLSPSAASFKEHEYLGNLSTVLPTGTGLQENVSEASKEV

SEKATLLIDRLTFESELYSEMGSSFSVPKASAVIVANPREEIIVKNKDEEKL

VSNKLLHQDLPTALTKLVEDEVSEKADSFNEKRVAVPEAPMREYADFPER

VWEVKDSKEDMLAAGKIENLESKVDKCFADSLQTNHEDKSSNDTSPFST

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DSEPVDLSDDSIPDPQKODETVMLVKESLTETSFSEMIYEYENKELSLAPRGGKP

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ETFSDDSPFIEDPFTLISKTSFSLKAREYTDLVSHKGEIATANAPAGAGSDPCTE

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LTVEFSIVSTAVYIALALISVTFIRYKGVITQAIQKSDGHPHPRAYLSEVAISEELV

QKYSNLSALGHVNCITKELRLFLVDLIVSLKFAVLMWVTVVGVCLFNGLTLLILALI

SLFSVPVYIERHQIDHYILGLANKVNDMAKIQAKIPGLKRAE"

ORIGIN

Alignment Scores:

Pred. No.: 1.65e-83 Length: 3579

Score: 908.00 Matches: 184

Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.35% Mismatches: 2

Query Match: 98.16% Indels: 0

DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x HSA251383 (1-3579)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspTleIysLysThrGlyValValPheGlyAla 20

Db 3010 TCAGTTGTTGACCTCCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCC 3069

Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 3070 AGCCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGAGGCTAACAGCCTACATT 3129

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCT 3189

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTACAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

Db 3250 TCTGAGGAGTGGTTCAGAACTACAGTAATTTCTGCTCTTGGTCATGTGAACCTGCAGATA 3309

Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

Db 3310 AAGAACTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTCAGGTG 3369

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140

Db 3370 TTGATGTGGGTATTACCTATGTTGGTGCCCTGTTTAATGGTCTGACACTACTGATTTTG 3429

Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160

Db 3430 GCTCTCATTTTCACCTCTTCAGTGTTCCTGTTTATTATGAACGGCATCAGCGCGCAGATAGAT 3489

Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 3490 CATTATCTAGGACTTGCAATTAAGAAATGTTAAAGATGCTATGGCTAAATAATCAACAGCAAAA 3549

Qy 181 IleProGlyLeuLysArgLysAlaAsp 189

Db 3550 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3576

RESULT 28

LOCUS CQ829486 3919 bp DNA linear PAT 05-JUL-2004

DEFINITION Sequence 4 from Patent WO2004052932.

ACCESSION CQ829486

VERSION CQ829486.1 GI:49732808

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Barske, C., Mir, A. K., Oertle, T., Schnell, L., Schwab, M. E.,

Vitaliti, A. and Zurini, M.

Nogo a binding molecules and pharmaceutical use thereof

Patent: WO 2004052932-A 4 24-JUN-2004;

Novartis AG (CH)

FEATURES

source

1..3919 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

1..3579

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VSNKLLHQDLPTALTKLVEDEVSEKADSFNEKRVAVPEAPMREYADFPER

VWEVKDSKEDMLAAGKIENLESKVDKCFADSLQTNHEDKSSNDTSPFST

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DSEPVDLSDDSIPDPQKODETVMLVKESLTETSFSEMIYEYENKELSLAPRGGKP

YLESFKSLDNKDTLLPDEYVSTLSKKEKIPLOMEELSTAVYSNDDLFIKKAQIRET

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LTVEFSIVSTAVYIALALISVTFIRYKGVITQAIQKSDGHPHPRAYLSEVAISEELV

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CDS



Db 3444 AAGAACTCAGCGCCTCTTCTAGTGATGATTTAGTTGATCTCTGAAAGTTTCAGGTG 3503

Qy 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuLeu 140

Db 3504 TTGATGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTG 3563

Qy 141 AlaLeuLeuSerLeuPheSerLeuProValIleTyrGluArgHisGlnValGlnIleAseP 160

Db 3564 GCTCTCACTTCACTCTTCACTGTTCTCTGTTATTTATGAAGCGCATCAGGCACAGATAGAT 3623

Qy 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 3624 CATTATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 3683

Qy 181 IleProGlyLeuLysArgLysAlaAseP 189

Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710

RESULT 30

AB020693

LOCUS Homo sapiens mRNA for KIAA0886 protein, partial cds. PRI 10-JAN-2004

ACCESSION AB020693

VERSION AB020693.1 GI:4240260

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirose,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

JOURNAL DNA Res. 5 (6), 355-364 (1998)

MEDLINE 99156230

REFERENCE 10048485

AUTHORS Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.

JOURNAL Direct Submission

FEATURES

source

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/db\_xref="taxon:9606"

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gene

CDS

## ORIGIN

Alignment Scores:

Pred. No.: 1.94e-83 Length: 4053

Score: 908.00 Matches: 184

Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.35% Mismatches: 2

Query Match: 98.16% Indels: 0

DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AB020693 (1-4053)

Qy 1 SerValValAspLeuLeuTyrTTPArgAspIleLysThrGlyValValPheGlyAla 20

Db 3144 TCAGTTGTGGTACCTCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGGTGGC 3203

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIle 40

Db 3204 AGCCTATTCTCTGCTTTCATTGACATTAATGAGCGTAAACAGCTTACATT 3263

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 3264 GCCTTGGCCCTGCTCTCTGTGACCATCATCTTAGGATATACAGGGGTGTGATCAAGCT 3323

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 3324 ATCCAGAANTCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGAGTGTCTATA 3383

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

Db 3384 TCTGAGGAGTTGGTTTCAAGATACAGTAATCTGCTCTGTGTCATGTGAACCTGCACGATA 3443

Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

Db 3444 AAGAACTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTCAGGTG 3503

Qy 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuLeu 140

Db 3504 TTGATGGGTATTTACCTATGTTGGTGGTCTGTTTAAATGGTCTGACACTACTGATTTG 3563

Qy 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAseP 160

Db 3564 GCTCTCACTTCACTCTTCACTGTTCTCTGTTATTTATGAAGCGCATCAGGCACAGATAGAT 3623

Qy 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 3624 CATTATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 3683

Qy 181 IleProGlyLeuLysArgLysAlaAseP 189

Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710

RESULT 31

AY123250

LOCUS Homo sapiens RTN4 isoform G (RTN4) mRNA, complete cds; alternatively spliced. 4060 bp mRNA linear PRI 23-SEP-2003

DEFINITION

ACCESSION AY123250

VERSION AY123250.1 GI:26800589

KEYWORDS



QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuLeu 140
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QY	141	AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB	2955	GCTCTCATTTCCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3014
QY	161	HisTyrLeuGlyLeuAlaAsnLysSerValIleAspAlaMetAlaLysIleGlnAlaLys 180
DB	3015	CATTATCTAGGACTTGCATTAAGATGTTAAGATGCTATGCTAATAATCCAGCAAAA 3074
QY	181	IleProGlyLeuLysArgLysAlaAsp 189
DB	3075	ATCCCTGGATTGAAGCGCAAGCTGAA 3101
RESULT	33	
BD270070		
LOCUS	BD270070	4093 bp DNA linear PAT 17-JUL-2003
DEFINITION	Secreted proteins and polynucleotides encoding them.	
ACCESSION	BD270070	
VERSION	BD270070.1	GI:33079838
KEYWORDS	JP 2002537757-A/32.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 4093)	
AUTHORS	Valenzuela, D., Yuan, O., Hoffman, H., Hall, J. and Rapiejko, P.	
TITLE	Secreted proteins and polynucleotides encoding them	
JOURNAL	Patent: JP 2002537757-A 32 12-NOV-2002;	
COMMENT	ALPHAGENE INC	
OS	Homo sapiens (human)	
PN	JP 2002537757-A/32	
PD	12-NOV-2002	
PF	24-AUG-1999 JP 2000566287	
PR	24-AUG-1998 US 60/097638, 24-AUG-1998 US 60/097659 PR	
09-SEP-1998 US 60/099618, 28-SEP-1998 US 60/102092 PR		
25-NOV-1998 US 60/109978, 23-DEC-1998 US 60/113645 PR		
23-DEC-1998 US 60/113646, 23-AUG-1999 US 09/379246 PI		
VALENZUELA, OLIVE YUAN, HEIDI HOFFMAN, JEFF HALL, PETER PI		
PC C12N15/09, A61K38/00, A61K48/00, A61P31/10, A61P11/06, A61P21/00, PC		
A61P29/00,		
PC A61P31/04, A61P31/10, A61P31/12, A61P31/18, A61P35/00, A61P37/00,		
PC C07K14/47,		
PC C12N5/10, C12P21/02, G01N33/15, G01N33/50, C12N15/00, A61K37/02, PC		
C12N5/00		
CC Secreted proteins and polynucleotides encoding them		
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ORIGIN		
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Score:	908.00	Matches: 184
Percent Similarity:	98.94%	Conservative: 3
Best Local Similarity:	97.35%	Mismatches: 2
Query Match:	98.16%	Indels: 0
DB:	9	Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x AY123249 (1-4070)		
QY	1	SerValValAspLeuLeuTyrTrpArgAspIleLysValThrGlyValValPheGlyAla 20
DB	2535	TCAGTTGTGACCTCTGTTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGCC 2594
QY	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB	2595	AGCATTCTCTGCTTTCATTGACAGTATTAGCATTGTGAGCGTAACAGCTACATT 2654
QY	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB	2655	GCCTTGGCCCTGCTCTGTGACCATCATGCTTTAGGATATACAGGGGTGTGATCCAGCT 2714
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB	2715	ATCCAGAAATCAGATGAGGCCACCCTCAGGGCATATCTGGAATCTGAAGTTGTCTATA 2774
QY	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB	2775	TCTGAGGAGTTGTTTCAGAGTACAGTAATTTCTGCTCTTGTCTATGTCAGTGCACGATA 2834
QY	101	LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB	2835	AAGGAACCTCAGCGCTCTTCTAGTTCATGATTTAGTTGATTTCTGAAGTTTGCAGTG 2894

QY	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	3220	AGCCTATTCTGCTGCTTTCAATGACAGTATTGACATTTGAGCGTAACAGCCTACATT	3279
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla	60
Db	3280	GCCTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAAAGGCTGTGATCCAAGCT	3339
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle	80
Db	3340	ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA	3399
QY	81	SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle	100
Db	3400	TCTGAGGAGTGTGTTGAGAAGTACAGTAATTCCTGCTTGGTCAATGAACTGCACGATA	3459
QY	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	3460	AGGAATCAGGCGCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTGCAGTG	3519
QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeu	140
Db	3520	TTGATGTGGGTATTTACCTATGTTGCTGCTGCTTTTAATGCTGACACTACTGATTTTG	3579
QY	141	AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
Db	3580	GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT	3639
QY	161	HisTyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	3640	CATTATCAGGACTTCGAATAAGATGTTAAAGATGCTGCTGAATAATCCAAAGCAAA	3699
QY	181	IleProGlyLeuLysArgLysAlaAsp	189
Db	3700	ATCCCTGGATTGAAGCGCAAGCTGAA	3726
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DEFINITION	Homo sapiens RTN4 isoform Aa (RTN4) mRNA, complete cds; alternatively spliced.		
ACCESSION	AY123245		
VERSION	AY123245.1	GI:26800574	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 4102)		
AUTHORS	Ceertle, T., Huber, C., van der Putten, H. and Schwab, M.E.		
TITLE	Genomic structure and functional characterisation of the promoters of human and mouse rttn4		
JOURNAL	J. Mol. Biol. 325 (2), 299-323 (2003)		
MEDLINE	22376540		
PUBMED	12488097		
REFERENCE	2 (bases 1 to 4102)		
AUTHORS	Van der Putten, H.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland		
REFERENCE	3 (bases 1 to 4102)		
AUTHORS	Ceertle, T. and Schwab, M.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland		
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DB:	9	Gaps:	0
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Db	2567	TCAGTTGTTGACCTCTCTGACTGGAGACATTAAGAACACTGGAGTGTGTTGGTGCC	2626
QY	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	2627	AGCCTATTCTGCTGCTTCATTGACAGTATTTCAGCATTTGAGCGGTACAGCCTACATT	2686
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla	60
Db	2687	GCCTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGCTGTGATCCAAGCT	2746
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle	80
Db	2747	ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA	2806
QY	81	SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle	100
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Db	2867	AAGGAATCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCAGTG	2926
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DEFINITION Homo sapiens RTN4 isoform E (RTN4) mRNA, complete cds;
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ACCESSION AY123248
VERSION AY123248.1 GI:26800583
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters
of human and mouse rtg4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
3 (bases 1 to 4109)
Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland

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Best Local Similarity: 97.35% Mismatches: 2
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DB: 9 Gaps: 0
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Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerileValSerValThrAlaTyrile 40
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DEFINITION Homo sapiens RTN4 isoform D (RTN4) mRNA, complete cds;
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VERSION AY123247.1 GI:26800580
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Score: 908.00 Matches: 184
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Query Match: 98.16% Indels: 0
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RESULT 38
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DEFINITION Homo sapiens mRNA for RTN-XL, complete cds.
ACCESSION AB040462
VERSION AB040462.1 GI:11610574
KEYWORDS reticulon.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.
A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity
Oncogene 19 (50), 5736-5746 (2000)
21010696
PUBMED 11126360
REFERENCE
2 (bases 1 to 4166)
Eguchi,Y., Tagami,S. and Tsujimoto,Y.
Direct Submission
Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate
School of Medicine, Biomedical Research Center, Department of
Medical Genetics, Yamadaoka 2-2, Suita, Osaka 567-0871, Japan
(E-mail:eguchi@genome.med.osaka-u.ac.jp, Tel:+81-6-6879-3363,
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Db	3554	AAGAACTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTGAGTG	3613
Qy	121	LeuMetTrrPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeu	140
Db	3614	TTGATGTGGGTATTTACCTATGTTGGTGCCTGTTTAATGGTCTGCACACTACTGATTTTG	3673
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
Db	3674	GCCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT	3733
Qy	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	3734	CATTATCTAGGACTTCGAATAAGATGTTAAGATGCTTATGGCTAAAAATCCAGCAAAA	3793
Qy	181	IleProGlyLeuLysArgLysAlaAsp	189
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RESULT 41	AY102279	4789 bp	linear	PRI 23-SEP-2003
LOCUS	AY102279			
DEFINITION	Homo sapiens RTN4 isoform A (RTN4) mRNA, complete cds;			
ACCESSION	AY102279			
VERSION	AY102279.1	GI:26800572		
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1. (bases 1 to 4789)			
AUTHORS	Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.			
TITLE	Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4			
JOURNAL	J. Mol. Biol. 325 (2), 299-323 (2003)			

J. Mol. Biol. 325 (2), 299-323 (2003)  
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 PUBMED 12488097  
 REFERENCE  
 2 (bases 1 to 4789)  
 AUTHORS Oertle, T. and Schwab, M.E.

**AUTHORS**  
Certei, T. and Schwab, M.B.  
**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland  
**REFERENCE**  
3 (bases 1 to 4789)  
**AUTHORS**  
Van der Putten, H.  
**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland

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Location/Qualifiers
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## 3' UTR

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,4e-83 Length: 4789  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY102279 (1-4789)

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 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3314 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGCTAACAGCTACATT 3373  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3374 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCT 3433  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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 QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100  
 DB 3494 TCTGAGGAGTTGGTTTCAGAAAGTACAGATAATCTGCTCTTGGTCATGTGAACCTGCACGATA 3553  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3554 AAGAACTCAGGCGCTCTCTCTAGTTGATGATTTAGTTGATCTCTGAGTTGAGTG 3613  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
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RESULT 42

## AR220865

LOCUS AR220865 4822 bp DNA linear PAT 26-SEP-2002  
 DEFINITION Sequence 106 from patent US 6426186.  
 ACCESSION AR220865  
 VERSION AR220865.1 GI:23327742  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 4822)  
 AUTHORS Jones,K.A., Volkmut,W. and Walker,M.G.  
 TITLE Bone remodeling genes  
 JOURNAL Patent: US 6426186-A 106 30-JUL-2002;  
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x AR220865 (1-4822)

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 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3325 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCTACATT 3384  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3385 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCT 3444  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3565 AAGGAACTCAGGCGCTCTCTCTAGTTGATGATTTAGTTGATCTCTGAGTTGAGTG 3624  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
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 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
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 QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3745 CATTATCTAGGACTTGCNAATAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3804  
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## RESULT 43

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 LOCUS AV114152  
 DEFINITION Mus musculus nogo-A mRNA, complete cds.

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ACCESSION AY114152
VERSION AY114152.1 GI:21898576
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3821)
AUTHORS Jin, W., Long, M., Li, R. and Ju, G.
TITLE Cloning and expression of the mouse Nogo-A protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3821)
AUTHORS Jin, W., Long, M., Li, R. and Ju, G.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi Road, Xi'an, Shaanxi 710032, China
FEATURES
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Query Match: 98.00% Indels: 1
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Qy 40 lleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 59
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Qy 80 lleserGluGluLeuValGlnLysTyrSerIleSerAlaLeuGlyHisValIleSerThr 99
3406 ATATCAGAGGAATTTGGTTTCAGAAATATATAGTAATTTCTGCTCTTGGTTCATGTGAACACCA 3465
Qy 100 lileysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAla 119
3466 ATAAAGAAATTTGAGCGGTCTCTTCTTAGTGTATGATTTAGTTGATTCCTCGAAGTTTGA 3525
Qy 120 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 139
3526 GTGTTGATGCGGTATTTTACCTGTTGTCCTTTGTTCAATGGTTTGACACTACTGATT 3585
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3586 TTAGCTCTGATCTCCTCTTCTCAGTATTTCTCTTATATATATGAACGCGCATCGCGCGAGATA 3645
Qy 160 AspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 179
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3706 AAAATCCCTCGATTGAAGCGCAAGCAGAA 3735
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BC016165
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IMAGE:3505850), complete cds.
ACCESSION BC016165
VERSION BC016165.1 GI:16740575
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1784)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Dietzchen, L., Narusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalek, U., Smalusz, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1784)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
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DB: 9 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AY102278 (1-2389)

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RESULT 46
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LOCUS
DEFINITION Homo sapiens mRNA for Nogo-C protein (Nogo gene).
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ACCESSION AJ251385
VERSION AJ251385.1 GI:9408099
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Prinjha,R., Moore,S.E., Vinson,M., Blake,S., Morrow,R.,
Christie,G., Michalovich,D., Simmons,D.L. and Walsh,F.S.
TITLE Inhibitor of neurite outgrowth in humans
JOURNAL Nature 403 (6768), 383-384 (2000)
MEDLINE 20129242
PUBMED 10667780
2 (bases 1 to 600)
AUTHORS Michalovich,D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
HERZEGOVINA
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Query Match: 97.73% Indels: 0
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US-09-830-972-2_COPY_975_1163 (1-189) x HSA251385 (1-600)

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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 274 GAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTTCATGTGAATCTGCACGATAAG 333
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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334 GAACCTCAGCGCCCTCTCTAGTGTGATGATTTAGTGTCTCTGAAGTTTGCAGTGTG 393
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RESULT 47
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LOCUS
DEFINITION
Sequence 2 from patent US 5858708.
ACCESSION
AR028522
VERSION
AR028522.1 GI:5940495
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 799)
AUTHORS
Bandman,O., Au-Young,J., Goli,S.K. and Hillman,J.L.
TITLE
Polynucleotides encoding two novel human neuroendocrine-specific proteins
JOURNAL
Patent: US 5858708-A 2 12-JAN-1999;
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Location/Qualifiers
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Query Match: 97.73% Indels: 0
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US-09-830-972-2_COPY_975_1163 (1-189) x AR028522 (1-799)

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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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IMAGE:4291127), complete cds.
ACCESSION
BC007109
VERSION
BC007109.1 GI:13937989
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1079)
AUTHORS
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshikiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Boutford,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smallu,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
REFERENCE
2 (bases 1 to 1079)
AUTHORS
Strausberg,R.
TITLE
Direct Submission
JOURNAL
Submitted (30-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found

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through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 21 Row: h Column: 12  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Similarity but not  
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 the longest cds in the locus.

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 ACCESSION BD249448  
 VERSION BD249448.1 GI:33059218  
 KEYWORDS JP 2002522016-A/3.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 1122)  
 AUTHORS Michalovich D. and Prinjha, R.K.  
 TITLE Protein similar to neuroendocrine-specific protein, and encoding  
 JOURNAL SMITHKLINE BEECHAM PLC  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002522016-A/3  
 PD 23-JUL-2002  
 PF 21-JUL-1999 JP 2000561310  
 PR 22-JUL-1998 GB 9816024.5, 19-JUL-1999 GB 9916898.1 PI  
 DAVID MICHALOVICH, RABINDER KUMAR PRINJHA  
 PC  
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
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 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAla 41  
 Db 616 CTATTCTCGCTCTTTCATTGACAGATTCAGCATTGTGACGTAACAGCCATCATGCC 675  
 QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61

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Qy      82  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      796  GAGGAGTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCACTGAGTGCACGATAAAG 855
Qy      102  GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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Qy      122  MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
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Qy      142  LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Qy      162  TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Qy      182  ProGlyLeuLysArgLysAlaAsp 189
Db      1096  CCTGGATTGAAGCGCAAAAGCTGAA 1119

RESULT 50
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LOCUS          Homo sapiens mRNA for Nogo-B protein (Nogo gene).
DEFINITION
ACCESSION     AJ251384
VERSION       AJ251384.1 GI:9408097
KEYWORDS      Nogo gene; Nogo-B protein.
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R.,
              Christie, G., Michalovich, D., Simmons, D.L. and Walsh, P.S.
              Inhibitor of neurite outgrowth in humans
              Nature 403 (6768), 383-384 (2000)
MEDLINE       20129242
PUBMED        10667780
REFERENCE     2 (bases 1 to 1122)
AUTHORS       Michalovich, D.
TITLE         Direct Submission
JOURNAL       Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
              Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
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Score:                98.94%      Conservative: 3
Best Local Similarity: 97.34%      Mismatches:  2
Query Match:          97.73%      Indels:      0
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Db      676  TTGGCCCTCTCTCTGTCACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 735
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VERSION       BC001035.2 GI:33875905
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REFERENCE     1
AUTHORS       Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,
              Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Db 1082 CCTGGATTGAAGCGCAAGCTGAA 1105

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IMAGE:3901353), complete cds.
ACCESSION BC010737
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshuler,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1485)
Strausberg,R.
Direct Submission
Submitted (12-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-f@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
```

```
Web site: http://www-sbgc.stanford.edu
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Place: 14 Row: n Column: 2
This clone was selected for full length sequencing because it
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analysis
This clone has the following problem: The cds is short compared to
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PPAPAPAPPTTAPAPKRGSGSVVDLLYWRDKTKGVVFGASLFLLSLTVFSIV
SVTAYIALALLSVTIFRIYKGIQAIQKSDGHPFRAYLESEVAISELVOKYNSA
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ORIGIN
Alignment Scores:
Pred. No.: 1.38e-83 Length: 1485
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: Gaps: 9
US-09-830-972-2_COPY_975_1163 (1-189) x BC010737 (1-1485)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 561 GTGTGTGACCTCTCTGTCTGAGAGACATTAAAGAGACTGGAGTGTGTGTGTCGACG 620
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 621 CTATTCTCTGCTCTTTCATTGACAGTATTACAGCATTTGTGAGCGTAAACAGCTACATTGCC 680
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 681 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGTATCCAAAGCTATC 740
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 741 CAGAAATCAGATGAAGGCCACCCATTACAGGCGCATATCTGGAATCTGAAGTGTCTATCT 800
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Db 801 GAGGAGTTGGTTCAGAGTACAGTAATCTCTCTTGGTTCATGTGAAGTGCACGATAAAG 860

Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 861 GAACTCAGCGCCCTCTTCTTAGTTCATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 920

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141

Db 921 ATGTGGGTATTACCTATGTTGGTCCCTGTTTAAATGGTCTGCACACTACTGATTTGGCT 980

Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 981 CTCAATTTCACTCTTCAGTGTCTCTCTGTTTATATGAACGGCATCAGGCACAGATAGATCAT 1040

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 1041 TATCTAGACCTTGCAATTAAGATGTTTAAGATGCTATGGCTTAATATCAAGCAAAATC 1100

Qy 182 ProGlyLeuLysArgLysAlaAsp 189

Db 1101 CCTGGATTGAAGCGCAAGCTGAA 1124

RESULT 56

AKI30812

LOCUS Homo sapiens cDNA FLJ27302 fis, clone TWS04776. linear PRI 10-SEP-2003

DEFINITION AKI30812

ACCESSION AKI30812

VERSION AKI30812.1 GI:34527696

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terashima, Y., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1525)

AUTHORS Sugano, S. and Suzuki, Y.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flicdha@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

FEATURES

source

1..1525

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="TWS04776"

/tissue\_type="thymus"

/clone\_lib="TWS"

/note="Cloning vector: pME18SFL3"

ORIGIN

Alignment Scores: 1.43e-83 Length: 1525

Pred. No.: 1525

Score: 904.00 Matches: 183

Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.34% Mismatches: 2

Query Match: 97.73% Indels: 0

DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AKI30812 (1-1525)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysValThrGlyValValPheGlyAlaSer 21

Db 615 GTTGTGACCTCCCTGCTACTGGAGAGACATTAAAGAGCTGGAGTGGTGTGGTCCAGC 674

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 675 CTATTCCTGCTGCTTTCATTCCAGCATTCAGCATTTGTGAGCGTAACAGCCTACATTC 734

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 735 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAAGCTATC 794

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 795 CAGAAATCAGATGAAGGCCACCCATTAGGCAATCTGGAATCTGAAGTTGCTATATCT 854

Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

Db 855 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGGTTCATGTGAACCTGCACGATAAG 914

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 915 GAACTCAGCGCCCTCTTCTTAGTTCATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 974

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141

Db 975 ATGTGGGTATTACCTATGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1034

Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 1035 CTCATTTCACTCTTCAGTGTCTCTGTTTATTATGAACGGCATCAGGCACAGATAGATCAT 1094

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 1095 TATCTAGACCTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 1154

Qy 182 ProGlyLeuLysArgLysAlaAsp 189

Db 1155 CCTGGATTGAAGCGCAAGCTGAA 1178

RESULT 57

LOCUS CO769577 1599 bp DNA linear PAT 04-MAR-2004

DEFINITION Sequence 303 from Patent WO2003058021.

ACCESSION CO769577

VERSION CO769577.1 GI:45113880

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Koenig-Hoffman, K., Kazinski, M., Schaefer, R. and Kasper, B.

TITLE Novel apoptosis-inducing dna sequences

JOURNAL Patent: WO 2003058021-A 303 17-JUL-2003;

FEATURES

source

1..1599

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores: 1.52e-83 Length: 1599

Pred. No.: 1599



Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CQ769577 (1-1599)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 671 GTTGTGACCTCTCTGACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 730  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 731 CTATTCTCTGCTCTCTCATTTGACAGTATTCAGCATTTGAGCGTAAACAGCTTACATTCGC 790  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 791 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 850  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 851 CAGAAATCAGATCAGAGCCACCCATTCAGGCGATATCTGGAATCTGAACTTGTATATCT 910  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 911 GAGGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACGTCGACGATAAG 970  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 971 GAACCTCAGGCGCTCTCTCTAGTTGATGATTTAGTTGATCTCTGAAAGTTGCGATGTTG 1030  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 DB 1031 ATGTGGCTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTGGCT 1090  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 DB 1091 CTCATTTCATCTCTCAGTGTCTCTGTTATTTATGAACGCGATCAGGCACAGATAGATCAT 1150  
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 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 DB 1211 CCTGGATTGAAGCGCAAGCTGAA 1234

RESULT 58  
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 DEFINITION Bone marrow secreted proteins and polynucleotides.  
 ACCESSION BD231889  
 VERSION BD231889.1 GI:33041659  
 KEYWORDS JP 2002511231-A/3  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Lin, H. and Cao, L.  
 TITLE Bone marrow secreted proteins and polynucleotides  
 JOURNAL Patent: JP 2002511231-A 3 16-APR-2002;  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002511231-A/3  
 PD 16-APR-2002  
 PF 18-DEC-1998 JP 2000526635  
 PR 30-DEC-1997 US 60/068958, 24-SEP-1998 US 60/101603 PR  
 PI HAISHAN LIN, LI CAO  
 PC C12N15/09, A61K38/00, A61P43/00, C07K14/47, C07K16/18, C12N5/10, PC  
 C12Q1/68,

PC C12N15/00, A61K37/02, C12N5/00  
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 FT Location/Qualifiers  
 FT source 1..1610  
 FT /organism='Homo sapiens (human)'.  
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 Location/Qualifiers  
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## ORIGIN

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 Query Match: 97.73% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BD231889 (1-1610)

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 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
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 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 807 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 866  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 867 CAGAAATCAGATCAGAGCCACCCATTCAGGCGATATCTGGAATCTGAACTTGTATATCT 926  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 927 GAGGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCACTGTCAACTGCGACGATAAG 986  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
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 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
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 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 1167 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1226  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 DB 1227 CCTGGATTGAAGCGCAAGCTGAA 1250

RESULT 59  
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 LOCUS AF087901 1617 bp mRNA linear PRI 09-SEP-2000  
 DEFINITION Homo sapiens reticulon 4c mRNA, complete cds.  
 ACCESSION AF087901  
 VERSION AF087901.1 GI:10039642  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



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REFERENCE
AUTHORS Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
TITLE Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14--2p13 by radiation hybrid mapping
JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
MEDLINE 20237542
PUBMED 10773680
REFERENCE 2 (bases 1 to 1617)
AUTHORS Yang,J., Yu,L., Dai,P.Y., Cui,W.C., Zheng,L.H. and Zhao,S.Y.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1998) Lab of Human Gene Research, Institute of
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
P.R.China
FEATURES
source Location/Qualifiers
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106..705
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polyA_signal 1590..1595
polyA_site 1608
ORIGIN
1608
Alignment Scores:
Pred. No.: 1,548-83 Length: 1617
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x AF087901 (1-1617)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 139 GTTGTGACCTCTCTACTGGAGACACATTAAAGAGACTGGAGTGTGTTGGTGCCAGC 198
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 199 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 258
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 259 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 318
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 319 CAGAAATCAGATGAGGCCACCCATTAGGCGATATCTGGAATCTGGAATCTGATATCT 378
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 379 GAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGTGTCATGTGAACTGCACGATAAG 438
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 439 GAATCAGCGCGCTCTCTTAGTGTGATTTAGTTGATTTCTGAAATTTGCGAGTGTG 498
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 499 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTATATGCTCTGACACTACTGATTTGGCT 558
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 679 CTGTGATTGAAGCGCAAGCTGAA 702
RESULT 60
AKI29806 Homo sapiens cDNA FLJ26295 fis, clone DMC07157.
LOCUS AKI29806
DEFINITION AKI29806.1 GI:34526422
ACCESSION AKI29806
VERSION Oligo capping; fis (full insert sequence).
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Suzuki,Y.,
Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T.,
Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1619)
AUTHORS Sugano,S. and Suzuki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: shirokane@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
FEATURES
Location/Qualifiers
1..1619
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue type="dermoid tumor"
/clone_lib="DMC"
/note="Cloning vector: pME18SFL3"
ORIGIN
Alignment Scores:
Pred. No.: 1,548-83 Length: 1619
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x AKI29806 (1-1619)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 713 GTTGTGACCTCTCTACTGGAGACACATTAAAGAGACTGGAGTGTGTTGGTGCCAGC 772
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 773 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 832
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

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833	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC	892	COMMENT	Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting	
62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
893	CAGAAATCAGATGAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTGTCTATATCT	952		Series: IRAL Plate: 19 Row: d Column: 8	
82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101		This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24431932	
953	GAGGAGTTGGTTTCAAGATACAGTAATCTCTCTTGGTCATGTGAACGCGATAAAG	1012		This clone has the following problem: The cds is short compared to the longest cds in the locus.	
102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121	FEATURES	Location/Qualifiers	
1013	GAACTCAGCGCGCTCTTCTTAGTGATGATTTAGTTGATCTCTGGAAGTTTCGAGGTGG	1072	source	1..1654 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4082756" /tissue_type="Brain, glioblastoma" /clone_lib="NIH MGC_57" /lab_host="DH10B" /note="Vector: pDNR-LIB"	
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1 (bases 1 to 1654)					
Klausner,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,					
Klausner,R.D., Collins,F.S., Wagner,L., Shermen,C.M., Schuler,G.D.,					
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,					
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,					
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,					
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,					
Scheetz,J.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,					
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,					
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,					
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,					
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,					
Villalon,D.K., Murny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,					
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,					
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,					
Boutford,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,					
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,					
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,					
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.					
Generation and initial analysis of more than 15,000 full-length					
human and mouse cDNA sequences					
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)					
12477932					
2 (bases 1 to 1654)					
Strausberg,R.					
Direct Submission					
Submitted (15-AUG-2001) National Institutes of Health, Mammalian					
Gene Collection (MGC), Cancer Genomics Office, National Cancer					
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,					
USA					
NIH-MGC Project URL: http://mgc.nci.nih.gov					

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BC026788

LOCUS

DEFINITION

Homo sapiens reticulon 4, transcr

ACCESSION

BC026788

VERSION

BC026788.1

KEYWORDS

GI:20070661

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Klausner,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

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Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smalusz,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis

of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99

(26), 16899-16903 (2002)

12477932

2 (bases 1 to 1668)

Strausberg,R.

Direct Submission

Submitted (04-APR-2002) National

Institutes of Health, Mammalian

Gene Collection (MGC), Cancer

Genomics Office, National Cancer

Institute, 31 Center Drive, Room

11A03, Bethesda, MD 20892-2590,

USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleaged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
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 This clone was selected for full length sequencing because it  
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CDS

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
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AUTHORS Ito, T. and Schwartz, S.M.			
TITLE Cloning of a member of the reticulon gene family in human: skeletal muscle type			
JOURNAL Unpublished			
REFERENCE			
2 (bases 1 to 1691)			
AUTHORS Ito, T. and Schwartz, S.M.			
TITLE Direct Submission			
JOURNAL Submitted (27-FEB-1999) Pathology, University of Washington, 1959 Pacific NE, Seattle, WA 98195, USA			
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1698)  
Straussberg, R.  
Direct Submission  
Submitted (17-SEP-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: CLONTECH  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
Contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
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Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Gu, J.R., Wan, D.F., Zhao, X.T., Zhou, X.M., Jiang, H.Q., Zhang, P.P.,  
Qin, W.X., Huang, Y., Qiu, X.K., Qian, L.F., He, L.P., Li, H.N., Yu, Y.,  
Yu, J. and Han, L.H.  
TITLE Novel human CDNA clone with function of inhibiting cancer cell  
growth  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1700)  
AUTHORS Gu, J.R., Wan, D.F., Zhao, X.T., Zhou, X.M., Jiang, H.Q., Zhang, P.P.,  
Qin, W.X., Huang, Y., Qiu, X.K., Qian, L.F., He, L.P., Li, H.N., Yu, Y.,  
Yu, J. and Han, L.H.  
TITLE Direct Submission  
JOURNAL Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related  
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai  
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Query Match: 97.73% Indels: 0  
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 393 GAGGAGTTGGTTTCTGAGAGTACAGTAATTCCTCTTGGTCTGATGAACTGCAGATAAG 452  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 453 GAACCTCAGCGCCCTCTCTTAGTGTAGATTTAGTTGATCTCTGAAAGTTTGAGTGTG 512  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 513 ATGTGGGTATTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 572  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 573 CTATTTCACCTCTTCAGTGTCTCTGTTATTTATGAAACGGCATCAGGCACAGATAGATCAT 632  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 633 TATCTAGGACTTGCAATATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAAAGCAAAATC 692  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 693 CTGGATTGAGCGCAAGCTGAA 716

## RESULT 66

AB040463  
LOCUS Homo sapiens mRNA for RTN-XS, complete cds. PRI 10-OCT-2001  
DEFINITION  
AB040463  
ACCESSION  
AB040463.1 GI:11610576  
VERSION  
KEYWORDS reticulon.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Tagami, S., Eguchi, Y., Kinoshita, M., Takeda, M. and Tsujimoto, Y.  
TITLE A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
endoplasmic reticulum and reduces their anti-apoptotic activity  
JOURNAL Oncogene 19 (50), 5736-5746 (2000)  
MEDLINE 21010696

11126360

PUBMED  
REFERENCE

2 (bases 1 to 1709)  
Eguchi, Y., Tagami, S. and Tsujimoto, Y.  
Direct Submission  
TITLE  
JOURNAL  
Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate  
School of Medicine, Biomedical Research Center, Department of  
Medical Genetics, Yamadaoka 2-2, Suita, Osaka 565-0871, Japan  
(E-mail: eguchi@gen.med.osaka-u.ac.jp, Tel: +81-6-6879-3363,  
Fax: +81-6-6879-3369)

FEATURES  
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## CDS

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PPAPAAPSTPAPKRRSGSVVLDLKKTKGVFGASIFLLSLTVPSIV  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1,66e-83 Length: 1709  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AB040463 (1-1709)

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DB 800 GTTGTGACCTCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 859  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 860 CTATTCTCTCTCTTTCATTGACAGTATTGACATTTGAGCGTAACAGCTACATGGC 919  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 920 TTGGCCCTCTCTCTGACCATTCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 979  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 980 CAGAAATCAGATGAGAGCCACCCATTCAGGCATATCTGGAATCTGGAAGTTGCTATATCT 1039  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1040 GAGGAGTTGGTTTCTGAAAGTACAGTAAATCTGCTCTTGGTCTGATGAACTGCAGATAAG 1099  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1100 GAACCTCAGCGCCCTCTCTTAGTGTAGTATTGATTTGATCTCTGAAAGTTTGAGTGTG 1159  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
DB 1160 ATGTGGGTATTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1219  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

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Db      1280 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 1339
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Qy      182 ProGlyLeuLysArgLysAlaAsp 189
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RESULT 67
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LOCUS      1721 bp      mRNA      linear      MAM 27-OCT-2003
DEFINITION      Bos taurus RTN4-C (RTN4) mRNA, complete cds.
ACCESSION      AY164744
VERSION      AY164744.2 GI:37992246
KEYWORDS
SOURCE
ORGANISM      Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
AUTHORS      Oertle,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
TITLE      A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family
JOURNAL      FASEB J. 17 (10), 1238-1247 (2003)
PUBMED      12832288
REFERENCE
AUTHORS      Oertle,T. and Schwab,M.E.
TITLE      Direct Submission
JOURNAL      Submitted (16-OCT-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
3 (bases 1 to 1721)
Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (27-OCT-2003) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
SEQUENCE update by submitter
COMMENT      On Oct 27, 2003 this sequence version replaced gi:32331288.
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Pred. No.:      1.67e-83      Length:      1721
Score:      904.00      Matches:      183
Percent Similarity:      98.94%      Conservative:      3
Best Local Similarity:      97.34%      Mismatches:      2
Query Match:      97.73%      Indels:      0
DB:      4      Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x AY164744 (1-1721)

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Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThralaTyIleAla 41
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      |||
Db      279 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGGTGTGATCCAGGCTATC 338
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Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyLLeuGluSerGluValAlaIleSer 81
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DEFINITION      Homo sapiens reticulon 4, transcript variant 2, mRNA (cdna clone
IMAGE:4634289), complete cds.
ACCESSION      BC068991
VERSION      BC068991.1 GI:46362518
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1728)
AUTHORS
Krausner,R.D., Collins,P.S., Wagner,L.H., Shenmen,C.M., Schuler,G.D.,
Alschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Sheetz,T.E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettnerman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length

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TITLE







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    QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
    DB 388 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 447
    QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
    DB 448 CAGAAATCAGATGAAAGCCACCATTACAGGCATATCTGGAATCTGAAGTTGCTATATCT 507
    QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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    QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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    QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAlaIle 141
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RESULT 70
AB015639
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DEFINITION Homo sapiens ASY mRNA, complete cds.
ACCESSION AB015639
VERSION AB015639.1 GI:5821139
KEYWORDS ASY.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 2052)
  Yutsudo,M.
  Isolation of a cell death-inducing gene
  Published Only in Database (1999)
REFERENCE
  2 (bases 1 to 2052)
  Yutsudo,M.
  Direct Submission
  Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of
  Tumor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka, Suita, Osaka
  565-0871, Japan (E-mail:yutsudo@biken.osaka-u.ac.jp,
  Tel:81-6-879-8313, Fax:81-6-879-8315)
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    Pred. No.: 2,09e-83 Length: 2052
    Score: 904.00 Matches: 183
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    Query Match: 97.73% Indels: 0
    DB: 9 Gaps: 0
    US-09-830-972-2_COPY_975_1163 (1-189) x AB015639 (1-2052)
    QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
    DB 622 GTTGTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 681
    QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
    DB 682 CTATTCTGCTGCTTCTTACGATGATTCACAGTATGAGCATTTGAGCGTACAGCTACATGCC 741
    QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
    DB 742 TTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 801
    QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

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QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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## RESULT 71

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 LOCUS Homo sapiens reticulon 4b mRNA, complete cds.

AF148538  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 2235)  
 Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.

Assignment of the human reticulon 4 gene (RTN4) to chromosome  
 2p14-->p13 by radiation hybrid mapping

Cytogenet. Cell Genet. 88 (1-2), 101-102. (2000)

## JOURNAL

MEDLINE 2023/7542

## PUBMED

10773680

## REFERENCE

2 (bases 1 to 2235)  
 Zhou, Y., Yu, L. and Zhao, S.Y.

Direct Submission

## AUTHORS

Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of  
 Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,  
 P.R.China

## JOURNAL

## FEATURES

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polyA\_site

2225

ORIGIN

## Alignment Scores:

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 Score: 904.00 Matches: 183

Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.34% Mismatches: 2

Query Match: 97.73% Indels: 0

DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AF148538 (1-2235)

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QY 2 ValValAspLeuLeuTyrTipArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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Db 697 GTTGTGGACCTCTCTACTGAGAGACATTAGAGACTGGAGTGGTGGTGGTGGTGGTGG 756
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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 876
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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Db 877 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGAAGTTGCTATATCT 936
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Db 937 GAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCACTGTGAACCTGCACGATAAG 996
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QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db 997 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 1056
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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
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Db 1057 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTATGCTGCACACTACTGATTTGGCT 1116
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QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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|||
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Db 1177 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGAAATC 1236
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QY 182 ProGlyLeuLysArgLysAlaAsp 189
|||||
Db 1237 CTGGATTGAAGCGCAAGCTGAA 1260

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## RESULT 72

AF132047 2276 bp mRNA linear PRI 18-MAY-1999  
 LOCUS Homo sapiens foocen-m mRNA, complete cds.

AF132047

DEFINITION

AF132047

ACCESSION

AF132047.1

VERSION

GI:4838516

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2276)

Cloning of a member of the reticulon gene family in human:

ubiquitous type

unpublished

JOURNAL

REFERENCE

2 (bases 1 to 2276)

Itto, T. and Schwartz, S.M.

Direct Submission

TITLE

Submitted (27-FEB-1999) Pathology, University of Washington, 1959

JOURNAL

Submitted (27-FEB-1999) Pathology, University of Washington, 1959

Pacific NE, Seattle, WA 98195, USA

FEATURES

Location/Qualifiers

1..2276

source



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Db      860 CTATTCTCTGCTCTTCATTGACGATTTTCAGCAATTTGTCAGCGTAAACAGCCTACATTGCC 919
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Db      920 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAAGCTATC 979
Qy      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      980 CAGAAATCAGATGAGCGCCACCCATTCAGGCGATATCTGGAATCTCGAAGTTGCTATATCT 1039
Qy      82  GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIleLys 101
Db      1040 GAGGAGTTGGTTCAGAAGTACAGTAATCTGCTCTTGGTCATGTCGAACTGCACGATAAAG 1099
Qy      102  GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerIleuLysPheAlaValLeu 121
Db      1100 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTTCAGTGTG 1159
Qy      122  MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrIleLeuLeuAla 141
Db      1160 ATGTGGGTATTTACCTATGTTGTGTCCTTTGTTTAATGGTCTGACACTACTGATTTTGGCT 1219
Qy      142  LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      1220 CTCATTTCACTCTTCAGTGTCTCTGTATTTATGAACGCGATCAGGCACAGATAGATCAT 1279
Qy      162  TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1280 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAATC 1339
Qy      182  ProGlyLeuLysArgLysAlaAsp 189
Db      1340 CCTGGATTGAAGCGCAAGCTGAA 1363

RESULT 74
AY114153
LOCUS      Mus musculus nogo-B mRNA linear ROD 17-JUL-2002
DEFINITION Mus musculus nogo-B mRNA, complete cds.
ACCESSION AY114153
VERSION    AY114153.1 GI:21898578
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1  (bases 1 to 1276)
AUTHORS   Jin,W., Li,R., Long,M., Shen,J. and Ju,G.
TITLE     Cloning and expression of the mouse Nogo-B protein
JOURNAL   Unpublished
REFERENCE  2  (bases 1 to 1276)
AUTHORS   Jin,W., Li,R., Long,M., Shen,J. and Ju,G.
TITLE     Direct Submission
JOURNAL   Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi
          Road, Xi'an, Shaanxi 710032, China

FEATURES   source
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FRYIKGVIQAIQKSDCHPFRAYLSEVAISELVQKYSNLSALGHVNSTIKELRRLF
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CDS
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               /strain="BALB/c"
               /db_xref="taxon:10090"
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               /protein_id="AA077069.1"
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KRGGSGVVDLLLYWRDIIKTKTVYFEGASLFLLLSTVFSIVSVTAIALLSVTIS
FRYIKGVIQAIQKSDCHPFRAYLSEVAISELVQKYSNLSALGHVNSTIKELRRLF
VDDLVDLKFVLMVTVYVGVLFNGLITLLILALISLFSIPVIYERHQIDHYLGIA
NKSVDKAMAKIQAKIFGLKRAE"

ORIGIN
Alignment Scores: 1.63e-83 Length: 1276
Pred. No.: 902.50 Matches: 186
Score: 902.50 Matches: 186
Percent Similarity: 98.94% Conservative: 1
Best Local Similarity: 98.41% Mismatches: 1
Query Match: 97.57% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x AY114153 (1-1276)
Qy      2  ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal---PheGlyAla 20
Db      624 GTTGTGACCTCTCTCTGACGACATTTAGAAAGATGGAGTGGTGTATTTTGGTCC 683
Qy      21  SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      684 AGCTTATTTCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGCGCTACATT 743
Qy      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db      744 GCCTTGGCCCTCTCTCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCT 803
Qy      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      804 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTTGAATCTCGAAGTTGCCATA 863
Qy      81  SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100
Db      864 TCAGAGGAATTTGTTTCAGAAATATAGTAATCTCTCTCTGTCATGTGAACAGCAATA 923
Qy      101  LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerIleLysPheAlaVal 120
Db      924 AAAGAATTCAGCGCTCTCTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGTG 983
Qy      121  LeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrIleLeuLeuLeu 140
Db      984 TTGATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTTTCACACTACTGATTTTA 1043
Qy      141  AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db      1044 GCTCTGATCTCACTCTTCAGTATTTCTGTATATATGAACGCGCATCAGCGCAGATAGAT 1103
Qy      161  HisTyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db      1104 CATTATCTAGGACTTGCAAAACAGAGCGTTAAGGATGCGCATGCCAAAATCCAAAGCAAAA 1163
Qy      181  IleProGlyLeuLysArgLysAlaAsp 189
Db      1164 ATCCCTGGATTGAAGCGCAAGCAAGAA 1190

RESULT 75
AF132046
LOCUS      Rattus norvegicus foocen-m1 mRNA, alternate splice product,
DEFINITION complete cds.
ACCESSION AF132046
VERSION    AF132046.1 GI:4838514
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE     Rattus norvegicus
ORGANISM   Rattus norvegicus
REFERENCE  1  (bases 1 to 2256)
AUTHORS   Ito,T. and Schwartz,S.M.
TITLE     Cloning of a member of the reticulon gene family in rat: One of two
          minor splice variants
JOURNAL   Unpublished
REFERENCE  2  (bases 1 to 2256)
AUTHORS   Ito,T. and Schwartz,S.M.
TITLE     Direct Submission

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JOURNAL Submitted (27-FEB-1999) Pathology, University of Washington, 1959  
Pacific NE, Seattle, WA 98195, USA  
FEATURES Location/Qualifiers  
source 1..2256

/organism="Rattus norvegicus"  
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/db\_xref="taxon:10116"  
/sex="male"  
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/dev\_stage="3 months old"  
238..1314

note="member of reticulon gene family; alternate splice product"  
/codon\_start=1  
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/protein\_id="AAD31020.1"  
/db\_xref="GI:483815"

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PAPKRGSGSVVDLLYWRDITKTVGVFGASLFLLSLTVFSVTVAYTALALLSV  
TISPIYKGVLOAKSDEGHPFRAYLESEVAISELVQKYSNAGLHVNSTIKELR  
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## ORIGIN

Alignment Scores:  
Pred. No.: 4,828-83 Length: 2256  
Score: 901.00 Matches: 186  
Percent Similarity: 98.94% Conservativeness: 0  
Best Local Similarity: 98.94% Mismatches: 0  
Query Match: 97.41% Indels: 2  
DB: 10 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AF132046 (1-2256)

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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
Db 814 TTATTCCTGCTGCTCTCTGACAGTGTGACAGTGTGACGTGAACGCCCTACATTC 873  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 874 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGCATCCAGC 933  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 934 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATTTAGATCTGAAGTTGCTATATCA 993  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
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Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValIle 121  
Db 1054 GAATGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTGCGAGTGTG 1113  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 1114 ATGTGGGTGTTACTATGTTGGTGGCTTGTTCATGCTGCTGACACTACTGATTTAGCT 1173  
Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 1174 CTGATCTCCTCTTCTCAGTATTCCTGTTATTTATGAACGCCAT-----CAGATGATCAT 1227  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIle 181  
Db 1228 TATCTAGGACTTGCAACAAGAGTGTAAAGATGCCATGGCGCAAAATCCAGCAAAATC 1287

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## RESULT 76

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LOCUS CQ783030 1694 bp DNA linear PAT 17-MAR-2004  
DEFINITION Sequence 3170 from Patent EP1396543.  
ACCESSION CQ783030  
VERSION CQ783030.1 GI:45502969  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
Koga,H.

TITLE Primers for synthesizing full length cDNA clones and their use  
JOURNAL Patent: EP 1396543-A 3170 10-MAR-2004;  
Research Association for Biotechnology (JP)

FEATURES Location/Qualifiers  
source 1..1694

/organism="Homo sapiens"  
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## ORIGIN

Alignment Scores:  
Pred. No.: 4,238-83 Length: 1694  
Score: 900.00 Matches: 182  
Percent Similarity: 98.40% Conservativeness: 3  
Best Local Similarity: 96.81% Mismatches: 3  
Query Match: 97.30% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CQ783030 (1-1694)

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Db 788 GTTGTGACCTCTCTGTTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 847  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
Db 848 CTATTCCTGCTGCTTCCTCATTGACAGTATTCAGCATTGTGACGCTACATTCGCC 907  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATAAGGGCGTGCATCCAGC 967  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 968 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATTCGGAATCTGAAGTTGCTATATCT 1027  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 1028 GAGGAGTGGTTTCAGAGTACAGTAATTCCTGCTCTGCTCATGTGACGCTCAGCAATAAG 1087  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValIle 121  
Db 1088 GAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTGCGAGTGTG 1147

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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
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QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Db 1268 TATCTAGGACTTGCAATAGATGTTTAAGATGCTATGCTAAATCCAGCAAAATC 1327
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Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351
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RESULT 77
BD127437
LOCUS BD127437 1694 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127437
VERSION BD127437.1 GI:23222382
KEYWORDS JP 2002017375-A/2868.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
AUTHORS Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1694)
TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2868 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
EN JP 2002017375-A/2868
PD 22-JAN-2002
PF 07-JUL-2000 JP 20020253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOgai, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUO OTSUKI, HISASHI KOGA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
(479). (1351).
FT CDS Location/Qualifiers
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/db_xref="taxon:9606"
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 4,23e-83 Length: 1694
Score: 900.00 Matches: 182
Percent Similarity: 98.40% Conservative: 3
Best Local Similarity: 96.81% Mismatches: 3
Query Match: 97.30% Indels: 0
DB: 6 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x BD127437 (1-1694)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAlaSer 21
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|
Db 788 GTTGTGACCTCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGCAGC 847
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|
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerIleValThrAlaTyrIleAla 41
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Db 848 CTATTCCTGCTGCTTTTCATTTGACATATTGACATTTGAGCTTAACAGCCTACATGCC 907
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QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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|
|
Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGTGATCCAGCTATC 967
|
|
|
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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|
|
Db 968 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCTGGAATCTGATTTATCT 1027
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|
|
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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|
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Db 1028 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTCTGTGTCATGTGAACATGCACGATAAG 1087
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QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db 1088 GAATCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTGTG 1147
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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141
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|
Db 1148 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAATGGTCTGACACTACTGATTTGGCT 1207
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QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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|
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Db 1208 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 1267
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QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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|
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Db 1268 TATCTAGGACTTGCAATAGATGTTTAAGATGCTATGCTAAATCCAGCAAAATC 1327
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|
QY 182 ProGlyLeuLysArgLysAlaAsp 189
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|
|
Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351
|
|
|
RESULT 78
AK075039 1694 bp mRNA linear PRI 03-SEP-2002
LOCUS AK075039
DEFINITION Homo sapiens cDNA FLJ90558 fis, clone OVARC1001030.
ACCESSION AK075039
VERSION AK075039.1 GI:22760874
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Sato,H., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Sato,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1694)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
Location/Qualifiers
1. .1694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
FEATURES
source

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 DB 1486 CATTATCTAGGACTTGCATAAATAGAGTGTAAAGATGCTATGGCTAAATCCCAAGCAAAA 1545

QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572

RESULT 80  
 BD097380 1980 bp DNA linear PAT 27-AUG-2002  
 LOCUS  
 DEFINITION Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma.

ACCESSION BD097380  
 VERSION BD097380.1 GI:22642954  
 KEYWORDS WO 0166733-A/22.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1980)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 TITLE Nakagawara, A.  
 JOURNAL Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma. Patent: WO 0166733-A 22 13-SEP-2001;  
 COMMENT CHIBA PREF. HISAMITSU PHARMACEUTICAL CO INC, AKIRA NAKAGAWARA

OS Homo sapiens (human)  
 FN WO 0166733-A/22  
 PD 13-SEP-2001  
 PF 02-MAR-2000 WO 2001JP001631  
 PR 07-MAR-2000 JP OOP 159195,12-MAY-2000 JP OOP 140387 PI  
 AKIRA NAKAGAWARA  
 PC C12N15/12.C12Q1/68  
 CC Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma  
 CC human neuroblastoma  
 CC human neuroblastoma and poor prognostic human neuroblastoma FH

Key source Location/Qualifiers  
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 Percent Similarity: 98.41% Conservative: 4  
 Best Local Similarity: 96.30% Mismatches: 3  
 Query Match: 97.08% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BD097380 (1-1980)

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 DB 1006 TCAGTTGTTGACCTCTCTACTGAGAGACATTAAAGAGCTGGAGTGGTGGTGGTGGC 1065

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 1066 AGCCTATTCAGCTGCTTTTCATGACAGTATTGAGCATTTGAGCGCTAACAGCTACATT 1125

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 1126 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT 1185

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 1186 ATCCGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGGAAGTTGCTATA 1245

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 1246 TCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCCTCTCTGGTCATGTGAACTGCACGATA 1305

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 1306 AAGGAACCTCAGCGCTCTCTTCTAGTGTATGATTTAGTTCTCTCGAGTTGCAGTG 1365

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 1365 TTGATGTGGTATTTTACCTATGTTGGTGCCTTTTAAATGGTCTGACACTACTGATTTTG 1425

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
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QY 161 HistTyrLeuGlyLeuAlaAsnLysSerVallyAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 1486 CATTATCTAGGACTTGCATAAATAGAGTGTAAAGATGCTATGGCTAAATCCCAAGCAAAA 1545

QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572

RESULT 81  
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 LOCUS  
 DEFINITION Extended cDNA of secretory protein.  
 ACCESSION BD139293  
 VERSION BD139293.1 GI:23234238  
 KEYWORDS JP 2002508182-A/45.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 994)  
 AUTHORS Bouguerel, L., Duclert, A. and Edwards, J.B.D.M.  
 TITLE Extended cDNA of secretory protein  
 JOURNAL Patent: JP 2002508182-A 45 19-MAR-2002;  
 COMMENT GENSET  
 OS Homo sapiens (human)  
 PN JP 2002508182-A/45  
 PD 19-MAR-2002  
 PF 17-DEC-1998 JP 2000539136  
 PR 17-DEC-1997 US 60/069957,09-FEB-1998 US 60/074121 PR  
 13-APR-1998 US 60/081563,10-AUG-1998 US 60/096116 PI LYDIE  
 BOUGUEREL, AYMERIC DUCLERT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS  
 PC C12N15/09.C12N15/09.C07K14/47.C07K16/18.C12N1/15.C12N1/19, PC  
 C12N1/21,  
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 Von Heijne matrix  
 CC score 8.6  
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 FT sig\_peptide 35..160  
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ORIGIN  
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 Pred. No.: 7e-83 Length: 994  
 Score: 895.00 Matches: 182



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Percent Similarity: 98.40%      Conservative: 3
Best Local Similarity: 96.81%    Mismatches: 3
Query Match: 96.76%            Indels: 0
DB: 6                          Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BD139293 (1-994)

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DB 68 GTTGTGACCTCTCTGCTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 127
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 128 CTATTCTCTGCTCTTCAATGACAGTATTACGCAATGTGAGCGGTAAACAGCTTACATTGCC 187
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGGTGTGATCCAGCTATC 247
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 248 CAGAAATCAGATGAAGGCCCAACCAATCTAGGCGATATCTGGAATCTGAGTTGCTATATCT 307
QY 82 GluGluLeuValGlnLysTyrSerIleValSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 308 GAGGAGTGTGGTTTCAGAAATGACAGTAAATCTGCTCTTGGTTCATGTGAACCTGCACGATAAAG 367
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 368 GAACCTAGCGCGCTCTCTTAGTGTGATGATTTAGTTGATTTCTGAAAGTTTCAGTGTG 427
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 428 ATGTGGGTATTACCTATGTTGGTGGCTGTTTAAATGTTGCTGACACTACTGATTTGGCT 487
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 488 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCGACAGATAGATCAT 547
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 548 TATCTAGTACTTGCAGAAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAGCAAAATC 607
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 608 CTGTGATTGAAGCGCAAGCTGAA 631

RESULT 82
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LOCUS AB049853 2162 bp mRNA linear PRI 14-OCT-2000
DEFINITION Macaca fascicularis brain cDNA, clone: QnpA-18952.
ACCESSION AB049853
VERSION AB049853.1 GI:10801643
KEYWORDS fis (full insert sequence).
SOURCE Macaca fascicularis (crab-eating macaque)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
REFERENCE 1 (sites)
AUTHORS Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
TITLE Isolation of full-length cDNA clones from macaque brain cDNA
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2162)
AUTHORS Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)

```

COMMENT Lab host: TOP10  
Vector: pME18S-FL3 (Acc.No. AB009864)  
R. Site1: DraIII (CACTGTGTG)  
R. Site2: DraIII (CACCATGTG)  
Description: 1st strand cDNA was primed with an oligo(dT) primer using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAGTGGC]; 3' end primer [CGACCTGCAGCTCGAGCACA]).

FEATURES  
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/clone="QnpA-18952"  
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CDS  
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ORIGIN  
Alignment Scores:  
Pred. NO.: 1.9e-82 Length: 2162  
Score: 895.00 Matches: 180  
Percent Similarity: 98.94% Conservative: 6  
Best Local Similarity: 95.74% Mismatches: 2  
Query Match: 96.76% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x AB049853 (1-2162)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 596 GTTGTGACCTCTCTGCTACTGGAGAGACATGAAGAGACTGGAGTGGTGTGGTCCAGC 655  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 656 CTATTCTCTGCTCTTCAATGACAGTATTACGCAATGTGAGGTAAACAGCTTACATTGCC 715  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 716 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 775  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 776 CAGAAATCAGATGAAGGCCCAACCAATCTAGGCGATATCTGGAATCTGGAAGTTGCGATATCT 835  
QY 82 GluGluLeuValGlnLysTyrSerIleValSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 836 GAGGAGTGTGGTTTCAGAAATGACAGTAAATCTGCTCTTGGTTCATGTGAACCTGCACGATAAAG 895  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 896 GAACCTAGCGCGCTCTCTTAGTGTGATTTAGTTGATTTCTGAGGTTGCGAGTGTG 955  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 956 ATGTGGGTATTACCTATGTTGGTGGCTTGTAAATGCTGCTGACGCTACTGATTTGGCT 1015

Qy	142	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
Db	1016	CTCATTTTCACCTCTTCAGTGTTCCTGTGTTATTTATGACGGCATCAGGCACAGATAGATCAT	1075
Qy	162	TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	1076	TATCTAGACTTGCAAATAGATGTTTAAAGATGCTATGGCTAAATCCAAAGCGAATATC	1135
Qy	182	ProGlyLeuLysArgLysAlaAsp	189
Db	1136	CCTGGATTGAAGCGCAAAAGCTGAA	1159
RESULT	83		
LOCUS	AR379837	2610 bp	DNA
DEFINITION	Sequence 382 from patent US 6607879.	linear	PAT 18-DEC-2003
ACCESSION	AR379837		
VERSION	AR379837.1	GI:40087471	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2610)		
AUTHORS	Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.		
TITLE	Compositions for the detection of blood cell and immunological response gene expression		
JOURNAL	Patent: US 6607879-A 382 19-AUG-2003;		
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Best Local Similarity:	96.83%	Mismatches:	2
Query Match:	96.32%	Indels:	1
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Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl	41
Db	1371	CTATTCTGTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGGCTAACAGCTCAATTGC	1430
Qy	41	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle	61
Db	1431	CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCTAT	1490
Qy	61	eGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIleSe	81
Db	1491	CCAGAAATTCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAAATCTCGAAGTTGCTATATC	1550
Qy	81	rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLy	101
Db	1551	TGAGGAGTTGGTTCAGAAGTACAGTAAATCTGCTCTTGGTCACTGTAACCTGCACGATAAA	1610
Qy	101	sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValle	121
Db	1611	GGAACCTCAGGCCCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAAGTGT	1670
Qy	121	uMetTrrValPheThrTrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleuAl	141
Db	1671	GATGTGGGTATTTACCTATGTGTGGTGCTGTGTTTAATGGTCTGACACTACTGATTTTGGC	1730
Qy	141	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi	161

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 365 ATCCAAAGATCCGATGAAGCCATCCATTAGGGCTTACTTGGAGTCTGATGACTGTG 424  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrtle 100  
 Db 425 TCTGAAGAGCTGATTACAGAAATACAGCAGTGTGTGCTTGGTTCACATCAACGGCAGTC 484  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 495 AAGGAGCTGAGAGCGCTCTCTCGTGTGATGATCTGTTGATCTCTGAAGTTTCCAGTG 544  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 545 TTGATGTGGGTGTTCACTTACGTGTGGTGGCTGTTTAAATGCTGACATTAAGTATG 604  
 QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 605 GCTTTGATTTCCGCTGTTCACTGTTCTCTGTTATTTATGAGAGACATCAGGCCCGATCGAC 664  
 QY 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 665 CATTATTGGGACTAGTGAACAAGAACGTCAAAGATGCGATGCGCAAGATCCAAAGCAAG 724  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 725 ATCCCTGGGCTGAAGCGCAAACTGAG 751

RESULT 85  
 LOCUS AY494005 2835 bp mRNA linear VRT 16-FEB-2004  
 DEFINITION Gallus gallus neurite outgrowth inhibitor NOGO-A (NOGO) mRNA, partial cds.  
 ACCESSION AY494005  
 VERSION AY494005.1 GI:42528324  
 KEYWORDS Gallus gallus (chicken)  
 SOURCE Gallus gallus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 CATHARP.S.A., Pira, C.U., McNeill, D.S., Liwnicz, B.H. and Oberg, K.C.  
 Expression and Regulation of NOGO-A During Development of the Avian Central Nervous System  
 Unpublished  
 JOURNAL 2 (bases 1 to 2835)  
 REFERENCE Caltharp, S.A., McNeill, D.S., Pira, C.U. and Oberg, K.C.  
 AUTHORS Direct Submission  
 TITLE Submitted (02-DEC-2003) Anatomy, Loma Linda University, 24785 Stewart St. Evans Hall B09, Loma Linda, CA 92350, USA  
 JOURNAL Location/Qualifiers  
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 Db 1409 TCAGTTGTGACCTCTTACTTGGCGAGACATTAAGAAGACAGGAGTGGTGTGGTGGC 1468  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrlaTyrIle 40  
 Db 1469 AGCTTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTACAGCTTACATT 1528  
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 Db 1529 GCCTTGGCCCTGCTTCTGTGACCATCAGCTTAGGATATACAGGGAGTATCCAGGCA 1588  
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 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrtle 100  
 Db 1649 TCTGAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGGTTCATCAACGGCAGTC 1708  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
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 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
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 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 1949 ATCCCTGGGCTGAAGCGCAAACTGAG 1975  
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 VERSION BX933922.1 GI:41634450  
 KEYWORDS Gallus gallus (chicken)  
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 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE  
AUTHORS  
Phasianinae; Gallus.  
1 (bases 1 to 1363)  
Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E.,  
Croning, M.D.R., Davies, R.M., Francis, M.D., Graham, D.V.,  
Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R.,  
Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G.,  
Tickle, C. and Wilson, S.A.  
Direct Submission  
Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: chickestbms.umist.ac.uk  
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cdna  
sequencing project.  
This sequence is from the  
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cdna collection,  
from a library constructed by Elizabeth Bosch. cdna was prepared  
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI  
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DEFINITION  
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ORGANISM Gallus gallus  
ARCHAEOLOGY Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus  
REFERENCE 1 (bases 1 to 1578)  
AUTHORS Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E.,  
Croning, M.D.R., Davies, R.M., Francis, M.D., Graham, D.V.,  
Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R.,  
Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G.,  
Tickle, C. and Wilson, S.A.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: chickestbms.umist.ac.uk  
COMMENT BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cdna  
sequencing project.  
This sequence is from the  
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cdna collection,  
from a library constructed by Elizabeth Bosch. cdna was prepared  
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI  
cut cdna was then ligated into the vector. Vector: pBluescript II  
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ORGANISM Gallus gallus
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Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1597)
Oertle,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family
RTN/Nogo gene family
JOURNAL FASEB J. 17 (10), 1238-1247 (2003)
PUBMED 12832288
REFERENCE 2 (bases 1 to 1597)
Oertle,T. and Schwab,M.E.
Direct Submission
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Submitted (16-OCT-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
JOURNAL Location/Qualifiers
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ACCESSION BD190738
VERSION BD190738.1 GI:33000477
KEYWORDS JP 2002515751-A/5.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2386)
JACOBS,K., MCCOY,J.M., LAVALLIE,E.R., RACIE,L.A., MERBERG,D.,
TRACY,M., SPAULDING,V. and AGOSTINO,M.J.
Secreted proteins and polynucleotides encoding them
Patent: JP 2002515751-A 5 28-MAY-2002;
GENETICS INSTITUTE INC
PN JP 2002515751-A/5
PD 28-MAY-2002
PR 24-OCT-1997 JP 1998519738
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE,PI
DAVID MERBERG,
PI MAURICE TRACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness:
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REFERENCE  
AUTHORS  
Jacobs, K., McCoy, J. M., Lavallie, E. R., Collins-Racie, L. A., Evans, C.,  
Merberg, D., Treacy, M., Bowman, M. R., Scauldung, V. and Agostino, M. J.  
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VERSION AY316196.1 GI:34809223
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SOURCE Xenopus laevis (African clawed frog)
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 4060)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.B. and Stuermer, C.A.
Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
JOURNAL
PUBMED 15019938
REFERENCE
2 (bases 1 to 4060)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.B. and
Stuermer, C.A.O.
Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetstrasse 10, Konstanz 78457, Germany
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Score: 764.00 Matches: 149
Percent Similarity: 89.95% Conservative: 21
Best Local Similarity: 78.84% Mismatches: 19
Query Match: 82.59% Indels: 0
DB: Gaps: 0
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Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40
Db 2769 AGCTTGTTCCTCCTGCTCTCTGAGTGTGTTCAGTATTTGTCAGGCTGCTCGCTTATATT 2828
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlleGlyValIleGlnAla 60
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Qy 61 IleGlnIleSerAspGluGlyHisProPheArgAlaTyrlleGluSerGluValAlaIle 80
Db 2889 ATCCAGAAGTCAGAGGAAGGACACCATTCAGATCCATCTTGGAGTCCAACTGGCGGTG 2948
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RESULT 94  
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 VERSION 1  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 REFERENCE  
 1 (bases 1 to 1467)  
 AUTHORS Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von  
 Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and Stuermer, C.A.  
 TITLE Identification of two NOGO/RTN4 genes and analysis of Nogo-A  
 expression in Xenopus laevis  
 JOURNAL Mol. Cell. Neurosci. 25 (2), 205-216 (2004)  
 PUBLISHED 15019938  
 REFERENCE 2 (bases 1 to 1467)  
 AUTHORS Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von  
 Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and Stuermer, C.A.O.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,  
 Universitaetsstrasse 10, Konstanz 78457, Germany  
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3' UTR

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 Best Local Similarity: 78.31% Mismatches: 19  
 Query Match: 82.27% Indels: 0  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY316191 (1-1467)

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 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 193 AGCTTGTTCCTCCTCTCTCTGAGTGTGTTCAGTATTGTTCAGCGTGTCTCCTTATAT 252  
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 Db 253 GCCCTGGCCCTCTCTCCGTCCACATCAGTTTAAGATATACAAGGGATTCGCGGCC 312  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
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 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
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 QY 161 HisTyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
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 Db 673 GTTCCGGGCTGAAACGCAAGCTGAA 699

RESULT 95  
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 LOCUS Xenopus laevis RTN4.1-B2 (RTN4) mRNA, complete cds; alternatively  
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 ACCESSION AY316193  
 VERSION 1  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 Xenopodinae; Xenopus; Xenopus.  
 REFERENCE 1 (bases 1 to 1758)  
 AUTHORS Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von  
 Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and Stuermer, C.A.  
 TITLE Identification of two NOGO/RTN4 genes and analysis of Nogo-A  
 expression in Xenopus laevis  
 JOURNAL Mol. Cell. Neurosci. 25 (2), 205-216 (2004)  
 PUBLISHED 15019938  
 REFERENCE 2 (bases 1 to 1758)  
 AUTHORS Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von  
 Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and Stuermer, C.A.O.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,  
 Universitaetsstrasse 10, Konstanz 78457, Germany  
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 /organism="Xenopus laevis"



This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency analysis, similarity but not identity to protein.

## FEATURES

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Query Match: 82.16% Indels: 0
DB: 5 Gaps: 0

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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 212 TTGTTCTCTGCTCTCTGAGTGTGTTTCAGTATTGTTCAGCGTGTCTGCTTATATGCC 271
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
Db 272 CTGGCCCTGCTCTCCGTCACCATCAGTTTAAGGATATACAAAGGAGTTCCTGCAGGCCATC 331
QY 62 GlnLysSerAspGlnGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 392 GAGGATCTGTCAGAAATACTGCAATGTGGCCCTGAACCATGTCAACTGCACAGTCAAG 451
QY 102 GluLeuArgArgPheLeuValAspAspLeuValValAspSerLeuLysPheAlaValLeu 121
Db 452 GAGCTCGGCACCTCTCTCTGTTAGAGACCTCGTGGATTCCTCGAAGTTTGAGTATTG 511
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spliced.
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VERSION
AY316192.1 GI:34809215
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Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 1543)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.
Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
REFERENCE
2 (bases 1 to 1543)
15019938
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and
Stuermer, C.A.O.
Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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Percent Similarity: 89.89% Conservative: 21
Best Local Similarity: 78.72% Mismatches: 19
Query Match: 82.16% Indels: 0

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Db	288	TGTTCCTCCCTGCTCTCTGAGTGTGTTAGTATTGTACGGTCTCGCTTATTATGCC	347
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	348	CTGGCCCTGCTCTCGCTCACCATCAGTTAAAGGATATACAAAGGATTCTCGAGCCATC	407
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	408	CAGAAGTCAGAGGAAGGACACCCATTTCAGATTCATCTTGGAGTCCAACTCGCGGTGCCA	467
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
Db	468	GAGATCTGGTCCAGAAATATCTGCAATGTGGCCCTGAACCATGTCAACTGCACAGTCAAG	527
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	528	GAGCTGGCGCACCTCTCTCTGTAGACACCTGGTGGATTCCCTGAAAGTTTGCAGTATTG	587
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuLeuAla	141
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Qy	142	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
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VERSION	AY316194.1		
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REFERENCE	1 (bases 1 to 1701)		
AUTHORS	Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrasch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.		
TITLE	Identification of two NOGO/RTN4 genes and analysis of Nogo-A expression in Xenopus laevis		
JOURNAL	Mol. Cell. Neurosci. 25 (2), 205-216 (2004)		
PUBMED	15019938		
REFERENCE	2 (bases 1 to 1701)		
AUTHORS	Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrasch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.O.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz, Universitaetstrasse 10, Konstanz 78457, Germany		
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Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
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Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	550	CAGAAGTCAGAGGAAGGACACCCATTTCAGATTCATCTTGGAGTCCAACTCGCGGTGCCA	609
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
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Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
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Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuLeuAla	141
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LOCUS
DEFINITION Xenopus laevis RTN4.2-A3 (RTN4) mRNA, complete cds; alternatively
spliced.
ACCESSION AY316188
VERSION AY316188.1 GI:34809209
KEYWORDS
SOURCE Xenopus laevis (African clawed frog)
ORGANISM
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 3886)
AUTHORS Klinger M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.
TITLE Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
JOURNAL Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
PUBMED 15019938
REFERENCE
2 (bases 1 to 3886)
AUTHORS Klinger M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and
Stuermer, C.A.O.
Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetstrasse 10, Konstanz 78457, Germany
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Best Local Similarity: 77.78% Mismatches: 19
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spliced.
ACCESSION AY316190
VERSION AY316190.1 GI:34811716
KEYWORDS
SOURCE Xenopus laevis (African clawed frog)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 3943)
AUTHORS Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.
TITLE Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
JOURNAL Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
PUBMED 15019938
REFERENCE
2 (bases 1 to 3943)
AUTHORS Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and
Stuermer, C.A.O.
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TITLE Direct Submission  
JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,  
Universitaetsstrasse 10, Konstanz 78457, Germany  
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Query Match: 80.76% Indels: 0  
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Job time : 2800 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005. Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PF 09-DEC-2003; 2003MO-EP013960.  
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PR 10-DEC-2002; 2002GB-00028832.

XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS PHARMA GMBH.  
PA (UYZU-) UNIV ZUERICH.  
XX  
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XX WPI; 2004-468818/44.  
DR P-PSDB; ADP45572.  
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XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-  
PT D20 or NogoA623-640, useful in preparing a composition for treating CNS  
PT injury or neurodegenerative disorders.  
XX  
XX Disclosure; SEQ ID NO 25; 121pp; English.  
XX  
XX The present invention describes a binding molecule which binds to human  
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a  
CC dissociation constant of less than 100nM. Also described: (1) a  
CC polynucleotide encoding the binding molecule; (2) an expression vector or  
CC system comprising the polynucleotide; (3) a host cell comprising the  
CC expression system; (4) a pharmaceutical composition comprising the  
CC binding molecule and a carrier or diluent; and (5) treating diseases  
CC associated with nerve repair. The binding molecule has neuroprotective  
CC activity, and can be used in gene therapy. The binding molecule is useful  
CC in preparing a composition for treating central nervous system (CNS)  
CC injury or neurodegenerative disorders. The present sequence encodes rat  
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SQ

Alignment Scores:  
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Score: 925.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADP45571 (1-3492)

QY 1 ServValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 2923 TCAGTTGTTGACCTCTCTACTGGAGAGACATTAAAGAACCTGGAGTGTGTGGTCC 2982  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 2983 AGCTTATTCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATT 3042  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3043 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCT 3102  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3103 ATCCAGAAATCAGATGAAGCCACCCATTGAGGGCATATTTAGAAATCTGAAGTTGCTATA 3162  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3163 TCAGAGGAATTGGTTCAGAAATACAGTAAATCTGCTCTGCTTGTGTGATGTGACACACAATA 3222  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3223 AAAGAACTCAGGCGGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTGCGATG 3282  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGluLeuThrLeuLeuIleLeu 140  
DB 3283 TTGATGTGGTGTGTTTACTTATGTGTGGTCTGTTCAATGGTGTGACACTACTGATTTTA 3342  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3343 GCTCTGATCTCACTCTTCAGTATCTCTGTTATTTATGAAAGCGCATCAGGTGCAGATAGAT 3402

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3403 CATTATCTAGGACTTGCACAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAGCAAA 3462  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3463 ATCCCTGGATTGAAGCGCAAGCAGAT 3489  
RESULT 2  
AAD01173  
ID AAD01173 standard; cDNA; 4684 BP.  
XX AC AAD01173;  
XX 02-NOV-2000 (first entry)  
XX Rat neurite growth inhibitor Nogo A cDNA.  
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; ss.  
XX Rattus sp.  
OS  
XX Key Location/Qualifiers  
FH 253..3744  
FT /\*tag= a  
FT /product= "Nogo A"  
FT /transl\_except= (pos:1462..1464, aa:Ile)  
XX WO200031235-A2.  
XX 02-JUN-2000.  
XX 05-NOV-1999; 99WO-US026160.  
XX 06-NOV-1998; 98US-0107446P.  
XX (SCHW/) SCHWAB M E.  
XX (CHEN/) CHEN M S.  
XX Schwab ME, Chen MS;  
XX WPI; 2000-400052/34.  
XX P-PSDB; AA711310.  
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
XX of the central nervous system and inducing regeneration of neurons.  
XX Claim 26; Fig 2A; 122pp; English.  
XX The present sequence is a cDNA encoding rat Nogo A protein which is a  
XX potent neural cell growth inhibitor and is free of all central nervous  
XX system (CNS) myelin material with which it is natively associated. The  
XX present sequence was generated by fusing RO18U37-3, R1-3U21 cDNA  
XX sequences isolated from hexanucleotides primed rat brain stem/spinal cord  
XX library, and Oli18 cDNA from an oligo d(7)-primed rat oligodendrocyte  
XX library. Nogo proteins and fragments displaying neurite growth inhibitory  
XX activity are used in the treatment of neoplastic disease of the CNS e.g.  
XX glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,  
XX pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,  
XX meningioma, neuroblastoma or retinoblastoma and degenerative nerve  
XX diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which  
XX promote Nogo activity can be used to treat or prevent hyperproliferative  
XX or benign dysproliferative disorders e.g. psoriasis and tissue  
XX hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to  
XX inhibit production of Nogo protein to induce regeneration of neurons or  
XX to promote structural plasticity of the CNS in disorders where neurite

CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers

XX SQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.7e-100 Length: 4684  
 Score: 925.00 Matches: 189  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AD01173 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3175 TCAGTGTGTGACTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGCC 3234  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3235 AGCTTATTCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATT 3294  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3295 GCCTTGGCCCTCTCTCGTGACTATCAGCTTTAGGATATATAAGGGCGGTATCCAGGCT 3354  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3355 ATCCAGAAATCAGATGAGCCACCCTTCAGGCAATATTAGAAATCTGAAGTTCCTATA 3414  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3415 TCAGAGGAATGGTTTCAGAAATACAGTAATCTCTGCTTGGTTCATGTGAACAGCAATA 3474  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3475 AAAGAACTGAGCGCGCTTCTTAGTGTATGATGATTTAGTTGATTCCTCCGAAGTTTCAGTG 3534  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 3535 TTGATGTGGGTGTTTACTTAAGTGGTGGCTTGCTTCATAGTGTGACACTACTGATTTTA 3594  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3595 GCTCTGATCTCACTCTTCAGTATTCTCTGTTATTTATGAACGGCATCAGTGCAGATAGAT 3654  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3655 CATTATCTAGGACTTGCACAAAGAGTGTTAGGATGCCATGGCCAAATTCACAGCAAAA 3714  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3715 ATCCCTGGATTGAGCGCAAGACAGAT 3741

## RESULT 3

ABN86600

ID ABN86600 standard; DNA; 4684 BP.

XX AC ABN86600;

XX DT 05-NOV-2002 (first entry)

XX DE Rat neurotransmitter receptor protein Nogo encoding DNA.

XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

XX KW central nervous system; peripheral nervous system; tranquilizer; Nogo;

XX KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW

XX Rattus norvegicus.

XX Key Location/Qualifiers

XX CDS 253..3744

XX FT /tag= a

XX FT /product= "Nogo-A"

XX US2002072493-A1.

XX 13-JUN-2002.

XX 28-JUN-2001; 2001US-00893348.

XX 19-MAY-1998; 98IL-00124500.

XX 21-JUL-1998; 98MO-US014715.

XX 22-DEC-1998; 98US-00218277.

XX 19-MAY-1999; 99US-00314161.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

XX Moalem G;

XX WPI; 2002-607255/65.

XX P-PsDB; ABB81074, ABB81076, ABB81077.

XX Promoting nerve regeneration and preventing neuronal degeneration in the

XX central/peripheral nervous system from injury/disease, comprises

XX administering nervous system-specific activated T cells/antigen, or

XX analogs/peptides.

XX Disclosure; Page 40-44; 93pp; English.

The invention relates to promoting nerve regeneration or conferring  
 neuroprotection and preventing or inhibiting neuronal degeneration in the  
 central/peripheral nervous system (NS). The method involves administering  
 NS-specific activated T cells, NS-specific antigen, its analogue or its  
 peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 combinations. The method is useful for promoting nerve regeneration and  
 preventing neuronal degeneration in central/peripheral nervous system  
 from injury/disease, where the injury is spinal cord injury, blunt  
 trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or  
 damages caused by surgery such as tumor excision. The disease is not an  
 autoimmune disease or neoplasm. The disease results in a degenerative  
 process occurring in either gray or white matter or both. The disease is  
 diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 vitamin deficiency, intervertebral disc herniation, prion diseases such  
 as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 neuropathies associated with various diseases, including but not limited  
 to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 pathies, complications of various drugs (e.g., metronidazole) and toxins  
 (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 telangiectasia, Friedreich's ataxia, amyloid polynuropathies,  
 adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 disease, or lipoproteinemia. The present sequence represents a DNA  
 encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B  
 and Nogo-C), an example of NS-specific antigen

SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.7e-100 Length: 4684

Score: 925.00 Matches: 189

Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABB86600 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3175 TCAGTTGTTGACCTCTCTACTGGAGAGACATTAAAGAGACTGGAGTGTGTTGGTGCC 3234

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3235 AGCTTATTCTGCTGCTCTGACAGTGTTCAGATTGTCAGTGTAAAGCGCTACATT 3294

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60  
 DB 3295 GCCTGGCCCTGCTCTCGTACTATCAGCTTTAGGATATATAAGGCGTGATCCAGGCT 3354

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
 DB 3355 ATCCAGAAATCAGATCAAGGCCACCCATTACAGGCGCATATTTAGAATCTGAAGTTGCTATA 3414

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3415 TCAGAGGAATTGTTTCAAGAAATACAGTAATCTGCTCTTGGTCAATGTCGACACCAATA 3474

QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3475 AAGAACTCAGGCGGCTTTCTTAGTTGATGATTAGTTGATTCCTGAAGTTGCGATG 3534

QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 3535 TTGATGTTGGTGTACTTATGTTGTTGCTGCTTCAATGGTCTGACACTACTGATTTTA 3594

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3595 GCTCTGATCTCACTCTTCAGTATCTCTGTTATTTATGAAGCGCATCAGTGCAGATAGAT 3654

QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3655 CATTATCTAGGACTTGCAAAACAGAGTGTAAAGGATGCCATGGCCAAAATCCAAAGCAAAA 3714

QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741

RESULT 4  
 ID ADB85284  
 XX ADB85284 standard; DNA; 2782 BP.  
 XX AC ADB85284;  
 XX DT 04-DEC-2003 (first entry)  
 XX DE Rat foocen-m2 reticulon gene SEQ ID NO:165.  
 XX KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
 KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
 KW protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.  
 XX OS Rattus norvegicus.  
 XX PN EP1284297-A2.  
 XX PD 19-FEB-2003.  
 XX PF 26-JUL-2002; 2002BP-00255228.  
 XX PR 27-JUL-2001; 2001GB-00018354.  
 XX PR 07-FEB-2002; 2002GB-00002880.  
 XX PA (WARN ) WARNER LAMBERT CO.  
 XX

PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;  
 XX WPI; 2003-364994/35.  
 DR P-PSDB; ADB85283.  
 XX  
 PT Use of gene sequence that is down-regulated in response to streptozocin-  
 PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in  
 PT screening of compounds for treating or diagnosing pain.  
 XX  
 PS Claim 1; Page 240-241; 256pp; English.  
 XX  
 CC The invention relates to a novel isolated gene sequence that is down-  
 CC regulated in the spinal cord in response to streptozocin-induced  
 CC diabetes, or comprising, hybridising or having at least 80% sequence  
 CC identity to a sequence whose expression products are kinases,  
 CC phosphatases, ion channel proteins, receptors, transporters, G-protein  
 CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
 CC given in the specification. A gene of the invention has analgesic  
 CC activity, and may have a use in gene therapy. The gene sequences, vector,  
 CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a gene of the invention.  
 XX  
 SQ Sequence 2782 BP; 635 A; 728 C; 765 G; 654 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1-89e-100 Length: 2782  
 Score: 922.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.47% Mismatches: 0  
 Query Match: 99.68% Indels: 0  
 DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADB85284 (1-2782)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 1271 GCAGTTGTTGACCTCTCTACTGGAGAGACATTAAAGAGACTGGAGTGTGTTGGTGCC 1330

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 1331 AGCTTATTCTGCTGCTCTGACAGTGTTCAGATTGTTCAGTGTAAAGCGCTACATT 1390

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 1391 GCCTTGGCCCTGCTCTCGTGTACTATCAGCTTTAGGATATATAAGGCGTGTATCCAGGCT 1450

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 1451 ATCCAGAAATCAGATCAAGGCCACCCATTACAGGCGCATATTTAGAATCTGAAGTTGCTATA 1510

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 1511 TCAGAGGAATTGTTTCAAGAAATACAGTAATCTGCTCTTGGTCAATGTCAGGCGCAATA 1570

QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 1571 AAAGAACTGAGCGGCTTTCTTAGTGTATTTAGTTGATTCCTCGAAGTTGCGATG 1630

QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 1631 TTGATGTTGGTGTCTTACTTATGTTGGTGTCTTCAATGCTGCTGACACTACTGATTTTA 1690

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 1691 GCTCTGATCTCACTCTTCAAGTATTTCTGTTATTTATGAAGCGCATCAGTGCAGATAGAT 1750

QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

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Db 1751 CATTATCTAGGACTTCAACAACAGAGTGTAAAGGATGCCATGCCCAAAATCAAGCAAAA 1810
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 1811 ATCCCTGGATTGAAGCCCAAGCAGAT 1837

RESULT 5
AAD01175
XX AAD01175 standard; cDNA; 1568 BP.
AC AAD01175;
XX 02-NOV-2000 (first entry)
XX Rat neurite growth inhibitor Nogo C cDNA.
XX Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.
XX OS
XX Rattus sp.
XX Key Location/Qualifiers
XX CDS 1..1566
XX /*tag= a
XX /product= "Nogo C protein (residues 40-238) flanked by 1-
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XX C-terminal"
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XX /transl_except= (pos:85..87, aa:Xaa)
XX /transl_except= (pos:787..789, aa:Xaa)
XX /transl_except= (pos:826..828, aa:Xaa)
XX /transl_except= (pos:841..843, aa:Xaa)
XX /transl_except= (pos:883..885, aa:Xaa)
XX /transl_except= (pos:889..891, aa:Xaa)
XX /transl_except= (pos:940..942, aa:Xaa)
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XX /transl_except= (pos:1003..1005, aa:Xaa)
XX /transl_except= (pos:1111..1113, aa:Xaa)
XX /transl_except= (pos:1120..1122, aa:Xaa)
XX /transl_except= (pos:1138..1140, aa:Xaa)
XX /transl_except= (pos:1216..1218, aa:Xaa)
XX /transl_except= (pos:1222..1224, aa:Xaa)
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XX /transl_except= (pos:1264..1266, aa:Xaa)
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XX /transl_except= (pos:1318..1320, aa:Xaa)
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XX /transl_except= (pos:1537..1539, aa:Xaa)
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XX /partial
XX 118..120
XX misc_feature
XX /*tag= b
XX /note= "Start codon of Nogo C coding region"
XX 715..717
XX misc_feature
XX /*tag= c
XX /note= "Stop codon of Nogo C coding region"
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1999; 98US-0107446P.
XX

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PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
XX Schwab ME, Chen MS;
XX
XX WPI; 2000-400052/34.
XX P-PSDB; AAY71312.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 23; Fig 14; 122pp; English.
XX
XX The present sequence is a cDNA encoding rat Nogo C protein which is a
XX potent neural cell growth inhibitor and is free of all central nervous
XX system (CNS) myelin material with which it is natively associated. Nogo
XX proteins and fragments displaying neurite growth inhibitory activity are
XX used in the treatment of neoplastic disease of the CNS e.g. glioma,
XX glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
XX haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
XX neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
XX Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
XX activity can be used to treat or prevent hyperproliferative or benign
XX dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
XX Ribozymes or antisense Nogo nucleic acids can be used to inhibit
XX production of Nogo protein to induce regeneration of neurons or to
XX promote structural plasticity of the CNS in disorders where neurite
XX growth, regeneration or maintenance are deficient or desired. The animal
XX models can be used in diagnostic and screening methods for predisposition
XX to disorders and to screen for or test molecules which can treat or
XX prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
XX referred in claim 32 and SEQ ID NO: 29 in disclosure of the
XX CC specification. However the specification does not include sequences for
XX these SEQ ID numbers
XX
XX Sequence 1568 BP; 435 A; 274 C; 375 G; 484 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1,11e-100 Length: 1568
XX Score: 921.00 Matches: 188
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 99.57% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-830-972-2_COPY_975_1163 (1-189) x AAD01175 (1-1568)
XX
XX Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
XX 151 GTTGTTCACCTCCTCTACTCGAGAGACATTAAGAAGACTGGAGTGTGTTGGTCCAGC 210
XX
XX Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41
XX 211 TTATTCCTCGCTGCTCTCTGACAGTGTTCAGCATTTGTCAAGTGTAAACGGCTTACATTGCC 270
XX
XX Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
XX 271 TTGGCCCTGCTCTCGTGACATTCAGCTTTAGGATATATAAGGGCGTGATTCAGGCTATC 330
XX
XX Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
XX 331 CAGAAATCAGATGAAGGCCACCCCATTCAGGCGCATTTAGAAATCTGAAGTTGCTATATCA 390
XX
XX Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
XX 391 GAGGAATTGGTTCAGAAATACAGTAATTTCTCTCTTGGTCTATGTGAACAGCACATATAA 450
XX
XX Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
XX 451 GAATGAGCGCGCTTTCTTCTAGTGTGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 510
XX
XX 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
XX

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Db 511 ATGTGGGTCTTACTTATGTTGGTGGCTTGTTCATATGGTCTGACACTACTGATTTTAGCT 570  
 QY 142 LeuileSerleuPheSerleProValileTyrGluArgHisGlnValGlnileAspHis 161  
 Db 571 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 630  
 QY 162 TyrLeuGluLeuAlaAsnlySerVallyAspAlaMetAlaAlaGlylleGlnAlaIlylle 181  
 Db 631 TATCTAGGACTTGCACAAACAGAGTGTAAAGGATGCCATGCCCAAAATCCCAAGCAAAATC 690  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 691 CCTGGATTGAGCGCAAGCAGAT 714  
 RESULT 6  
 ADF42781  
 ID ADF42781 standard; cDNA; 734 BP.  
 AC ADF42781;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Mouse CYP27 nucleotide sequence SEQ ID NO:87.  
 XX  
 KW diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy;  
 XX diabetes; insulin resistance; metabolic disease; mouse; gene; ss.  
 OS Mus sp.  
 XX  
 PN WO2003102163-A2.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PF 04-JUN-2003; 2003WO-US017825.  
 XX  
 PR 04-JUN-2002; 2002US-0385857P.  
 PR 04-JUN-2002; 2002US-0386013P.  
 PR 04-JUN-2002; 2002US-0386074P.  
 PR 04-JUN-2002; 2002US-0386107P.  
 PR 05-JUN-2002; 2002US-0386314P.  
 PR 05-JUN-2002; 2002US-0386326P.  
 PR 05-JUN-2002; 2002US-0386332P.  
 PR 05-JUN-2002; 2002US-0386481P.  
 PR 05-JUN-2002; 2002US-0386512P.  
 PR 05-JUN-2002; 2002US-0386513P.  
 PR 05-JUN-2002; 2002US-0386558P.  
 PR 05-JUN-2002; 2002US-0386600P.  
 PR 05-JUN-2002; 2002US-0386615P.  
 PR 05-JUN-2002; 2002US-0386654P.  
 PR 06-JUN-2002; 2002US-0386838P.  
 PR 06-JUN-2002; 2002US-0386861P.  
 PR 06-JUN-2002; 2002US-0386944P.  
 PR 06-JUN-2002; 2002US-0386955P.  
 PR 06-JUN-2002; 2002US-0387017P.  
 PR 06-JUN-2002; 2002US-0387026P.  
 PR 06-JUN-2002; 2002US-0387039P.  
 PR 20-JUN-2002; 2002US-0386865P.  
 XX  
 PA (META-) METABOLEX INC.  
 XX  
 PI Allan B, Gregoire F, Lavan B, Moodie S, Waters S, Wong C;  
 XX  
 DR WPI; 2004-053469/05.  
 DR P-PSDB; ADF42782.  
 XX  
 PT Identifying an agent for treating diabetic or pre-diabetic individuals  
 PT comprises contacting an agent with a polypeptide, e.g., human ceramidase,  
 PT and selecting an agent that modulates the expression or activity of the  
 PT polypeptide.  
 XX  
 PS Disclosure; SEQ ID NO 87; 209pp; English.  
 XX  
 XX The present invention describes a method for identifying an agent for

CC treating a diabetic or pre-diabetic individual. The method comprises  
 CC contacting an agent to a mixture comprising a polypeptide encoded by a  
 CC nucleic acid that hybridises under stringent conditions to a nucleic acid  
 CC encoding any of the 23 fully defined amino acid sequences given in the  
 CC specification, and selecting an agent that modulates the expression or  
 CC activity of the polypeptide. Also described: (1) a method of treating a  
 CC diabetic or pre-diabetic animal, comprising administering to the animal a  
 CC therapeutic amount of an agent identified by the method described above;  
 CC (2) a method of introducing an expression cassette into a cell,  
 CC comprising introducing into the cell an expression cassette comprising a  
 CC promoter operably linked to a polynucleotide encoding a polypeptide,  
 CC where the polynucleotide hybridises under stringent conditions to a  
 CC nucleic acid encoding the above amino acid sequences; and (3) a method of  
 CC diagnosing an individual who has type 2 diabetes or is pre-diabetic,  
 CC comprising detecting in a sample from the individual the level of a  
 CC polypeptide or the level of the above-mentioned polynucleotide encoding  
 CC the polypeptide, where a modulated level of the polypeptide or  
 CC polynucleotide in the sample compared to a level of the polypeptide or  
 CC polynucleotide in either a lean individual or a previous sample from the  
 CC individual indicates that the individual is diabetic or pre-diabetic. The  
 CC method is useful in diagnosing and treating diabetes, insulin resistance  
 CC or related metabolic diseases in human subjects. The method may also be  
 CC used in identifying agents for treating diabetic or pre-diabetic  
 CC individuals. The present sequence is used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 734 BP; 202 A; 138 C; 179 G; 215 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3-54e-100 Length: 734  
 Score: 913.00 Matches: 186  
 Percent Similarity: 99.47% Conservative: 1  
 Best Local Similarity: 98.94% Mismatches: 1  
 Query Match: 98.70% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADF42781 (1-734)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 100 GTTGTTCACCTCCTCTACTCTGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCACG 159  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThralaTyrIleAla 41  
 Db 160 TTATTCCTGCTGCTGCTCTGACAGTGTTCAGATGTTCAGTGTACGGCCTACATGGC 219  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 220 TTGGCCCTGCTCTCTGTGACTATATCAGCTTTAGGATATATAAGGGTGTGATCCAAAGTATC 279  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 280 CAGAAATCAGATGAAGGCCACCACCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 339  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 340 GAGGAATGGTTTCAGAAATATAGTAATTTCTGCTCTGTGTCATGTGAACAGCAATATAAA 399  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 400 GAATTTGAGCGCTCTCTTCTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 459  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
 Db 460 ATGTGGGTATTTACTTACGTTGGTCCCTTGTTCATATGGTTTGCACACTACTGTATTTAGCC 519  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 520 CTGATCTCACTCTTCAGTATTTCTGTTATATATGAACGGCATCAGCGCGAGATAGATCAT 579  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIlylle 181  
 Db 580 TATCTAGGACTTGCACAAACAGAGTGTAAAGGATGCCATGGGCCAAATCCCAAGCAAAATC 639





PT gene and may be useful in the treatment of neural disorders including  
PT Alzheimer's and Parkinson's diseases.

XX Disclosure; Page 25-26; 25pp; English.

XX The present sequence is that of cDNA encoding human Nogo-A (see  
CC AAB82349). Nogo-A is a previously known splice variant of the human Nogo  
CC gene on chromosome 2p21. Nogo-A cDNA was obtained by PCR amplification of  
CC human spinal cord cDNA. The invention relates to a novel splice variant,  
CC Nogo-C (see AAF90323). It provides Nogo-C polypeptides and  
CC polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilizing Nogo-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric disorders and developmental disorders. Also  
CC provided are methods for identifying agonists and agonists for use in  
CC treating conditions associated with Nogo-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate Nogo-C  
CC activity or levels

XX Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.31e-98 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF90324 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTGCTAGTGGAGAGACATTAAAGAGCTGGAGTGGTGGTGGCC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3070 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCTACATT 3129  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATCAGAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValLysSerThrIle 100  
Db 3250 TCTGAGGAGTTGGTTGAGAGTACAGATAATCTGCTCTTGGTCATGTGAACCTGCACGATA 3309  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3370 TTGATGTTGGTATTACCTATGTTGTTGCTGCTTGTAAATGCTGACACTGATGTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTTTCAGTGTCTCTGTTATTTATTAAGCGGCATCAGGCGCATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCATTAATAGAAATGTTAAGATGCTATGGCTAAATCCAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 9

ABK90134

ID ABK90134 standard; DNA; 3579 BP.

XX

AC ABK90134;

XX

DT 21-OCT-2002 (first entry)

XX

DE DNA encoding human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;  
KW Nogo-associated disease; metastasis; gene; ds.

OS Homo sapiens.

XX

XX Location/Qualifiers

Key

CDS 1..3579

FT

FT /\*tag= a

FT /product= "Human NogoA protein"

XX

XX WO200257483-A2.

XX

XX 25-JUL-2002.

XX

XX 18-JAN-2002; 2002WO-GB000228.

XX

XX 18-JAN-2001; 2001GB-00001312.

XX

XX (GLAX ) GLAXO GROUP LTD.

XX

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX

XX Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

XX WPI; 2002-599722/64.

XX

XX P-PSDB; ABG30938.

XX

PT Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
PT providing and monitoring interaction between Nogo and BACE polypeptides.

XX

PS Disclosure; Page 53-58; 68pp; English.

XX

CC The present invention relates to a new method of identifying modulators  
CC of Nogo function or BACE activity. The method involves providing Nogo and  
CC BACE polypeptides capable of binding with each other, monitoring the  
CC interaction between these polypeptides, and determining if the test agent  
CC is a modulator of Nogo or BACE activity. The method is useful in treating  
CC acute neuronal injuries, such as spinal or head injury, stroke,  
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
CC hypertrophy) of the central nervous system. The BACE polypeptide is  
CC useful in screening methods to identify agents that may act as modulators  
CC of BACE activity and in particular agents that may be useful in treating  
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
CC and the polynucleotide encoding the BACE polypeptide are useful in  
CC manufacturing a medicament for the treatment or prevention of disorders  
CC responsive to the modulation of Nogo activity, in alleviating the  
CC symptoms or improving the condition of a patient suffering from this  
CC disorder, in axon regeneration, or in preventing metastasis or spreading  
CC of a cancer. The polynucleotide may also be an essential component in  
CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
CC techniques. The present nucleic acid sequence encodes the human NogoA  
CC protein of the invention

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.31e-98 Length: 3579



```
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservativity: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x ABK90134 (1-3579)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTGACCTCTGCTGCTTCAATGACAGTATTAAGAGACTGGAGTGGTGTGGTCC 3069

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCTGCTGCTTCAATGACAGTATTAAGAGACTGGAGTGGTGTGGTCC 3129

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTTGGCCCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTATCCAAGCT 3189

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3250 TCTGAGGAGTTGGTTTCAGAAATACAGTAATCTGCTCTTGGTCATGTGAAGTGCAGATA 3309

Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGSAACCTACAGCGCTCTCTTAGTGTGATGATTTAGTTGATCTCTGAAGTTTGCAGTG 3369

Qy 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3370 TTGATGTGGTATTTACCTAGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTTG 3429

Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3430 GCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTTATGAAGCGCATCGGCGCAGATAGAT 3489

Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTTATCAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3549

Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 10
ID ABN86601
XX ABN86601 standard; DNA; 3579 BP.
AC ABN86601;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human neurotransmitter receptor protein Nogo encoding DNA.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;
KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; human; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..3579
FT /tag= a
FT /product= "Nogo"
FT /note= "Nogo-A, Nogo-B and Nogo-C"
FT
XX
```

US2002072493-A1.  
13-JUN-2002.  
28-JUN-2001; 2001US-008933348.  
19-MAY-1998; 98IL-00124500.  
21-JUL-1998; 98WO-US014715.  
22-DEC-1998; 98US-00218277.  
19-MAY-1999; 99US-00314161.  
(YEDA ) YEDA RES & DEV CO LTD.  
Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
Moalem G;  
WPI; 2002-607255/65.  
P-PSDB; ABB81078, ABB81079, ABB81080.  
Promoting nerve regeneration and preventing neuronal degeneration in the  
central/peripheral nervous system from injury/disease, comprises  
administering nervous system-specific activated T cells/antigen, or  
analogs/peptides.  
Disclosure; Page 49-53; 93pp; English.  
The invention relates to promoting nerve regeneration or conferring  
neuroprotection and preventing or inhibiting neuronal degeneration in the  
central/peripheral nervous system (NS). The method involves administering  
NS-specific activated T cells, NS-specific antigen, its analogue or its  
peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
combinations. The method is useful for promoting nerve regeneration and  
preventing neuronal degeneration in central/peripheral nervous system  
from injury/disease, where the injury is spinal cord injury, blunt  
trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or  
disease caused by surgery such as tumour excision. The disease is not an  
autoimmune disease or neoplasm. The disease results in a degenerative  
process occurring in either gray or white matter or both. The disease is  
diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
amyotrophic lateral sclerosis, non-articular optic neuropathy, and  
vitamin deficiency, intervertebral disc herniation, prion diseases such  
as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
neuropathies associated with various diseases, including but not limited  
to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
pathies, complications of various drugs (e.g., metronidazole) and toxins  
(e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
adrenomyeloneuropathy, giant axonal neuropathy, Refsum's disease, Fabry's  
disease, or lipoproteinemia. The present sequence represents a DNA  
encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B  
and Nogo-C), an example of NS-specific antigen  
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.31e-98 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservativity: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABN86601 (1-3579)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
|||||  
Db 3010 TCAGTTGTGACCTCTGCTGCTTCAATGACAGTATTAAGAGACTGGAGTGGTGTGGTCC 3069  
|||||

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
|||||  
Db 3070 AGCCTATTCTGCTGCTTCAATGACAGTATTAAGAGACTGGAGTGGTGTGGTCC 3129  
|||||

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
|||||  
Db 3130 GCCTTTGGCCCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTATCCAAGCT 3189  
|||||

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
|||||  
Db 3190 ATCCAGAAATCAGATGAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
|||||

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
|||||  
Db 3250 TCTGAGGAGTTGGTTTCAGAAATACAGTAATCTGCTCTTGGTCATGTGAAGTGCAGATA 3309  
|||||

Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
|||||  
Db 3310 AAGSAACCTACAGCGCTCTCTTAGTGTGATGATTTAGTTGATCTCTGAAGTTTGCAGTG 3369  
|||||

Qy 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
|||||  
Db 3370 TTGATGTGGTATTTACCTAGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTTG 3429  
|||||

Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
|||||  
Db 3430 GCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTTATGAAGCGCATCGGCGCAGATAGAT 3489  
|||||

Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
|||||  
Db 3490 CATTTATCAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 3549  
|||||

Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
|||||  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
|||||

Db 3070 AGCCTATTCTGCTGCTTTTCATTCAGCATTTTCAGCATTTGTGAGCGTAAACAGCTACATT 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db 3130 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACCTGCAGATA 3309  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTAGTTGATTTCTGAAGTTTGCAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
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QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGCGCGAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTAATCAGGACTTGCMAATAAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 11  
ID ADO07886 standard; cDNA; 3579 BP.  
AC ADO07886;  
XX 01-JUL-2004 (first entry)  
DT Human polynucleotide #65.  
DE Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
KW anorectic; antidiabetic.  
XX Homo sapiens.  
XX US2004071700-A1.  
XX 15-APR-2004.  
XX 09-OCT-2002; 2002US-00267502.  
XX 09-OCT-2002; 2002US-00267502.  
PR (LIFE-) LIFE SCI DEV CORP.  
XX Kim J, Galant R;  
XX WPI; 2004-328526/30.  
DR P-PSDB; ADO08103.  
XX Identifying compounds that influence fat cell number or size for treating  
PT or preventing obesity or diabetes by exposing the cell to the agent and  
PT identifying fat cell number or size relative to cells not exposed to the  
PT agent.  
XX Claim 1; SEQ ID NO 212; 275pp; English.  
PS The invention relates to a method of identifying compounds that influence

CC fat cell number or size comprising providing a cell that expresses a gene  
CC and an agent, exposing the cell to the agent and identifying fat cell  
CC number or size relative to cells not exposed to the agent. The method  
CC also comprises providing an expression vector and an agent, exposing the  
CC vector to the agent, detecting a change in expression of the gene  
CC relative to expression of the gene in an expression vector not exposed to  
CC the agent, treating a subject with the agent and identifying fat cell  
CC number or size in the subject. The agent comprises an antisense  
CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
CC method also comprises providing a polypeptide and an agent, exposing the  
CC polypeptide to the agent, detecting binding of the agent to the  
CC polypeptide or a change in an activity of the polypeptide, treating a  
CC subject with the agent and identifying fat cell number or size in the  
CC subject. The agent comprises an antibody. A method of regulating fat cell  
CC number or size comprises providing a subject containing fat cells and an  
CC agent that changes the expression of a gene, and treating the subject  
CC with the agent under conditions so that fat cell size or number in the  
CC subject is altered. The method is useful for identifying compounds that  
CC influence fat cell number or size, for preparing a composition for  
CC treating or preventing obesity or diabetes. This sequence represents  
CC human cDNA used in the scope of the invention.  
XX SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1,318-98 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 12 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADO07886 (1-3579)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAAGAGACTGGAGTGTGTTGTGTC 3069  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3070 AGCCTATTCTGCTGCTTTTCATTGACGATTAATCAGCATTTGTGAGCGTAAACGCTACATT 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3130 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACCTGCAGATA 3309  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTAGTTGATTTCTGAAGTTTGCAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAAATGGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGCGCGAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTAATCAGGACTTGCMAATAAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

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RESULT 12
ADRI13965
ID ADRI13965 standard; cDNA; 3579 BP.
XX
AC ADRI13965;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human NIGO-A cDNA.
XX
KW ss; gene; human; myelin-associated glycoprotein; MAG; neural growth;
KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW multiple sclerosis; Creutzfeldt-Jacob disease; Kuru;
KW multiple system atrophy; Lou Gehrig's disease;
KW progressive supranuclear palsy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3579
FT /tag= a
FT /product= "NIGO-A"
XX
XX US2004121341-A1.
XX
XX 24-JUN-2004.
XX
XX 20-DEC-2002; 2002US-00327213.
XX
XX 20-DEC-2002; 2002US-00327213.
XX
XX (FILB/) FILBIN M T.
XX (DOME/) DOMENICONI M.
XX (CAOZ/) CAO Z.
XX
XX Filbin MT, Domeniconi M, Cao Z;
XX
XX WPI: 2004-479666/45.
XX P-PSDB; ADRI13966.
XX
XX New myelin-associated glycoprotein (MAG) derivative comprises a mutation
XX in or flanking MAG Ig-like domain 5 (Igds), excluding the MAG derivative
XX MAG (dl-3)-Fc, useful promoting neural growth and regeneration.
XX
XX Disclosure; SEQ ID NO 8; 81pp; English.
XX
XX The invention relates to a myelin-associated glycoprotein (MAG)
XX derivative comprising a mutation in or flanking MAG Ig-like domain 5
XX (Igds), excluding the MAG derivative MAG (dl-3)-Fc, where the mutation
XX reduces or eliminates the ability of the derivative to regulate neurite
XX outgrowth as compared to endogenous or soluble MAG without eliminating
XX binding to neuronal surfaces. The inhibitors of MAG are useful for
XX promoting neural growth and regeneration. They are also useful for
XX treating neural degeneration associated with injuries, disorders, or
XX diseases. The disorder, disease, or condition is associated with
XX apoptosis or results from a demyelinating disease and includes
XX amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
XX Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease,
XX Kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou
XX Gehrig's disease), or progressive supranuclear palsy. The present
XX sequence represents the human NIGO-A cDNA.
XX
XX Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,31e-98 Length: 3579
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservatives: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 12 Gaps: 0

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US-09-830-972-2_COPY_975_1163 (1-189) x ADRI13965 (1-3579)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyVal 20
DB 3010 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTGTTGGTCC 3069
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3070 AGCCTATTCTCTGCTCTTCATTGACAGTATTACAGATTGTGAGCGTAACAGCTACATT 3129
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGlnAla 60
DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCT 3189
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100
DB 3250 TCTGAGGAGTTGGTTTCAGNAGTACAGTAATTCTCTCTTGGTCATGTGAATCGACGATA 3309
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3310 AAGGAACTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCACTG 3369
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeu 140
DB 3370 TTGATGTGGTATTTACCTATGTTGGTGCCTTTGTTTAATGGTCTGACACTACTGATTTTG 3429
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 3430 GCTCTCATTTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCGCGCGCATAGAT 3489
QY 161 HistyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3490 CATTATCTAGGACTTGCAAATGAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAA 3549
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576
RESULT 13
ADRI1174
ID AAD01174 standard; cDNA; 3833 BP.
XX
AC AAD01174;
XX
DT 02-NOV-2000 (first entry)
XX
DE Bovine neurite growth inhibitor Nogo cDNA.
XX
KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menigioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; Benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.
XX
OS Bos sp.
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.

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XX Schwab ME, Chen MS;  
XX WPI; 2000-400052/34.  
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
XX of the central nervous system and inducing regeneration of neurons.  
XX Claim 26; Fig 12; 122pp; English.  
XX The present sequence is a cDNA encoding bovine Nogo protein which is a  
XX potent neural cell growth inhibitor and is free of all central nervous  
XX system (CNS) myelin material with which it is natively associated. The  
XX present sequence was obtained from bovine spinal cord white matter cDNA  
XX library. Nogo proteins and fragments displaying neurite growth inhibitory  
XX activity are used in the treatment of neoplastic disease of the CNS e.g.  
XX glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,  
XX pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,  
XX meningioma, neuroblastoma or retinoblastoma and degenerative nerve  
XX diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which  
XX promote Nogo activity can be used to treat or prevent hyperproliferative  
XX or benign dysproliferative disorders e.g. psoriasis and tissue  
XX hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to  
XX inhibit production of Nogo protein to induce regeneration of neurons or  
XX to promote structural plasticity of the CNS in disorders where neurite  
XX growth, regeneration or maintenance are deficient or desired. The animal  
XX models can be used in diagnostic and screening methods for predisposition  
XX to disorders and to screen for or test molecules which can treat or  
XX prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
XX referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
XX specification. However the specification does not include sequences for  
XX these SEQ ID numbers  
XX Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 U; 0 Other;  
XX SQ

Alignment Scores:  
Pred. No.: 1,44e-98 Length: 3833  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 0 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAD01174 (1-3833)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 2301 TCAGTTGTTGACCTCTCTACTCGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCC 2360  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 2361 AGCTTGTTCCTGCTGCTGCTGACAGTATTTCAGCATTTGTGAGTGTAAAGCGGCTACATT 2420  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 2421 GCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCT 2480  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 2481 ATCCAGAAATCTGATGAAGGCCACCCATTTCAGGCGATATTTGGAATCTGAAGTTGCTATA 2540  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 2541 TCTGAGGAGTTGGTTCTGAGAAGTACAGCAATTCCTGCTCTGTCATGTTAACTGCACAATA 2600  
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 2601 AAAGAACTCAGACGCTCTCTTAGTGTGATGATTTAGTTGATTTCTCTGAAGTTGAGTG 2660  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 2661 TTGATGTGGGTATTACCTATGTTGGTCTTGTTCATGCTGTGACACTACTAAATTTTG 2720

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 2721 GCTCTGATTTCACCTCTCAGTGTCTGTATTATGAACGGCATCAGCGCAAAATAGAT 2780  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 2781 CATTATCTGGGACTTGCATAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 2840  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 2841 ATCCCTGGATTGAAGCGTAAAGCTGAA 2867  
RESULT 14  
ADP45550  
ID ADP45550 standard; cDNA; 3919 BP.  
XX AC ADP45550;  
XX DT 09-SEP-2004 (first entry)  
XX DE Human NogoA encoding cDNA SEQ ID NO:4.  
XX KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;  
XX KW nerve repair; neuroprotective; gene therapy;  
XX KW central nervous system injury; CNS injury; neurodegenerative disorder;  
XX KW gene; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 1..3579  
FT FT /\*tag= a  
FT FT /product= "NogoA"  
XX PN WO2004052932-A2.  
XX PD 24-JUN-2004.  
XX PF 09-DEC-2003; 2003WO-EP013960.  
XX PR 10-DEC-2002; 2002GB-00028832.  
XX PA (NOVS ) NOVARTIS AG.  
XX PA (NOVS ) NOVARTIS PHARMA GMBH.  
XX PA (UYZU-) UNIV ZUERICH.  
XX PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;  
XX PI Zurini M;  
XX DR WPI; 2004-468818/44.  
XX DR P-PSDB; ADP45551.  
XX PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.  
XX PS Example 1; SEQ ID NO 4; 121pp; English.  
XX The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes human NogoA, which is used in the exemplification of the present invention.  
XX Sequence 3919 BP; 1168 A; 857 C; 890 G; 1004 T; 0 U; 0 Other;  
XX SQ

## Alignment Scores:

Pred. No.: 1.48e-98 Length: 3919  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: 12 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADP45550 (1-3919)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3010 TCAGTTGTTGACCTCTCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGC 3069  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3070 AGCCTATTCTCTGCTTTCATTGACAGTATTCAGCATTTGTGAGGTAACACCTACATT 3129  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3130 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCT 3189  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3250 TCTGAGGAGTTGGTTCAGAGTACAGTAATTCCTCTTGGTCATGTGNACTGCACGATA 3309  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3310 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTGCAGTG 3369  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140  
 DB 3370 TTGATGTGGGTATTTACCTATCTTGGTCTGCTTTGTTAAATGGTCTGACACTACTGATTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3430 GCTCTCATTTCTCTTCTAGTGTCTCTGTTATTTATGAAGGCATCAGGCACAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCACGCAAAA 3549  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

## RESULT 15

AAS09453

ID AAS09453 standard; cDNA; 4053 BP.

XX AC AAS09453;

XX DT 26-SEP-2001 (first entry)

XX DE Human cDNA encoding the Nogo protein.

XX KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

XX KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

XX KW demyelinating disease; multiple sclerosis; monophasia demyelination;

XX KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;

XX KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;

XX KW Pelizaeus-Werzbacher disease; Spongy degeneration; Alexander's disease;

XX KW Canavan's disease; metachromatic leukodystrophy; viral infection;

XX KW Krabbe's disease; AB020693; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT 135..3713

FT /\*tag= a  
 XT /product= "Nogo protein"  
 PN WO200151520-A2.  
 XX 19-JUL-2001.  
 XX 12-JAN-2001; 2001WO-US001041.  
 XX 12-JAN-2000; 2000US-0175707P.  
 PR 26-MAY-2000; 2000US-0207366P.  
 PR 29-SEP-2000; 2000US-0236378P.  
 XX (UYVA ) UNIV YALE.  
 PA Strittmatter SM;  
 PI WPI; 2001-442138/47.  
 DR P-PSDB; AAU09453.  
 XX Novel Nogo receptor protein useful for identifying modulator of Nogo  
 PT protein or Nogo receptor protein, which is useful for treating central  
 PT nervous system disorders.  
 XX Example 1; Page 95-100; 109pp; English.  
 XX The sequence (Genbank accession number AB0202693) encodes the human Nogo  
 CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention  
 CC relates to the use of the nogo receptor, nogo protein, their nucleic  
 CC acids, vectors expressing them and antibodies against them, to isolate  
 CC agents which block nogo receptor mediated axonal growth. The agent is  
 CC useful for treating a central nervous system disorder which is a result  
 CC of cranial or cerebral trauma, spinal cord injury, stroke or a  
 CC demyelinating disease selected from multiple sclerosis, monophasia  
 CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,  
 CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,  
 CC adrenoleukodystrophy, Pelizaeus-Werzbacher disease, Spongy degeneration,  
 CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,  
 CC viral infection and Krabbe's disease  
 XX Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.56e-98 Length: 4053  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAS09453 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3144 TCAGTTGTTGACCTCTCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGC 3203  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3204 AGCCTATTCTCTGCTTTCATTGACAGTATTCAGCATTTGTGAGGTAACACCTACATT 3263  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3264 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCT 3323  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3324 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3383  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3384 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTCACTGTAACCTGCAGATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

Db 3444 AAGGAAGTCTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTGAGTG 3503  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 3504 TTGATGTGGTATTTACCTATGTTGGTGGCTTTTAAAGTCTGACACTACTGATTTTG 3563  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 3564 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3623  
 QY 161 HisTyrLeuGlyLeuAlaLeuLeuSerValIleAspAlaMetAlaIleGlnAlaLys 180  
 Db 3624 CATTTATCTAGGACTTCCAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 3684 ATCCCTGGATTGAGCGCAAGCTGAA 3710  
 RESULT 16  
 ACC81048  
 ID ACC81048 standard; cDNA; 4053 BP.  
 XX  
 AC ACC81048;  
 XX  
 DT 22-JUL-2003 (first entry)  
 XX  
 DE Human NogoA gene.  
 XX  
 KW Human: Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT 135. .3713  
 CDS /\*tag= a  
 FT /\*product= "Human NogoA"  
 FT  
 XX WO2003031462-A2.  
 XX  
 PN 17-APR-2003.  
 XX  
 PD 04-OCT-2002; 2002WO-US032007.  
 XX  
 PF 06-OCT-2001; 2001US-00972599.  
 XX  
 PR (UYAA ) UNIV YALE.  
 XX  
 PA Strittmatter SM;  
 XX  
 PI WPI; 2003-393433/37.  
 XX  
 DR P-PSDB; ABR59667.  
 XX  
 PT New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 PT injury, e.g. spinal cord injury.  
 XX  
 PS Disclosure; Page 126-131; 148pp; English.  
 XX  
 CC The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 CC human Nogo receptor (Ngr) NLRRT domain), or residues 27-309 of P1 with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of

CC axonal growth by a central nervous system (CNS) neuron. The Ngr  
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an Ngr protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention  
 XX  
 SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.56e-98 Length: 4053  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ACC81048 (1-4053)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 3144 TCAGTGTGTGACCTCTGCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCC 3203  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 3204 AGCCTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACAT 3263  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3264 GCCTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGTCAAGCT 3323  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3324 ATCCAGAAATCAGATGAAGCCACCCATTCAGGCATATCTGGAATCTGGAATGCTGATA 3383  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 3384 TCTGAGGAGTGTGTTTCTGAGAAGTACAGTAATCTCTGCTCTTGGTTCATGTGAACGCACATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3444 AAGGAAGTCTCAGCGCTCTCTTCTTAGTATGATTTAGTTGATTTCTCTGAAGTTTGAGTG 3503  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 3504 TTGATGTGGTATTTACCTATGTTGGTGGCTTTTAAAGTCTGACACTACTGATTTTG 3563  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 3564 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3623  
 QY 161 HisTyrLeuGlyLeuAlaLeuLeuSerValIleAspAlaMetAlaIleGlnAlaLys 180  
 Db 3624 CATTTATCTAGGACTTCCAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 3684 ATCCCTGGATTGAGCGCAAGCTGAA 3710  
 RESULT 17  
 ADP13574  
 ID ADP13574 standard; DNA; 4053 BP.  
 XX  
 AC ADP13574;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Renal cell carcinoma differentially expressed gene #310.  
 XX

KW ds; diagnosis; non-blood disease; solid tumor; gene expression;  
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
KW head/neck cancer; differential expression.

OS Homo sapiens.

XX WO2004048933-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037481.

XX 21-NOV-2002; 2002US-0427982P.

PR 03-APR-2003; 2003US-0459782P.

XX (AMHP ) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

XX WPI; 2004-460799/43.

PS Disclosure; SEQ ID NO 310; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a gene that  
CC is differentially expressed and detected by the method of the invention.  
CC (Note: this sequence is not given as part of the printed specification  
CC but was obtained from WIPO in electronic format at  
CC ftp.wipo/pub/published\_pct\_sequences).

XX SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,568-98 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADP13574 (1-4053)

Qy 1 SerValAlaLeuLeuSerValThrPheSerIleValSerValPheGlyAla 20  
Db 3144 TCAGTTTGTGACCTCCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCC 3203  
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3204 AGCCTATTCTGCTCTTTCATTGACGATTTACGATTTGAGCGTAACGACCTACATT 3263

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT 3323  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATA 3383  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3384 TCTGAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGGTCATGTGACACGATA 3443  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAACCTCAGCGCCTCTCTTAGTTGATGATTAGTTGATCTCTCAAGTTTCAGTGTG 3503  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu 140  
Db 3504 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTATTAATGGTCTGACACTACTGATTTTG 3563  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3564 GCTCTCATTTTCCCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3623  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3624 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCAACGAAAA 3683  
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710  
RESULT 18  
AAA23454  
ID AAA23454 standard; cDNA; 4093 BP.  
XX AC AAA23454;  
XX 19-JUN-2000 (first entry)  
XX cDNA encoding human secreted protein vb22\_1, SEQ ID NO:63.  
XX Human; secreted protein; cancer; tumour; cardiovascular disorder;  
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
KW neurodegenerative disease; asthma; contraceptive; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 152..1006  
XX /\*tag= b  
XX /product= "Clone vb22\_1 ORF2"  
XX CDS 1048..3729  
XX /\*tag= a  
XX /product= "Human secreted protein vb22\_1"  
XX WO200011015-A1.  
XX 02-MAR-2000.  
XX 24-AUG-1999; 99WO-US019351.  
XX 24-AUG-1998; 98US-0097638P.  
XX 24-AUG-1998; 98US-0097659P.  
XX 09-SEP-1998; 98US-0099618P.  
XX 28-SEP-1998; 98US-0102092P.  
XX 25-NOV-1998; 98US-0109978P.  
XX 23-DEC-1998; 98US-0113645P.  
XX 23-DEC-1998; 98US-0113646P.  
XX 23-AUG-1999; 99US-00379246.  
XX (ALPH-) ALPHAGENE INC.  
PA



XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
 XX WPI; 2000-224657/19.  
 XX P-PSDB; AAY95012, AAY95030.  
 XX New secreted or transmembrane proteins and polynucleotides encoding them,  
 XX useful for treating neurodegenerative disorders, autoimmune diseases and  
 XX cancer.  
 XX  
 XX Claim 72; Page 321-322; 357pp; English.  
 XX  
 XX The invention relates to 40 human secreted proteins (AAY94981-Y95020),  
 CC and cDNA sequences encoding them (AAA3423-A23462). The secreted proteins  
 CC of the invention include those that are thought to be only partially  
 CC secreted, i.e., transmembrane proteins. The proteins of the invention may  
 CC exhibit one or more activities selected from the following: cytokine  
 CC activity; cell proliferation; differentiation; immune modulation;  
 CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
 CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
 CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
 CC proteins may be administered to patients as vaccines, and the nucleotides  
 CC may be used as part of a gene therapy regime. Diseases or conditions that  
 CC may be treated using the proteins or nucleotides of the invention include  
 CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
 CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
 CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
 CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
 CC allergic reactions such as asthma and anaemia. They may also be used for  
 CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
 CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
 CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
 CC activity may additionally be useful as contraceptives. Nucleic acid  
 CC sequences of the invention may be used in chromosome mapping, and as a  
 CC source of diagnostic primers and probes. The present sequence represents  
 CC cDNA encoding one of the 40 proteins of the invention  
 XX  
 XX Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1-58e-98 Length: 4093  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAA23454 (1-4093)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrClyValValPheGlyAla 20  
 DB 3160 TCAGTTGTTGACCTCTCTGACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGC 3219  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3220 AGCCTATTCTGCTGCTTTCAITGACAGTATTGAGCATTTGAGCCGTAAACAGCCTACATT 3279  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3280 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3339  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleLeuGluSerGluValAlaIle 80  
 DB 3340 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCCATATCTGGAATCTGAGTTGCTATA 3399  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3400 TCTGAGAGTTGGTTTCAGAAAGTACAGTAATTCGCTCTGCTCATGTGAACTGCACGATA 3459  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3460 AAGGAACCTCAGGCGCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTTCAGTGTG 3519

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 3520 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGGTCTGACACTACTGATTTTG 3579  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3580 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTAAGCGGCATCAGGCACAGATAGAT 3639  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3640 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGCTAAATCAAGCAAAA 3699  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3700 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3726  
 RESULT 19  
 ABV94680  
 ID ABV94680 standard; cDNA; 4632 BP.  
 XX  
 AC ABV94680;  
 XX  
 DT 14-JAN-2003 (first entry)  
 XX  
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.  
 XX  
 KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
 KW cytostatic; tumour; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200260317-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 XX 30-JAN-2002; 2002WO-US002781.  
 XX  
 PR 30-JAN-2001; 2001US-0265305P.  
 PR 31-JAN-2001; 2001US-0265682P.  
 PR 09-FEB-2001; 2001US-0267568P.  
 PR 21-MAR-2001; 2001US-0278651P.  
 PR 28-APR-2001; 2001US-0287112P.  
 PR 16-MAY-2001; 2001US-0291631P.  
 PR 12-JUL-2001; 2001US-0305484P.  
 PR 20-AUG-2001; 2001US-0313999P.  
 PR 27-NOV-2001; 2001US-0333626P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
 XX  
 DR WPI; 2002-627435/67.  
 DR P-PSDB; ABP68600.  
 XX  
 XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
 PT cancer.  
 XX  
 PS Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.  
 CC  
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)  
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
 CC complements of (a); (c) sequences consisting of at least 20 contiguous  
 CC residues of (a); (d) sequences that hybridize to (a), under moderately  
 CC stringent conditions; (e) sequences having at least 75% or 90% identity  
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
 CC in a patient and compositions comprising polypeptides, polynucleotides,  
 CC antibodies, fusion proteins, T cell populations and antigen presenting  
 CC cells expressing the polypeptide are useful in treating pancreatic cancer  
 CC and stimulating an immune response. The polynucleotides can be used as  
 CC probes or primers for nucleic acid hybridisation, in the design and  
 CC preparation of ribozyme molecules for inhibiting expression of the tumour



CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.88e-98 Length: 4632  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABV94680 (1-4632)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 3151 TCAGTTGTTGACCTCCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC 3210  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCTGCTCTTTCATGTGACATTTACAGCATTTGAGCGTAACAGCCTACATT 3270  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3330  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAAGTTGCTATA 3390  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3391 TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACTGCACGATA 3450  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGNACTCAGCGCCCTCTTCTAGTGATGATTTAGTTGATTTCTGGAAGTTGTCAGTG 3510  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3511 TTGATGTGGTATTATACATGTTGGTGGCTTGTGTTTAATGCTGTGACACTACTGATTTG 3570  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3571 GCTCTCATTTTCACCTTTCAGTGTCTCTGTTTATGTAACGGCATCAGGCACAGATAGAT 3630  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3631 CATATCTAGACTTGCAAAATAGAAATGTTAAGATGCTATGGCTAAATATCAAGCAAAA 3690  
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3691 ATCCCTGGATTGAAGCGCAAGCTGAA 3717

RESULT 20

ADG32772

ID ADG32772 standard; DNA; 4632 BP.

XX AC ADG32772;

XX DT 26-FEB-2004 (first entry)

XX Human DNA differentially expressed in patients with SLE SeqID96.

XX human; ds; autoimmune; chronic inflammatory disease; SLE;

XX systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;

XX Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;

XX ulcerative colitis; primary sclerosing cholangitis; appendicitis;

XX diverticulitis; primary biliary sclerosis.

OS Homo sapiens.

PN WO2003090694-A2.

XX 06-NOV-2003.

PD 24-APR-2003; 2003WO-US013015.

XX 24-APR-2002; 2002US-00131827.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgenuth J, Fry K, Woodward R, Ly N;

XX WPI; 2003-877243/81.

XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases,

XX such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative

XX colitis, psoriasis and asthma by detecting the expression level of one or

XX more genes.

XX Claim 18; SEQ ID NO 96; 877pp; English.

XX This invention relates to novel methods for diagnosing and monitoring

XX autoimmune and chronic inflammatory diseases. Specifically, it refers to

XX the identification of genes that have a clinical utility as diagnostic

XX tools for the management of, in particular, patients with systemic lupus

XX erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the

XX present invention describes a method for determining the levels of

XX multiple differentially expressed genes of a patient, in a concerted

XX manner, in order to achieve an improved diagnostic assay with sensitivity

XX and specificity for the disease in question. As such, these genes are

XX useful for the diagnosis of various other inflammatory disorders

XX including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,

XX ankylosing spondylitis, ulcerative colitis, primary sclerosing

XX cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.

XX This polynucleotide is a DNA sequence representing human mRNA that is

XX differentially expressed in patients with SLE, used in an exemplification

XX of the invention.

XX SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.88e-98 Length: 4632

Score: 908.00 Matches: 184

Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.35% Mismatches: 2

Query Match: 98.16% Indels: 0

DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADG32772 (1-4632)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20

Db 3151 TCAGTTGTTGACCTCCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC 3210

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 3211 AGCCTATTCTCTGCTCTTTCATGTGACATTTACAGCATTTGAGCGTAACAGCCTACATT 3270

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3330

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 3331 ATCCAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAAGTTGCTATA 3390

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

Db 3391 TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACTGCACGATA 3450

Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120



ID ADR83534 standard; DNA; 4789 BP.  
XX AC ADR83534;  
XX DT 02-DEC-2004 (first entry)  
XX DE Human reticulon 4 DNA, target gene of miRNA.  
XX KW human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;  
KW immune disease; nerve disorder; amyotrophic lateral sclerosis;  
KW Parkinson's disease; Alzheimer's disease; inflammatory disease;  
KW siRNA silencing precursor; cytostatic; immunosuppressive; neurotropic;  
KW neuroprotective; antiinflammatory; immunotherapy; reticulon 4.  
XX OS Homo sapiens.  
XX PN WO2004076622-A2.  
XX PD 10-SEP-2004.  
XX PF 10-FEB-2004; 2004WO-JP001433.  
XX PR 10-FEB-2003; 2003US-0445829P.  
XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
XX PI Taira K, Kawasaki H;  
XX WPI; 2004-653393/63.  
XX PT Modulating expression of a target gene in a cell, for treating cancer, an  
PT immune disease, or a nerve disorder, comprises introducing into the cell  
PT a polynucleotide that forms a duplex region with an mRNA transcribed from  
PT the target gene.  
XX PS Claim 9; SEQ ID NO 436; 865pp; English.  
XX CC This invention relates to a novel method for modulating the expression of  
CC a target gene in a cell. Specifically, it refers to the introduction into  
CC a cell of a polynucleotide that forms a duplex region with an mRNA  
CC transcribed from the target gene, where the duplex region comprises a  
CC mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that  
CC regulates mRNA at a post-transcriptional level. The present invention  
CC describes a method for controlling ontogenesis of a mammal, function of a  
CC mammalian cell, differentiation of a mammalian cell or viability of a  
CC mammalian cell in the post-transcriptional phase, which comprises  
CC introducing a plasmid vector comprising a promoter and nucleic acid  
CC molecule expressing an miRNA or siRNA silencing precursor to the miRNA.  
CC Accordingly, it provides a cell therapy method for treating cancer,  
CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,  
CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease  
CC by introducing into the cell the miRNA, siRNA silencing precursor to the  
CC miRNA or the plasmid vector. As such, they can be developed into  
CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,  
CC neurotropic, neuroprotective and antiinflammatory activities and hence can  
CC be used for immunotherapy. This polynucleotide sequence is a human target  
CC gene whose expression is modulated by miRNAs of the invention.  
SQ Sequence 4789 BP; 1422 A; 1052 C; 1075 G; 1240 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1.97e-98 Length: 4789  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.38% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 13 Gaps: 0  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADR83534 (1-4789)  
  
QY 1 SerValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAla 20  
Db TCAGTTGTTGACCTCTGTTACTGAGAGACATTAAGAGACTGGAGTGGTGTGTTGGTCC 3313

QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db AGCCTATTCTGCTGCTTTTCATTGACAGTATTGACAGTATTGAGGGTACAGCCTACATT 3373  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCT 3433  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerClnuValAlaIle 80  
Db ATCCAGAAATCAGATGAAGGCCACCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3493  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db TCTGAGGAGTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTCATGTGACTGCAGATA 3553  
QY 101 LysGluLeuAArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db AAGGAACCTCAGGGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTG 3613  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140  
Db TTGATGTGGGTATTTACCTATATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTTG 3673  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db GCTCTCATTTTCATCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGAT 3733  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db CATTATCTAGGACTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAA 3793  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db ATCCCTGGATTGAAGCGCAAGCTGAA 3820  
  
RESULT 23  
ABS70449  
ID ABS70449 standard; cDNA; 4822 BP.  
XX AC ABS70449;  
XX DT 27-NOV-2002 (first entry)  
XX DE Human bone remodelling gene #106.  
XX KW Bone remodelling; osteoporosis; human; gene; ss.  
XX OS Homo sapiens.  
XX PN US6426186-B1.  
XX PD 30-JUL-2002.  
XX PF 18-JAN-2000; 2000US-00484970.  
XX PR 18-JAN-2000; 2000US-00484970.  
XX PA (INCY-) INCYTE GENOMICS INC.  
XX PI Jones KA, Volkmut W, Walker MG;  
XX WPI; 2002-673014/72.  
XX PT A combination of polynucleotides which are co-expressed with genes known  
PT to be involved in bone remodeling and osteoporosis are useful in an array  
PT for the diagnosis of bone remodeling and osteoporosis associated  
PT disorders.  
XX PS Claim 1; Col 283-288; 206pp; English.  
XX CC The invention relates to a combination comprising a number of

CC substantially purified and isolated polynucleotides which are co-  
 CC expressed with genes known to be involved in bone remodelling and  
 CC osteoporosis. The invention is used to diagnose disorders associated with  
 CC bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone  
 CC remodelling genes of the invention  
 XX  
 SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;

Alignment Scores:  
 Pred. No.: 1.98e-98 Length: 4822  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABS70449 (1-4822)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3265 TCAGTTGTTGACCTCTCTGCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGGTGGC 3324  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3325 AGCTATTTCTGCTGCTTTTCATTCAGATTCAGCATTTGTGAGCGTAACAGCTACATT 3384  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGlnAla 60  
 DB 3385 GCCTTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCT 3444  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluAlaIle 80  
 DB 3445 ATCCAGAAATCAGATCAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3504  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3505 TCTGAGGAGTTGGTTCAGAGTACAGTAACTCTGCTCTTGGTCATGTGACTGCAGATA 3564  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3565 AAGGAACCTCAGGCGCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTGCAAGTG 3624  
 QY 121 LeuMetTyrValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleu 140  
 DB 3625 TTGATGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTG 3684  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3685 GCTCTCATTTCACTCTTCAGTGTCTCTGTTTATTTATGACGGCATCAGGCACAGATAGAT 3744  
 QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3745 CATTATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGCTGCTAAAGTAAATCCAAAGCAAAA 3804  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3805 ATCCCTGGATTGAAGCGCAAGCTGAA 3831

RESULT 24

AD007888

ID AD007888 standard; cDNA; 3492 BP.

XX

AC

XX

XX

01-JUL-2004 (first entry)

XX

DE

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XX

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XX

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XX

XX

PN

US2004071700-Al.

XX

15-APR-2004.

XX

09-OCT-2002; 2002US-00267502.

XX

09-OCT-2002; 2002US-00267502.

XX

(LIFE-) LIFE SCI DEV CORP.

XX

Kim J, Galant R;

XX

WPI; 2004-328526/30.

DR

P-PSDB; ADO08105.

XX

Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.

PS Claim 1; SEQ ID NO 214; 275pp; English.

XX

The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC polypeptide or a change in an activity of the polypeptide, treating a  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC mouse cDNA used in the scope of the invention.

XX Sequence 3492 BP; 1035 A; 800 C; 817 G; 840 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.91e-98 Length: 3492  
 Score: 906.50 Matches: 187  
 Percent Similarity: 98.95% Conservative: 1  
 Best Local Similarity: 98.42% Mismatches: 1  
 Query Match: 98.00% Indels: 1  
 DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADO07888 (1-3492)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal---PheGly 19

DB 2920 TCAGTTGTTGACCTCTCTGCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTATTGGT 2979

QY 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39

DB 2980 GCCAGCTTATCTCTGCTGCTCTGACAGTGTTCAGCATTTGTCAAGTGAAGCGCTAC 3039

QY 40 IleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGln 59

DB 3040 ATTGCTTGGCCCTGCTCTCTGCTACTATCAGCTTTAGGATATATAAGGGTGTGATCCAA 3099

QY 60 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAla 79

DB 3100 GCTATCCAGAAATCAGATGAGAGGCCACCCATTCAGGGCATATTTTGGAAATCTGAAGTTGCC 3159



RESULT 26  
AAF90323  
ID AAF90323 standard; cDNA; 600 BP.  
XX  
AC AAF90323;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Human NOGO-C cDNA.  
XX  
KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200136531-A1.  
XX  
PD 25-MAY-2001.  
XX  
PF 14-NOV-2000; 2000WO-GB004345.  
XX  
PR 15-NOV-1999; 99GB-00026995.  
XX  
PR 24-JAN-2000; 2000GB-00001550.  
XX  
PA (SMIK ) SMITHLINE BECHAM PLC.  
XX  
PI Michalovich D, Prinjha R;  
XX  
XX WPI; 2001-343822/36.  
DR P-PSDB; AAB82348.  
XX  
XX  
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO  
PT gene and may be useful in the treatment of neural disorders including  
PT Alzheimer's and Parkinson's diseases.  
XX  
PS Claim 1; Page 25; 25pp; English.  
XX  
CC The present sequence is that of cDNA encoding human NOGO-C (see  
CC AAB82348). NOGO-C is a novel splice variant of the human NOGO gene on  
CC chromosome 2p21. 2 Other splice variants, NOGO-A and NOGO-B, have  
CC previously been identified. The invention provides NOGO-C polypeptides  
CC and polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilizing NOGO-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric disorders and developmental disorders. Also  
CC provided are methods for identifying agonists and agonists for use in  
CC treating conditions associated with NOGO-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate NOGO-C  
CC activity or levels  
XX  
SQ Sequence 600 BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3,24e-99 Length: 600  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF90323 (1-600)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 34 GTTGTGACCTCTGCTAGTGGAGAGACATTAAAGACACTGGAGTGGTGTGGTGCAGC 93  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 94 CTATTCCTGCTGCTTTCATTGACAGTATTTCAGCATTTGTCAGCGTAACACCTACATTGCC 153  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATC 213  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerClnuValAlaIleSer 81  
Db 214 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATGCTATATCT 273  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 274 GAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTTGGTCACTGTGAACGACGATAAG 333  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 334 GAACTCAGGCGCTCTCTCTAGTGTATGATGATTTAGTATTCTCTGAAGTTGCAAGTGTG 393  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
Db 394 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATTATGATGGTCTGACACTACTGATTTGGCT 453  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 454 CTCATTTCACTCTTTCAGTGTCTCTGTTATTATGAACGCGATCAGGCACAGATAGCAT 513  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 514 TATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 573  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 574 CCTGGATTGAAGCGCAAAAGCTGAA 597

RESULT 27  
AAF72983  
ID AAF72983 standard; cDNA; 770 BP.  
XX  
AC AAF72983;  
XX  
DT 24-NOV-2000 (first entry)  
XX  
DE Human NSPH encoding cDNA sequence SEQ ID NO:3.  
XX  
KW Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1253180-A.  
XX  
PD 17-MAY-2000.  
XX  
PF 30-OCT-1998; 98CN-00121473.  
XX  
PR 30-OCT-1998; 98CN-00121473.  
XX  
PA (UYFU-) UNIV FUDAN.  
XX  
PI Yu L, Zhao Y, Zhang H;  
XX  
DR WPI: 2000-466537/41.  
DR P-PSDB; AAB12805.  
XX  
PT Specific protein of human neuroendocrine, coding sequence and its  
PT preparing process and application.  
XX  
PS Claim 1; Page 14; 21pp; Chinese.  
XX  
CC The present invention relates to a new member of the human neuroendocrine  
CC specific protein family, designated NSPH. The present sequence encodes  
CC the human NSPH protein  
XX  
SQ Sequence 770 BP; 215 A; 136 C; 190 G; 229 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4,6e-99 Length: 770  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservatives: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAA72983 (1-770)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysLysThrGlyValValPheGlyAlaSer 21  
 Db 114 GTTGTGACCTCTCTGACGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 173

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 174 CTATTCTGCTGCTCTTCATTGACGATTAATCAGCATTTGAGCGTAACAGCCCTACATTGCC 233

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 234 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 293

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 294 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 353

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 354 GAGGAGTTGGTTTCAAGATACAGTAATCTCTCTGTCATGTGAACCTGACGATNAAG 413

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 414 GAATCAGCGCGCTCTCTTAGTGATGATTTAGTTGATCTCTGAGTTTGCAGTGTG 473

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 474 ATGTGGGTATTACCTATGTTGGTGCCTGTTTAATGGTCTGACACTACTGATTTGGCT 533

QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 534 CTCAATTCACCTCTCAGTGTCTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 593

QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 594 TATCTAGGACTTGCAATTAAGATGTTAAAGTGTGCTATGGCTTAATTCAGCAAAATC 653

QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 654 CTGGATTGAAGCGCAAGCTGAA 677

RESULT 28  
 AAV23695  
 ID AAV23695 standard; cDNA; 799 BP.  
 AC  
 AC AAV23695;  
 XX  
 DT 24-JUL-1998 (first entry)  
 XX  
 DE Human NSPLP protein A coding sequence.  
 DE  
 KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;  
 KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT 75..674  
 FT CDS /tag= a  
 FT /product= "NSPLPA"  
 FT  
 XX  
 PN W09806841-A2.  
 XX

PD 19-FEB-1998.  
 XX  
 PF 24-JUL-1997; 97WO-US013469.  
 XX  
 PR 12-AUG-1996; 96US-00700607.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Bandman O, Au-Young J, Goli SK, Hillman J;  
 XX  
 DR WPI; 1998-159533/14.  
 DR P-PSDB; AAW53947.  
 XX  
 PT Human neuro-endocrine-specific protein-like proteins - useful for  
 PT diagnosis, monitoring and treatment of cancer and neuro-degenerative  
 PT disease.  
 XX  
 PS Claim 3; Page 38-39; 73pp; English.  
 XX  
 CC This sequence encodes a human neuroendocrine-specific protein-like  
 CC protein (NSPLP) of the invention. Recombinant cells transformed with the  
 CC DNA are used to express the NSPLP proteins, which are used to treat  
 CC cancer and neurodegenerative diseases such as amyotrophic lateral  
 CC sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be  
 CC used to inhibit activity of the NSPLP proteins. Antibodies specific for  
 CC NSPLP are used for diagnosis and monitoring treatment of diseases  
 CC associated with NSPLP expression, in usual immunoassays, and to isolate  
 CC NSPLP from natural sources. The NSPLP proteins, or their fragments can  
 CC also be used in drug screening to identify NSPLP antagonists. The nucleic  
 CC acid can be used diagnostically and for monitoring treatment (in  
 CC hybridisation or amplification assays); to isolate closely related  
 CC sequences; in gene therapy for both sense and antisense applications  
 CC (including use of ribozymes) and for mapping the natural genomic sequence  
 XX  
 SQ Sequence 799 BP; 218 A; 141 C; 196 G; 242 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 4,85e-99 Length: 799  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservatives: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 2 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAV23695 (1-799)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysLysThrGlyValValPheGlyAlaSer 21  
 Db 108 GTTGTGACCTCTCTGACGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 167

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 168 CTATTCTGCTGCTCTTCATTGACGATTAATCAGCATTTGAGCGTAACAGCCCTACATTGCC 227

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 228 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 287

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 288 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 347

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 348 GAGGAGTTGGTTTCAAGATGACAGTAATCTCTCTTGGTCTATGTGAACCTGACCGATAAG 407

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 408 GAATCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAGTTTGCAGTGTG 467

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 468 ATGTGGGTATTACCTATGTTGGTGCCTGTTTAATGGTCTGACACTACTGATTTGGCT 527







(SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha R;

XX WPI: 2001-343822/36.

XX P-PSDB; AAB82350.

XX New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.

XX Disclosure; Page 27; 25pp; English.

XX The present sequence is that of cDNA encoding human NOGO-B (see AAB82350). NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel NOGO gene splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels

XX Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 7.8e-99 Length: 1122  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF90325 (1-1122)

QY 2 ValValAspLeuLeuTyrTrpArgaspIleLysThrGlyValValPheGlyAlaSer 21  
DB 556 GTTGTGTACCTCTCTACTGAGACACATTAAAGACTGGAGTGTCTTTGGTGCCAGC 615  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 616 CTATTCTGCTGCTTTCATTGACAGTATTACAGATTGTGAGCTTACAGCTTACATTGCC 675  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAAAGGTGTGATCCAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 736 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 795  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 796 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTGTGTTCATGTGAATCTGACACGATTAAG 855  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 856 GAACCTCAGCGCCTCTCTAGTTCATGATTAGTTAGTTCTCTGAAGTTTGCAGTGTG 915  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 916 ATGTGGGTATTACCTATGTTGGTCCCTTGTATTATGCTGTGACACTACTGATTGGCT 975  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 976 CTCATTTCACCTCTTCAGTGTCTCTCTTATTATGACGGCATCAGGCACATGATCAT 1035  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 1036 TATCTAGGACTTGCAATAGAAATGTTAAAGATGCTATGCTATAAATCCAGCAAAATC 1095  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 1096 CCTGATTGAAGCCAAAGCTGAA 1119  
RESULT 31  
AA04379  
ID AAX04379 standard; DNA; 1213 BP.  
XX AC AAX04379;  
XX DT 13-APR-1999 (first entry)  
XX DE Human secreted protein gene 69 clone HAGFT48.  
XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX OS Homo sapiens.  
XX PN WO9856904-A1.  
XX PD 17-DEC-1998.  
XX PF 11-JUN-1998; 98WO-US012125.  
XX PR 13-JUN-1997; 97US-0049547P.  
PR 13-JUN-1997; 97US-0049548P.  
PR 13-JUN-1997; 97US-0049549P.  
PR 13-JUN-1997; 97US-0049550P.  
PR 13-JUN-1997; 97US-0049566P.  
PR 13-JUN-1997; 97US-0049606P.  
PR 13-JUN-1997; 97US-0049607P.  
PR 13-JUN-1997; 97US-0049608P.  
PR 13-JUN-1997; 97US-0049609P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 13-JUN-1997; 97US-0049611P.  
PR 13-JUN-1997; 97US-0050901P.  
PR 13-JUN-1997; 97US-0052989P.  
PR 08-JUL-1997; 97US-0051919P.  
PR 18-AUG-1997; 97US-0055984P.  
PR 12-SEP-1997; 97US-0058665P.  
PR 12-SEP-1997; 97US-0058666P.  
PR 12-SEP-1997; 97US-0058669P.  
PR 12-SEP-1997; 97US-0058750P.  
PR 12-SEP-1997; 97US-0058971P.  
PR 12-SEP-1997; 97US-0058972P.  
PR 12-SEP-1997; 97US-0058975P.  
PR 02-OCT-1997; 97US-0060834P.  
PR 02-OCT-1997; 97US-0060844P.  
PR 02-OCT-1997; 97US-0060865P.  
PR 02-OCT-1997; 97US-0061059P.  
PR 02-OCT-1997; 97US-0061060P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;  
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;  
PI Feng P;  
XX WPI: 1999-080881/07.  
DR P-PSDB; AAW78194.  
XX New isolated human genes and the secreted polypeptides they encode -





DE	CDNA encoding a bone marrow secreted protein designated BMS112.
XX	
XX	Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW	cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW	myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW	erythroid progenitor cell; colony stimulating factor; granulocyte;
KW	monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW	platelet disorder; thrombocytopenia; hematopoietic stem cell;
KW	stem cell disorder; aplastic anaemia; bone differentiation;
KW	paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW	ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW	bone fracture; cartilage damage; artificial joint; ss.
XX	
XX	Homo sapiens.
OS	
XX	
XX	Key Location/Qualifiers
FH	132. .1253
FT	/*tag= a
FT	/product= "bone marrow secreted protein"
FT	polyA_signal 1516. .1521
FT	/tag= b
XX	
XX	WO9933979-A2.
PN	
XX	
PD	08-JUL-1999.
XX	
XX	18-DEC-1998; 98WO-US027008.
PF	
XX	
PR	30-DEC-1997; 97US-0068958P.
PR	24-SEP-1998; 98US-0101603P.
PR	30-SEP-1998; 98US-0102540P.
XX	
XX	(CHIR ) CHIRON CORP.
PA	
XX	
XX	Lin H, Cao L;
FI	
XX	WPI; 2000-038344/03.
DR	P-PSDB; AAV53624.
DR	
PT	New isolated human polynucleotide and secreted proteins can induce
PT	production of other cytokines in certain cell populations.
XX	
PS	Claim 11; Page 72-74; 120pp; English.
XX	
XX	AAZ36228-49 encode bone marrow secreted proteins of human bone marrow
CC	stromal cells. The proteins can exhibit cytokine, cell proliferation, or
CC	cell differentiation activity (either inducing or inhibiting). They can
CC	be used to support colony forming cells or factor-dependent cell lines,
CC	to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC	deficiencies. In addition, they may be used to support the growth and
CC	proliferation of erythroid progenitor cells, and to treat various
CC	anaemias. They can have colony stimulating factor (CSF) activity and can
CC	be used to support the growth and proliferation of myeloid cells such as
CC	granulocytes, monocytes or macrophages, to prevent or treat myelo-
CC	suppression, to support the growth and proliferation of megakaryocytes
CC	and platelets, thereby allowing prevention or treatment of platelet
CC	disorders such as thrombocytopenia, to support the growth and
CC	proliferation of hematopoietic stem cells, either in place of or in
CC	conjunction with platelet transfusions, to treat stem cell disorders,
CC	such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC	repopulate the stem cell compartment after irradiation or chemotherapy.
CC	They can be used for growth or differentiation of bone, cartilage,
CC	tendon, ligament, or nerve tissue, as well as for wound healing and
CC	tissue repair and replacement, and in the treatment of burns, incisions
CC	and ulcers, to induce cartilage and/or bone growth in circumstances where
CC	bone is not normally formed and thus have an application in healing bone
CC	fractures and cartilage damage or defects, prophylactic use in fracture
CC	reduction and also in the improved fixation of artificial joints
XX	
SQ	Sequence 1610 BP; 354 A; 458 C; 426 G; 372 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	1,29e-98 Length: 1610

XX Anne TW, Olsen NJ;  
PI WPI; 2004-061002/06.  
XX  
XX Detecting an autoimmune disorder in a subject comprising comparing the  
PT expression level of each gene determined with a standard, where the  
PT comparing detects the presence of an autoimmune disorder in the subject.  
XX  
XX Claim 10; SEQ ID NO 62; 86pp; English.  
XX  
XX The invention relates to a method of detecting an autoimmune disorder in  
CC a subject comprising obtaining a biological sample, preferably a  
CC peripheral blood mononuclear cell, from a subject, determining expression  
CC levels of at least two genes in the biological sample, and comparing the  
CC expression level of each gene determined with a standard, where the  
CC comparison detects the presence of an autoimmune disorder in the subject.  
CC The method is useful for detecting or diagnosing an autoimmune disorder,  
CC e.g. rheumatoid arthritis, systemic lupus erythematosus, multiple  
CC sclerosis, or type 1 (insulin-dependent) diabetes. The present sequence  
CC represents one of seventy genes used to detect autoimmune disorders with  
CC the described method.  
XX  
SQ Sequence 1785 BP; 520 A; 316 C; 402 G; 547 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1.5e-98 Length: 1785  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 12 Gaps: 0  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADK14166 (1-1785)  
  
QY 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 247 GTTGTGACCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 306  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 307 CTATTCCTGCTGCTTTCATTCAGCAGTATTCAGCATTTGAGCGTAACAGCTTACATGCC 366  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 367 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 426  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 427 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGAAAGTTGCTATATCT 486  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 487 GAGGAGTTGGTTTCAGAACTACAGTAATCTCTCTTGTGTCATGTGAACCTGCACATAAG 546  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 547 GAATCAGGCCCTCTCTTGTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTGTG 606  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleAla 141  
DB 607 ATGTGGGTATTTACCTATGTTGGTCTCTTGTATGATGCTCTGACACTACTGATTTGGCT 666  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 667 CTCAATTCACCTCTCAGTGTCTCTGTTTATGTAACGGCATCAGGCACATAGATCAT 726  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 727 TATCTAGGACTTGCAGTAATGATTTAAGATGCTATGGCTTAATCAAGCAAAATC 786  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
|||||

Db 787 CTGTGATTGAAGCGCAAAAGCTGAA 810  
RESULT 36  
ABK90133  
ID ABK90133 standard; DNA; 2052 BP.  
XX  
AC ABK90133;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE DNA encoding human NogoB protein.  
XX  
KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hypertrophy; central nervous system; axon regeneration; NogoB;  
KW Nogo-associated disease; metastasis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1188  
FT /\*tag= a  
FT /product= "Human NogoB protein"  
XX  
PN WO200257483-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 18-JAN-2002; 2002WO-GB000228.  
XX  
PR 18-JAN-2001; 2001GB-00001312.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
XX  
DR WPI; 2002-599722/64.  
XX P-PSDB; ABG30937.  
XX  
PT Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
PT providing and monitoring interaction between Nogo and BACE polypeptides.  
XX  
PS Disclosure; Page 50-52; 68pp; English.  
XX  
CC The present invention relates to a new method of identifying modulators  
CC of Nogo function or BACE activity. The method involves providing Nogo and  
CC BACE polypeptides capable of binding with each other, monitoring the  
CC interaction between these polypeptides, and determining if the test agent  
CC is a modulator of Nogo or BACE activity. The method is useful in treating  
CC acute neuronal injuries, such as spinal or head injury, stroke,  
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
CC hypertrophy) of the central nervous system. The BACE polypeptide is  
CC useful in screening methods to identify agents that may act as modulators  
CC of BACE activity and in particular agents that may be useful in treating  
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
CC and the polynucleotide encoding the BACE polypeptide are useful in  
CC manufacturing a medicament for the treatment or prevention of disorders  
CC responsive to the modulation of Nogo activity, in alleviating the  
CC symptoms or improving the condition of a patient suffering from this  
CC disorder, in axon regeneration, or in preventing metastasis or spreading  
CC of a cancer. The polynucleotide may also be an essential component in  
CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
CC techniques. The present nucleic acid sequence encodes the human NogoB  
CC protein of the invention  
XX  
SQ Sequence 2052 BP; 511 A; 512 C; 506 G; 523 T; 0 U; 0 Other;

```
Alignment Scores: 1.82e-98 Length: 2052
Pred. No.: 904.00 Matches: 183
Score: 98.94% Conservative: 3
Percent Similarity: 97.34% Mismatches: 2
Best Local Similarity: 97.73% Indels: 0
Query Match: 97.73% Gaps: 0
DB: 6

US-09-830-972-2_COPY_975_1163 (1-189) x ABK90133 (1-2052)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleValLysThrGlyValValPheGlyAlaSer 21
DB 622 GTTGTGACCTCTCTGACGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 681
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 682 CTATTCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTAAACAGCTACATTGCC 741
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
DB 742 TTGGCCCTGCTCTCTGTGACCATCTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 801
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 802 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAAATCTGAAATGCTATATCT 861
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 862 GAGGAGTTGGTTCAGAAATACAGTAATTTCTGCTCTTTGGTTCATGTGAATGCACGATAAAG 921
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 922 GAATCAGGCGCTCTCTTAGTGTGATGATTTAGTTGATTTCTGAAATTTGCAAGTTGCGTGTG 981
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaIle 141
DB 982 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1041
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 1042 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1101
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 1102 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGCTAAATCCAAAGCAAAATC 1161
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 1162 CCTGGATTGAGCGCAAGCTGAA 1185

RESULT 37
ABV94681
ID ABV94681 standard; cDNA; 2235 BP.
AC ABV94681;
XX
XX
XX 14-JAN-2003 (first entry)
XX
XX Human pancreatic cancer expressed cDNA SEQ ID NO 54.
DE
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytosolic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX W0200260317-A2.
XX
XX 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US0002781.
XX
XX 30-JAN-2001; 2001US-0265305P.
PR
XX 31-JAN-2001; 2001US-0265682P.
PR
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PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI: 2002-627435/67.
XX P-PSDB; ABP68601.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
XX cancer.
XX
XX Claim 1; SEQ ID NO 54; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a); under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridisation, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;
SQ

Alignment Scores: 2.05e-98 Length: 2235
Pred. No.: 904.00 Matches: 183
Score: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 6

US-09-830-972-2_COPY_975_1163 (1-189) x ABV94681 (1-2235)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 697 GTTGTGACCTCTCTGACGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 756
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 757 CTATTCTGCTCTTTCATTGACAGTATTGAGCATTTGAGCGTAAACAGCTACATTGCC 816
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAAGTATC 876
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 877 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGCAAGTTGCTATATCT 936
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 937 GAGGAGTTGGTTCAGAAATGACAGTAAATCTGCTCTTTGGTCAATGTAACGTCAGATAAAG 996
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
```

Db 997 GAACCTCAGCGGCTCTCTTAGTGTGATGATTTAGTGTGATTTCTCTGAAGTTTCAGCTGTTG 1056  
QY 122 MetTTPValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1057 ATGTGGTATTACCTATGTTGGTCTGTTTAAAGTGTGACACTACTGATTTGGCT 1116  
QY 142 LeuileSerLeuPheSerileProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 1117 CTCAITTCACCTCTCAGTGTCTCTGTATTATTAAGCGCATCAGGCACAGATGATCAT 1176  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysile 181  
Db 1177 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAAATC 1236  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 1237 CCTGATTGAAGCGCAAGCTGAA 1260  
RESULT 38  
AAC64406  
ID AAC64406 standard; cDNA; 2240 BP.  
XX  
AC AAC64406;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human Nogo B nucleotide sequence SEQ ID NO:1.  
XX  
KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;  
KW stress-phosphorylated endoplasmic reticulum protein; cytosolic;  
KW gene therapy; cell growth; cellular stress response; neuron growth;  
KW regulator of oxidative stress; inhibitor of neurite outgrowth;  
KW axon regeneration; diagnosis; cancer; identification; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200060083-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 07-APR-2000; 2000WO-US009393.  
XX  
PR 08-APR-1999; 99US-0128372P.  
PR 21-JUN-1999; 99US-0140331P.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Wei D, Halenbeck R, Williams LT;  
XX  
DR WPI; 2000-665007/64.  
DR P-PSDB; AAB24242.  
XX  
XX Novel protein associated with cell stress response useful for modulating  
PT stress levels, cell growth, diagnosis and treatment of cancer and  
PT malignant growth and for identifying agonists and antagonists.  
XX  
PS Claim 2; Page 63-64; 68pp; English.  
XX  
CC The present sequence encodes a human stress-phosphorylated endoplasmic  
CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and  
CC is a modulator of the storage and exchange of calcium, cell growth and  
CC cellular stress response. It can: regulate oxidative stress; inhibit  
CC neurite outgrowth, neuron growth and axon regeneration. Nogo B  
CC polypeptides and polynucleotides are useful for modulating stress levels  
CC and cellular stress-response, cell growth and viability, diagnosis and  
CC treatment of cancer, malignant growth and other Nogo B related diseases.  
CC Nogo B polypeptides are also useful to screen combinatorial libraries to  
CC identify agonist or antagonist. Antibodies against Nogo B polypeptides  
CC are useful for affinity chromatography and distinguishing Nogo B  
CC polypeptides  
XX  
SQ Sequence 2240 BP; 570 A; 558 C; 536 G; 576 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,06e-98 Length: 2240  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAC64406 (1-2240)  
QY 2 ValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 693 GTTGTGTACCTCTCTGCTACTGGAGACACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 752  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerileValSerValThrAlaTyrIleAla 41  
Db 753 CTATTCTCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTAACAGCCTACATTGCC 812  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 813 TTGGCCCTGCTCTCTGTCAGCCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 872  
QY 62 GlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 873 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATCT 932  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 933 GAGGAGTTGGTTCAGAAAGTACAGTAATTTCTCTCTTGGTCATGTGAACCTGCACGATAAG 992  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 993 GAACTCAGGCGCTCTCTTAGTTAGTATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTG 1052  
QY 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1053 ATGTGGGTATTACCTATGTTGGTGGCTTGTATTAATGGTCTGCACACTACTGATTTGGCT 1112  
QY 142 LeuileSerLeuPheSerileProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 1113 CTCAITTCACCTCTCAGTGTCTCTGTATTATTAAGCGCATCAGGCACAGATGATCAT 1172  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysile 181  
Db 1173 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAAATC 1232  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 1233 CCTGATTGAAGCGCAAGCTGAA 1256  
RESULT 39  
AAK94408  
ID AAK94408 standard; cDNA; 1694 BP.  
XX  
AC AAK94408;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human full-length cDNA, SEQ ID NO: 3170.  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX  
OS Homo sapiens.  
XX  
FN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.



XX (HELI-) HELIX RES INST.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI: 2001-524255/58.  
DR P-PSDB; AAW93484.  
XX 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.  
XX The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly  
CC from EPO  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 4,22e-98 Length: 1694  
Score: 900.00 Matches: 182  
Percent Similarity: 98.40% Conservative: 3  
Best Local Similarity: 96.81% Mismatches: 0  
Query Match: 97.30% Indels: 0  
DB: Gaps: 0  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAK94408 (1-1694)  
  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGACCTCTCTGTGACCATTCAGCATTTGAGGAGATTAAGAGACTGGAGTGTGTTGGTGCAGC 847  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 848 CTATTCCTGCTGCTTTCATGACAGTATTGAGCATTTGAGCGTAAACGCCCTACATGTC 907  
  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 908 TTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGATATACAGGCTGTGATCCAGCTATC 967  
  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 968 CAGAAATCAGATGAGAGCCACCCCATTCAGGCGATATCTGGAATCTGAGTTGCTATCT 1027  
  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1028 GAGGAGTTGCTTTCAGAGTACAGTAAATCTGCTCTTGGTCATGTGAACGATTAAG 1087  
  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1088 GAACCTCAGCGGCTCTCTTGTAGTATGATTTAGTATCTCTGAGTTGCGAGTTG 1147  
  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 1148 ATGTGGGTATTTACCTATGTTGGTCTGCTTTTAATGGTCTGACACTACTGATTTGGCT 1207  
  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 1208 CTCAITTCATCTCTCAGTGTCTCTGTTATTATTAAGACGGCATCAGGCAGATGATCAT 1267  
  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 1268 TATCTAGGACTTGCAATAAGAAATCTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1327  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 1328 CCTGGATTGAGCGCAAAAGCTGAA 1351  
  
RESULT 40  
ADL31137  
ID ADL31137 standard; cDNA; 1694 BP.  
XX AC ADL31137;  
XX DT 20-MAY-2004 (first entry)  
XX DE Full length human cDNA clone SeqID 3170.  
XX KW human; medicine; signal transduction; glycoprotein; transcription;  
XX oligo-capping method; ss; gene.  
XX OS Homo sapiens.  
XX PN EP1396543-A2.  
XX PD 10-MAR-2004.  
XX PF 07-JUL-2000; 2003EP-00025638.  
XX PR 08-JUL-1999; 95JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
PI WPI: 2004-204755/20.  
DR P-PSDB; ADL31138.  
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
PT length human cDNAs.  
XX Example 1; SEQ ID NO 3170; 1340pp; English.  
XX This invention relates to a novel primers useful for synthesising full  
CC length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction,  
CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
CC ends using the oligo-capping method. This polynucleotide sequence is a  
CC full length human cDNA clone of the invention.  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 4,22e-98 Length: 1694  
Score: 900.00 Matches: 182  
Percent Similarity: 98.40% Conservative: 3  
Best Local Similarity: 96.81% Mismatches: 3  
Query Match: 97.30% Indels: 0  
DB: Gaps: 12  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADL31137 (1-1694)  
  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGACCTCTCTGTGACCATTCAGCATTTGAGGAGATTAAGAGACTGGAGTGTGTTGGTGCAGC 847  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41



Db 848 CTATTCTGCTGCTTTTCATTGACAGTATTCAGCAATGTGAGCGTAACAGCCTACATTTGCC 907  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 967  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 968 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAATTTGCTATATCT 1027  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 1028 GAGGAGTTGGTTTCAGAACTACAGTAAATCTGCTCTTGGTCTATGTGAAGTGCACGATAAAG 1087  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 1088 GAACTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAATTTGCAAGTTTG 1147  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 1148 ATGTGGGTATTACCTATGTTGGTGCCTTGTATATGCTCTGACACTACTGATTTGGCT 1207  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 1208 CTCATTTTCACCTCTTCAGTGTTCCTGTTATTTATGAAACGCGCATCAGGCGCAGATAGATCAT 1267  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIleIle 181  
 Db 1268 TATCTAGACCTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1327  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351

## RESULT 41

AAI98079  
 ID AAI98079 standard; cDNA; 1980 BP.

AC AAI98079;  
 XX AAI98079;

DT 04-DEC-2001 (first entry)  
 XX Human neuroblastoma expressed polynucleotide SEQ ID NO 22.

DE Human; neuroblastoma; ss.  
 KW Homo sapiens.  
 OS WO200166733-Al.

PN 13-SEP-2001.  
 XX 02-MAR-2001; 2001WO-JP001631.

XX 07-MAR-2000; 2000JP-00159195.  
 PR 12-MAY-2000; 2000JP-00140387.

XX (CHIB-) CHIBA PREFECTURE.  
 PA (HISM) HISAMITSU PHARM CO LTD.

XX Nakagawara A;  
 XX WPI; 2001-602630/68.

XX Nucleic acids for prognosis of human neuroblastoma comprise nucleic acids  
 PT expressed by human neuroblastomas.

XX Claim 1; Page 69-70; 159pp; Japanese.  
 PS The invention relates to nucleic acids (AAI98058-AAI98161) or their

CC homologues expressed by human neuroblastomas useful for detecting genes  
 CC expressed by neuroblastoma and for analysing their structure and  
 CC function. The nucleic acids are useful for the diagnosis and prognosis of

CC neuroblastoma  
 XX Sequence 1980 BP; 601 A; 373 C; 423 G; 583 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.15e-98 Length: 1980  
 Score: 898.00 Matches: 182  
 Percent Similarity: 98.41% Conservative: 4  
 Best Local Similarity: 96.30% Mismatches: 3  
 Query Match: 97.08% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAI98079 (1-1980)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 1006 TCAGTTGTGGACCTCCCTGCTGACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCC 1065  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1066 AGCCTATTCCAGCTGCTTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATT 1125  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 1185  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 1186 ATCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATA 1245  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 1246 TCTGAGGAGTTGGTTTCAGAGTACAGTAAATCTCTCTCTGTCATGTGAACCTGCACGATA 1305  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1306 AAGGAACCTCAGCGCGCTCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGGAGTTTCAGTG 1365  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 1366 TTGATGGGTATTACCTATGTTGGTGCCTTGTATAGTCTGACACTACTGATTTTG 1425  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 1426 GCTCTCATTTTCACCTCTTCAGTGTTCCTGTTATTATGAACGCGCATCAGGCGCAGATAGAT 1485  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1486 CATTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 1545  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572

## RESULT 42

AAI97587  
 ID AAI97587 standard; DNA; 991 BP.

AC AAI97587;  
 XX 13-SEP-1999 (first entry)

DT Extended human secreted protein coding sequence, SEQ ID NO. 51.  
 DE Secreted protein; human; cytokine; cellular proliferation; cell movement;  
 KW cellular differentiation; immune system regulator; anti-inflammatory;  
 KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
 KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
 KW genetic disease; ss.

OS Homo sapiens.  
 XX WO9931236-A2.

XX PD 24-JUN-1999.  
XX PF 17-DEC-1998; 98WO-IB0002122.  
XX PR 17-DEC-1997; 97US-0069957P.  
XX PR 09-FEB-1998; 98US-0074121P.  
XX PR 13-APR-1998; 98US-0081563P.  
XX PR 10-AUG-1998; 98US-0096116P.  
XX (GEST ) GENSET.  
XX PA Bougueleret L, Duclert A, Dumas Milne Edwards J;  
XX PI WPI; 1999-385906/32.  
XX DR P-PSDB; AAY35903.  
XX New isolated human secreted proteins.  
XX PT Claim 1; Page 185-186; 516pp; English.  
XX PS This sequence represents an extended human secreted protein coding  
CC sequence of the invention. The secreted proteins can be used in treating  
CC or controlling a variety of human conditions. The secreted proteins may  
CC act as cytokines or may affect cellular proliferation or differentiation  
CC or may act as immune system regulators, haematopoiesis regulators, tissue  
CC growth regulators, regulators of reproductive hormones or cell movement  
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or  
CC tumour inhibition activity. The DNAs can be used in forensic procedures  
CC to identify individuals or in diagnostic procedures to identify  
CC individuals having genetic diseases resulting from abnormal expression of  
CC the genes corresponding to the extended cDNAs. They are also useful for  
CC constructing a high resolution map of the human chromosomes. They can  
CC also be used for gene therapy to control or treat genetic diseases  
XX SQ Sequence 991 BP; 280 A; 175 C; 232 G; 304 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 7,97e-98 Length: 991  
Score: 895.00 Matches: 182  
Percent Similarity: 98.40% Conservative: 3  
Best Local Similarity: 96.81% Mismatches: 3  
Query Match: 96.76% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAX97587 (1-991)  
  
QY 2 ValValAspLeuLeuThrValPheSerLeuValPheGlyAlaSer 21  
DB 68 GTTGTGACCTCTCTGACGACATTTAGAGACCTGGAGTGGTGGTGGCCAC 127  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaVal 41  
DB 128 CTATTCCTGCTGCTTTTCATTACAGTATTTCAGCATTTGAGCGTACAGCTACATGGC 187  
  
QY 42 LeuAlaLeuLeuSerValThrLeuSerPheArgIleThrValGlyValIleGlnAla 61  
DB 188 TTGGCCCTGCTCTCTGACCATTCAGCTTTAGGATATACAGGGGTGTGATCCAGGTATC 247  
  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaValLeuGluSerGluValAlaIleSer 81  
DB 248 CAGAAATCAGATGAGGCCACCCATTCAGGCATATCTCGAATCTGAAGTTGCTATATCT 307  
  
QY 82 GluGluLeuValGlnLysThrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 308 GAGGAGTTGGTTTGCAGAGTACAGTAAATCTGCTCTTGGTTCATCGAATCGACGATAAAG 367  
  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 368 GAACCTCAGCGCCTCTCTTAGTTGATTTAGTTGATTTCTGAAGTTTGCAGGTGG 427  
  
QY 122 MetTyrValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141

DB 428 ATGTGGGTATTACCTATGTTGGTGCCTTGTAAATGCTGCACACTACTGATTTGGCT 487  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 488 CTCATTTCACTCTTCCAGTGTCTCTTATGTAACGGCATCAGGCACAGATAGTATCAT 547  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 548 TATCTAGTACTTGCCTCAATTAAGTATGTTAAGATGCTATGGCTTAATCCAGCAAAATC 607  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 608 CCTGGATTGAGCGCAAGCTGAA 631  
  
RESULT 43  
ADP18854  
ID ADP18854 standard; cDNA; 994 BP.  
XX AC ADP18854;  
XX DT 26-AUG-2004 (first entry)  
XX DE Human secreted polynucleotide #110.  
XX KW Human; secreted protein; gene; ss; genetic disease.  
XX OS Homo sapiens.  
XX PN US2004110939-A1.  
XX PD 10-JUN-2004.  
XX PF 15-OCT-2001; 2001US-00978360.  
XX PR 17-DEC-1998; 98WO-IB002122.  
XX PR 09-FEB-1999; 99WO-IB000282.  
XX PR 21-JUN-2000; 2000WO-IB000951.  
XX PR 15-SEP-2000; 2000US-00663600.  
XX (GEST ) GENSET SA.  
XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;  
XX Duclert A;  
XX WPI; 2004-440404/41.  
XX DR P-PSDB; ADP19259.  
XX New isolated polynucleotide encoding secreted polypeptide, useful for  
PT gene therapy, or in diagnostic procedures to identify individuals having  
PT genetic diseases resulting from abnormal expression of the genes.  
XX Claim 1; SEQ ID NO 110; 113pp; English.  
XX The invention relates to human cDNA sequences that encode human secreted  
CC proteins. The invention also relates to an antibody that specifically  
CC binds to a polypeptide of the invention and a method of binding the  
CC polypeptide to an antibody. The polynucleotides are useful for expressing  
CC the entire secreted proteins which they encode and for distinguishing  
CC human tissues and cells from non-human tissues and cells, and for  
CC distinguishing between human tissues and cells that do or do not express  
CC the polynucleotides comprising the cDNAs. The polynucleotides and  
CC polypeptides are useful in forensic procedures or diagnostic procedures  
CC to identify individuals with genetic diseases resulting from abnormal  
CC expression of the genes corresponding to the cDNAs. The sequences are  
CC also useful in gene therapy to control or treat genetic diseases. This  
CC sequence represents a human secreted polynucleotide of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC sequata.uspto.gov/sequence.html.  
XX SQ Sequence 994 BP; 283 A; 175 C; 232 G; 304 T; 0 U; 0 Other;  
  
Alignment Scores:

```
Pred. No.: 8e-98 Length: 994
Score: 895.00 Matches: 182
Percent Similarity: 98.40% Conservativity: 3
Best Local Similarity: 96.81% Mismatches: 3
Query Match: 96.76% Indels: 0
DB: 12 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x ADP18854 (1-994)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValSerValThrGlyValValPheGlyAlaSer 21
Db 68 GTTGTGACCTCTCTGTACCTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 127
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
Db 128 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGCGTAACAGCTTACATTGCC 187
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 247
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 248 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTCAAGTTGCTATATCT 307
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 308 GAGGAGTTGGTTCAGAGTACAGTAACTCTGCTCTGTGTCATGTGACTGACGATTAAG 367
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 368 GAACCTCAGCGGCTCTCTTGTAGTATGATTTAGTTGATCTCTCAAGTTTCAGTGTG 427
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAlaIle 141
Db 428 ATGTGGGTATTTACTATGTTGGTGGCTGTTTAAATGTTGCTGACACTACTGATTTGGCT 487
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 488 CTCATTTTCACTCTTCAGTGTCTCTGTTATTAAGACGGCATCAGGCACAGATAGATCAT 547
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 548 TATCTAGTACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 607
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 608 CTTGATTTGAAGCGCAAGCTGAA 631

RESULT 44
ADI31056
ID ADI31056 standard; cDNA; 2610 BP.
XX AC ADI31056;
XX AC ADI31056;
XX 17-JUN-2004 (first entry)
XX DE Human cDNA #382.
XX KW Human; gene; ss; immunological response; immunopathological condition;
XX KW Crohn's disease; asthma; ulcerative colitis; hyperesoinophilia;
XX KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
XX KW acute monocytic leukaemia; antiinflammatory; antistaphylococcal; antiulcer;
XX KW osteopathic; antiarthritis; antirheumatic; cytostatic.
XX OS Homo sapiens.
XX PN US6607879-B1.
XX XX 19-AUG-2003.
XX PD 09-FEB-1998; 98US-00023655.
XX PF
XX XX
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PR 09-FEB-1998; 98US-00023655.
XX (INCY-) INCYTE CORP.
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2003-895307/82.
XX A composition comprising a plurality of cDNAs, useful for detecting
XX altered expression of genes in an immunological response or for
XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX or osteoarthritis.
XX Claim 1; SEQ ID NO 382; 50pp; English.
XX The invention relates to a composition comprising a plurality of cDNAs
XX for detecting the altered expression of genes in an immunological
XX response. The invention also relates to a method of diagnosing or
XX monitoring the treatment of an immunopathological condition in a sample,
XX comprising obtaining nucleic acids from a sample, contacting the nucleic
XX acids of the sample with an array comprising the plurality of cDNAs under
XX conditions to form one or more hybridisation complexes, detecting the
XX hybridisation complexes and comparing the levels of the detected
XX hybridisation complexes with the level of hybridisation complexes
XX detected in a non-diseased sample, where an altered level of the detected
XX hybridisation complexes correlates with the presence of an
XX immunopathological condition. Also disclosed are an expression profile
XX comprising a microarray and a plurality of detectable complexes and a
XX method for identifying a plurality of polynucleotide probes. The cDNAs
XX are useful as hybridisable array elements in a microarray for monitoring
XX the expression of target polynucleotides. The microarray can be used in
XX the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX ulcerative colitis, hyperesoinophilia, irritable bowel syndrome,
XX osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX identifying agents for the treatment of the diseases. The microarray may
XX also be used in drug discovery and development, toxicological and
XX carcinogenicity studies, forensics or pharmacogenomics. The composition
XX may also be used in purification of a subpopulation of mRNAs, cDNAs or
XX genomic fragments. This sequence represents a human cDNA of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification but was obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 2610 BP; 773 A; 434 C; 557 G; 820 T; 0 U; 26 Other;
```

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Alignment Scores:
Pred. No.: 9.4e-97 Length: 2610
Score: 891.00 Matches: 183
Percent Similarity: 98.41% Conservativity: 3
Best Local Similarity: 96.83% Mismatches: 2
Query Match: 96.32% Indels: 1
DB: 11 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x ADI31056 (1-2610)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValSerValThrGlyValValPheGlyAlaSer 21
Db 1311 GTTGTGACCTCTCTGTACCTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 1370
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
Db 1371 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGCGTAACAGCTTACAAATTC 1430
Qy 41 aleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 1490
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 1491 CCAGAAATCAGATGAAGGCCACCATTCAGGCATATCTGGATCTGAAGTTGCTATATC 1550
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Db 1551 TGAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTTGTGTCATGTAAGTGCAGATATA 1610  
 Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLeuPheAlaValle 121  
 Db 1611 GGAACCTCAGCGCCTCTCTTAGTTCATGATTAGTTGATCTCTGAAGTTTCAGAGTTT 1670  
 Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAl 141  
 Db 1671 GATGTGGGTATTTACCTATGTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGC 1730  
 Qy 141 aleulleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161  
 Db 1731 TCTCATTTTCACTCTTCAGTGTTCCTGTTATTTAATGACCGCATCAGGCACAGATATCA 1790  
 Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 1791 TTATCTAGGACTTGCATTAAGAATCTTAAAGATGCTATGGCTAAATCCAGCAAAAT 1850  
 Qy 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 1851 CCCTGGGTTTGAAGCGCAAGCTGAA 1875

## RESULT 45

AAV30920

ID AAV30920 standard; cDNA; 2386 BP.

XX

AC AAV30920;

DT 14-SEP-1998 (first entry)

XX

DE Human secreted protein BG160\_1 cDNA.

XX

KW BG160\_1; secreted protein; protein factor; human; ds.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 102..2030

FT /\*tag= a

FT sig\_peptide 1863..1899

FT /\*tag= b

FT /\*note= "putative leader/signal peptide"

FT mat\_peptide 1900..2027

FT /\*tag= c

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FN W09817687-A2.

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CC predicted AT415\_4 amino acid sequence shows homology to neuroendocrine-specific proteins. Novel cDNA clones (see AAV30916-32) coding for human secreted proteins (see AAV5880-90) are claimed. These can be used for recombinant production of the secreted proteins for analysis, characterisation, diagnostic or therapeutic use. They can also be used as tissue or mol.wt. markers, for chromosome identification, to identify genetic disorders, to isolate new related DNA, as sources of primers for PCR, to generate antibodies, and in interaction trap assays. The secreted proteins may also have many biological activities, e.g. cytokine, immunomodulator, haematopoiesis regulating activity, tissue growth activity, activin or inhibin activity, chemotactic or chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, antiinflammatory, cadherin and tumour invasion suppressor activity, and tumour inhibition activity. The proteins can be expressed in vivo from DNA, introduced in gene therapy vectors

XX

SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.86e-94 Length: 2386  
 Score: 871.50 Matches: 179  
 Percent Similarity: 96.30% Conservative: 3  
 Best Local Similarity: 94.71% Mismatches: 2  
 Query Match: 94.22% Indels: 5  
 DB: Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAV30920 (1-2386)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 1476 TCAGTTGTGACCTCTCTGACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGC 1535  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1536 AGCCTATTCTGCTGCTTTCATTGACAGTATTTCAGCAATTTGTCAGCGTAACAGCTACATT 1595  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 1596 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCT 1655  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 1656 ATCCAGAAATCAGATGAGGCCACCCCATTCAGG-----GAAGTTGCTATA 1700  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 1701 TCTGAGGAGTTGGTTTCAGAAATACAGTAATTTCTGCTCTTGGTTCATGTGAACGACGATA 1760  
 Qy 101 LysGluLeuArgArgPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1761 AAGGAACTCAGCGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTCAGTG 1820  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 1821 TTGATGTGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTG 1880  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 1881 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATTAATGAACGGCATCAGGCACAGATAGAT 1940  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1941 CATTATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTAAATTCAGCAAAA 2000  
 Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 2001 ATCCCTGGATTGAGCGCAAGCTGAA 2027

## RESULT 46

ABK90135

ID ABK90135 standard; DNA; 1798 BP.

XX

AC ABK90135;

CC This cDNA clone, designated BG160\_1, codes for a novel human secreted protein (see AAV58383). It was isolated from a human adult brain cDNA library using methods selective for cDNAs that encode secreted proteins. The clone is deposited in composite clone ATCC 98232; an oligonucleotide (see AAV99725) is designed to isolate the clone from the composite. The

Claim 20; Page 74-75; 114pp; English.

CC This cDNA clone, designated BG160\_1, codes for a novel human secreted protein (see AAV58383). It was isolated from a human adult brain cDNA library using methods selective for cDNAs that encode secreted proteins. The clone is deposited in composite clone ATCC 98232; an oligonucleotide (see AAV99725) is designed to isolate the clone from the composite. The

XX 21-OCT-2002 (first entry)  
XX DNA encoding human NogoC protein.  
XX Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
XX stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
XX neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
XX cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
XX tissue hypertrophy; central nervous system; axon regeneration; NogoC;  
XX Nogo-associated disease; metastasis; Gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 215..814  
XX /tag= a  
XX /product= "Human NogoC protein"  
XX WO200257483-A2.  
XX 25-JUL-2002.  
XX 18-JAN-2002; 2002WO-GB000228.  
XX 18-JAN-2001; 2001GB-00001312.  
XX (GLAX ) GLAXO GROUP LTD.  
XX (SMK ) SMITHKLINE BEECHAM PLC.  
XX Blackstock WP, Hale RS, Prinjha R, Rowley A;  
XX WPI: 2002-599722/64.  
XX P-PSDB; ABG30939.  
XX Identifying modulators of Nogo or BACE activity for treating acute  
XX neuronal injuries, neoplastic or dysproliferative disorders, comprises  
XX providing and monitoring interaction between Nogo and BACE polypeptides.  
XX Disclosure; Page 62-64; 68pp; English.  
XX The present invention relates to a new method of identifying modulators  
XX of Nogo function or BACE activity. The method involves providing Nogo and  
XX BACE polypeptides capable of binding with each other, monitoring the  
XX interaction between these polypeptides, and determining if the test agent  
XX is a modulator of Nogo or BACE activity. The method is useful in treating  
XX acute neuronal injuries, such as spinal or head injury, stroke,  
XX peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
XX neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
XX cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
XX hypertrophy) of the central nervous system. The BACE polypeptide is  
XX useful in screening methods to identify agents that may act as modulators  
XX of BACE activity and in particular agents that may be useful in treating  
XX Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
XX and the polynucleotide encoding the BACE polypeptide are useful in  
XX manufacturing a medicament for the treatment or prevention of disorders  
XX responsive to the modulation of Nogo activity, in alleviating the  
XX symptoms or improving the condition of a patient suffering from this  
XX disorder, in axon regeneration, or in preventing metastasis or spreading  
XX of a cancer. The polynucleotide may also be an essential component in  
XX assays, a probe, in recombinant protein synthesis, and in gene therapy  
XX techniques. The present nucleic acid sequence encodes the human NogoC  
XX protein of the invention  
SQ Sequence 1798 BP; 540 A; 314 C; 392 G; 552 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1e-93 Length: 1798  
Score: 864.00 Matches: 182  
Percent Similarity: 97.88% Conservative: 3  
Best Local Similarity: 96.30% Mismatches: 3  
Query Match: 93.41% Indels: 2  
DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABK90135 (1-1798)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleuLysLysThrGlyValValPheGlyAlaSer 21  
DB 248 GTTGTGTACCTCCCTGTAAGAGAGACTTAAAGAGACTGGAGTGGTGTGGTGGCAGC 307  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 308 CTATTCCTGCTGCTTCATTGACAGTATTGAGCATTTGAGCGTAAACAGCCTACATTGCC 367  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAAGCTATC 427  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerCysValAlaIleSer 81  
DB 428 CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 487  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 488 GAGGAGTTGGTTCAAGAGTACAGTAATTTCTGCTCTTGGTCACTGTAATCTGCAAGTAAG 547  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 548 GAACCTAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 607  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 608 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATATGTTGCTGACACTACTGATTTGGCT 667  
QY 142 LeuIleSerLeu-PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161  
DB 668 CTCATTTCACTCTCTTCAGTGTCTCTGTTATTTA-GAAGGCATCATGACAGATAGATCA 726  
QY 161 sTYrIeUGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIl 181  
DB 727 TTATCTAGGACTTGCATAATAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAAT 786  
QY 181 eProGlyLeuLysArgLysAlaAsp 189  
DB 787 CCTGGATTGAAGCGCAAAAGCTGAA 811  
RESULT 47  
ID AAF98399 standard; cDNA; 2386 BP.  
XX AAF98399;  
XX AAF98399;  
XX 07-JUN-2001 (first entry)  
XX Human cDNA clone BG160\_1 sequence SEQ ID 41.  
XX Human; secreted protein; nutrient; cytokine modulator; proliferation;  
XX differentiation; immune system modulator; tissue growth; chemotactic;  
XX haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;  
XX haematopoiesis.  
XX Homo sapiens.  
XX WO200119988-A1.  
XX 22-MAR-2001.  
XX 14-SEP-2000; 2000WO-US025135.  
XX 17-SEP-1999; 99US-00398829.  
XX (GEMY ) GENETICS INST INC.  
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
XX Merberg D, Treacy M; Bowman MR, Spaulding V, Agostino MJ;  
XX

DR WPI; 2001-244801/25.  
DR P-PSDB; AAB90682.  
XX  
XX Isolated nucleic acids encoding polypeptides, useful for modulating e.g.  
PT cytokine and cell proliferation/differentiation activity, the immune  
PT system and hematopoiesis regulating activity.  
XX  
PS Claim 1; Page 408-409; 557pp; English.  
XX  
XX Human cDNA clones represented in AAF98374 - AAF98489 encode secreted  
CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various  
CC tissue types, and may be used in the prevention, treatment and diagnosis  
CC of diseases associated with inappropriate protein expression. The  
CC polypeptides and nucleic acids may be used as nutrients or to modulate  
CC cytokine and cell proliferation/differentiation activity and may also be  
CC involved in modulation of the immune system. The cDNA sequences,  
CC proteins, their agonists and/or antagonists exhibit hematopoiesis  
CC regulating activity; tissue growth activity; activin/inhibin activity;  
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;  
CC receptor/ligand activity; anti-inflammatory activity; hematopoiesis  
CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition  
CC activity. Included in the invention are probes represented in AAF98490 -  
CC AAF98572 which are specific for the cDNA clones encoding the secreted  
CC proteins  
XX  
SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2-26e-93 Length: 2386  
Score: 862.50 Matches: 178  
Percent Similarity: 95.77% Conservative: 3  
Best Local Similarity: 94.18% Mismatches: 3  
Query Match: 93.24% Indels: 5  
DB: Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF98399 (1-2386)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThyGlyValValPheGlyAla 20  
Db 1476 TCAGTGTGTGACCTCTGCTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCT 1535  
QY 21 SerLeuPheLeuLeuSerLeuThyValPheSerIleValSerValThrAlaTyrIle 40  
Db 1536 AGCTATTCTCTGCTGCTTCTATGACAGTATTACAGCATTTGTGAGCGTAACAGCTACATT 1595  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db 1596 GCCTTGCCCTGCTCTCTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCT 1655  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 1656 ATCCAGAAATCAGATGAAGGCCACCCATTCAGG-----GAAGTTGCTATA 1700  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 1701 TCTGAGGAGTGTGTTTCTGAGAGTACAGTAATCTGCTCTGCTGATGTGACGTGCGATA 1760  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 1761 AAGGAATCAGGCGCTCTCTTAGTTAGTATTTAGTTAGTTCTCTGAAGTTGCGATG 1820  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 1821 TTGATGTGGGTATTTACCTATGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1880  
QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 1881 GCTCTCATTTCTCTCTGAGT 1940  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1941 CATTTATCAGGACTTCGAAATGAAGATGTTAAAGATGCTTAAAGATGCTTAAATCCAGCAAA 2000

QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 2001 ATCCCTGGATTGAGCGCAAGCTGAA 2027  
RESULT 48  
ABK34580  
ID ABK34580 standard; cDNA; 1514 BP.  
XX  
XX AC ABK34580;  
XX  
XX 08-MAY-2002 (first entry)  
XX Human cDNA for novel secreted protein, SEQ ID 349.  
XX Human; ss; gene; secreted protein; immune deficiency; viral infection;  
KW bacterial infection; fungal infection; autoimmune disorder; burn;  
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;  
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;  
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;  
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;  
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;  
KW lymphoid cell deficiency.  
XX Homo sapiens.  
XX  
XX WO200177290-A2.  
XX 18-OCT-2001.  
XX 29-MAR-2001; 2001WO-US010295.  
XX 06-APR-2000; 2000US-0194941P.  
XX (GEMY ) GENETICS INST INC.  
XX  
XX Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
PI Gulukota K, Graham JR;  
PI WPI; 2002-179323/23.  
XX  
XX Six hundred and twenty five polynucleotides derived from a variety of  
PT human tissue sources which encode secreted proteins, useful for treating  
PT immune deficiencies and disorders such as autoimmune disorders.  
XX  
XX Claim 1; Page 173; 339pp; English.  
XX  
XX The invention relates to 625 polynucleotides which have been derived from  
CC a variety of human tissue sources and which encode novel secreted  
CC proteins, their complements and sequences that hybridise to them. Also  
CC included are a vector comprising the polynucleotide, a host cell.  
CC transformed with the vector, the proteins encoded by the polynucleotides,  
CC antibodies that bind to the proteins and identification of modulators of  
CC the proteins or the expression of the polynucleotide. The polynucleotides  
CC can be used as probes for the identification and isolation of full length  
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used  
CC as nutritional supplements. The protein is useful in the treatment of  
CC various immune deficiencies and disorders such as viral infections,  
CC bacterial infections, fungal infections, autoimmune disorders (e.g.  
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and  
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are  
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's  
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders  
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and  
CC tumours. They are also useful for tissue regeneration, for wound healing  
CC and in the treatment of burns, incisions and ulcers. The proteins are  
CC also useful for regulating haematopoiesis, for treating myeloid or  
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA  
CC sequences encoding a secreted protein  
XX  
SQ Sequence 1514 BP; 455 A; 258 C; 313 G; 488 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2.03e-91 Length: 1514





```
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 848 CTATTCCTGCTGCTTTTCATGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTTGCC 907
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAAAGCTATC 967
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 968 CAGAAATCAGATGAGGCCACCCATTCAGGCATATCTGGAATCTCAAGTTGCTATATCT 1027
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 1028 GAGGAGTTGGTTTTCAGAAATACAGTAAATCTGCTCTTGGTTCATGTGAACCTGCACGATAAG 1087
QY 102 GluLeuArgArgPheLeuValAlaAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 1088 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGCT----- 1137
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 1137 ----- 1137
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1138 CTCAATTCACCTCTTCAGTGTCTGCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1197
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1198 TATCTAGGACTTGCATAATAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1257
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1258 CTGGATTGAGCGCAAACTGAA 1281
RESULT 50
ID ADJ56527 standard; cdna; 1520 BP.
XX
AC ADJ56527;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat cdna differentially expressed in MYCN activated cells SegID 333.
XX
KW rat; differential expression; transactivator; proto-oncogene;
KW neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;
KW MYCN activated cell.
XX
OS Rattus norvegicus.
XX
PN US2003119009-A1.
XX
PD 26-JUN-2003.
XX
PF 25-FEB-2002; 2002US-00084817.
XX
PR 23-FEB-2001; 2001US-0270784P.
XX
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHE J M.
XX
PI Stuart SG, Nuchtern JG, Plon SE, Shohet JM;
XX
DR WPI; 2003-635698/60.
XX
PT New genes regulated by MYCN activation, useful in gene therapy,
PT particularly for treating a subject with e.g. neuroblastoma or
PT cancers, or for diagnosing, staging or monitoring the treatment of the
```

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PT cancer.
XX Claim 1; SEQ ID NO 333; 27pp; English.
XX
CC This invention relates to novel isolated cDNAs that are differentially
CC expressed in MYCN activated cells. Specifically, it refers to
CC polynucleotide sequences that exhibit differential expression patterns in
CC cells activated by the transactivator MYCN, where MYCN is a proto-
CC oncogene that is amplified in neuroblastoma cells and is common in small
CC cell lung cancers. The present invention describes these cDNA molecules
CC as useful for in hybridisation assays to detect expression of nucleic
CC acids (or complementary nucleic acids) in a present in a given sample, as
CC well as for screening assays by identifying molecules or compounds that
CC specifically bind the cDNA as a ligand and modulate function or activity.
CC Accordingly, these compositions exhibit cytostatic activity and can also
CC be used for gene therapy purposes. This polynucleotide sequence is a cDNA
CC that is differentially expressed in MYCN activated cells, given in an
CC exemplification of the invention. NOTE: This sequence does not appear in
CC the printed specification but has been obtained in electronic format from
CC the US Patent Office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20030119009.
XX
SQ Sequence 1520 BP; 398 A; 354 C; 336 G; 432 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.57e-71 Length: 1520
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 10 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x ADJ56527 (1-1520)
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 176 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCGTTGGAGATTTCCCTG 235
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 236 CTGCTGCTCTTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCCCTACCTGGCCCTG 295
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 296 GCGGCACCTCAGCCACCATCATGTTCCGCATCTCAAGTCTGTTTACAGAGTGCAG 355
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 356 AAAACCGACGAGGCCACCCCTTTCAAGGCTACTTTGGAGCTTGAGATCACCCCTTTCTCAG 415
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 416 GAGCAGATTTCAGAAATGACAGGACTGCTGTCAGTTCTACGTGAACAGCACACTTAAGGAA 475
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 476 CTGAGGAGGCTCTTCCTTCTCCAGGACCTGGTGGATTCCTTAATTTGAGTCTCTGATG 535
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
Db 536 TGGCTCCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTGTG 595
QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 596 GTTTCAAATGTTTACTCTACCTAGTGTATGTTAAGCACCAGCACAGATTGACCAATAT 655
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 656 CTGGGACTTGTGAGGACTCACATTAATGCTGTTGTGGCAAGATTCAGGCTAAATCCCA 715
QY 183 GlyLeuLysArgLysAlaAsp 189
Db 716 GCGCTTAAGAGGACGCTGAG 736
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RESULT 51  
 ID ADO07887 standard; cDNA; 2331 BP.  
 XX  
 AC ADO07887;  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human polynucleotide #66.  
 XX  
 KW Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 KW anorectic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2004071700-A1.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 09-OCT-2002; 2002US-00267502.  
 XX  
 PR 09-OCT-2002; 2002US-00267502.  
 XX  
 PA (LIFE-) LIFE SCI DEV CORP.  
 XX  
 PI Kim J, Galant R;  
 XX  
 DR WPI; 2004-328526/30.  
 DR P-PSDB; ADO08104.  
 XX  
 PT Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX  
 PS Claim 1; SEQ ID NO 213; 275pp; English.  
 XX  
 CC The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC human cDNA used in the scope of the invention.  
 XX  
 SQ Sequence 2331 BP; 552 A; 698 C; 649 G; 432 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 2,866-71 Length: 2331  
 Score: 679.00 Matches: 127  
 Percent Similarity: 84.49% Conservative: 31  
 Best Local Similarity: 67.91% Mismatches: 29  
 Query Match: 73.41% Indels: 0  
 DB: 12 Gaps: 0  
 XX  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADO07887 (1-2331)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 Db 1768 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGACGGCGATCGTGTGGGAGTTTCCTG 1827  
 QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 1828 CTGCTGCTCTTCTCCCTGACCCAGTTACGCGTGGTGGCGTCTGCTGCCCTACCTGCCCTG 1887  
 QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 1888 GCCGACCTCTCAGCCACCATCAGTTTCGCACTACCAAGTCTGTTTTACACAGCTGCAG 1947  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 1948 AAACCGACGAGGCCACCTTTCAAGCCCTACTTTGGAGCTTGAGATCACCCCTTTCTCAG 2007  
 QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 2008 GAGCAGATTCAAGAGTACACGAGCTGCTCTTACGTGAAACAGCACACTTAAGGAA 2067  
 QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 2068 CTGAGGAGCTCTTCTTGTCCAGACCTGTGGATTCCTTAAATTTGCAGTCTCTGATG 2127  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142  
 Db 2128 TGGCTCCTGACCTAGTTGGCGCTCTCTTCAATGSCCTGACCTCTGCTCATGCTG 2187  
 QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 2188 GTTTCATATGTTTACTCTACCTGATGTATGTTAAGCACCAGGCACAGATTGACCAATAT 2247  
 QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 2248 CTGGACCTTGAGGAGCTCACATAATCTGTTGTGGCAAGATTTCAGCTTAATATCCCA 2307  
 QY 183 GlyLeuLysArgLysAlaAsp 189  
 Db 2308 GCGCTAAGAGCGACGCTGAG 2328  
 RESULT 52  
 AAX75770  
 ID AAX75770 standard; DNA; 3202 BP.  
 XX  
 AC AAX75770;  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE Human neuroendocrine-specific protein NSP-A DNA.  
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; senaphorin II; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGB-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9845322-A2.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 02-APR-1998; 98WO-IB000705.  
 XX  
 PR 10-APR-1997; 97US-0043163P.  
 XX  
 PA (ROYA-) ROYAL NETHERLANDS ACAD AGTS & SCI.  
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.



PR 03-OCT-2000; 2000US-0237604P.  
 PR 03-OCT-2000; 2000US-0237606P.  
 PR 03-OCT-2000; 2000US-0237608P.  
 PR 01-NOV-2000; 2000US-0244867P.  
 PR 01-NOV-2000; 2000US-0245084P.  
 XX  
 PA (AVAL-) AVALON PHARM.  
 XX  
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 XX  
 XX WPI; 2002-188264/24.  
 DR

XX Screening for anti-neoplastic agent involves exposing cells to a chemical  
 PT agent to be tested for anti-neoplastic activity, and determining a change  
 PT in expression of a gene of a signature gene set.  
 XX

PS Claim 1; SEQ ID NO 3237; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
 CC to ABL70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC the data collected with respect to the anti-neoplastic agent as a result  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms  
 CC tumour  
 XX

SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.47e-71 Length: 3202  
 Score: 679.00 Matches: 127  
 Percent Similarity: 84.49% Conservative: 31  
 Best Local Similarity: 67.91% Mismatches: 29  
 Query Match: 73.41% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABL64900 (1-3202)

Qy 3 ValAspLeuThrTyTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
 Db 1890 ATTGACCTGTTGATTGGCGGACATCAAGCAGCGGCATCGTGTGGAGTTCTCTG 1949  
 Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAlaLeu 42  
 Db 1950 CTGCTGCTCTTCTCCCTCACCAGTTACGCGTGGTGGAGCGTGGCTACCTGCGCCCTG 2009  
 Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyRileLysGlyValIleGlnAlaIleGln 62  
 Db 2010 GCGGACCTCTCAGCCACCATCAGTTTCGCGCATCTACAAGTGTGTTTACAGCAGTGCAG 2069  
 Qy 63 LysSerAspGluGlyHisProPheArgAlaTyRileuGluSerGluValAlaIleSerGlu 82  
 Db 2070 AATACCGACGAGGCCACCTTTTCAGCGCTTCTGGAGCTTGAGATCACCCTTCTCTGAG 2129  
 Qy 83 GluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 2130 GAGCAGATTACAGAGTACACGACTCCCTGCGATTTCTACGTTGACAGCACACTTAAGGAA 2189  
 Qy 103 LeuArgLeuPheLeuValAspLeuValAspSerLeuValAspPheAlaValLeuMet 122  
 Db 2190 CTGAGGAGGCTCTTCTTGTGCCAGACCTGGTGGATTCTCTTAAATTTGCAGTCTGATG 2249

Qy 123 TrpValPheThrTyTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142  
 Db 2250 TGGCTCTGACTAGCTTGGCGCTCTCTCAATGGCCTGACCTGCTCTCATGCTGTG 2309  
 Qy 143 IleSerLeuPheSerIleProValIleTyRileuArgHisGlnValGlnIleAspHisTyR 162  
 Db 2310 GTTTCATATGTTTACTCTACCTGATGTATGTTAAGCACCGACGACAGATTGACCAATAT 2369  
 Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 2370 CTGGACTTGTGAGGACTCACATTAATGCTGTTGTGGCAAGATTGAGCTAAATCCCA 2429  
 Qy 183 GlyLeuLysArgLysAlaAsp 189  
 Db 2430 GCGCTAAGACGACGCTGAG 2450

RESULT 54

ADQ18661

ID ADQ18661 standard; DNA; 3202 BP.

AC ADQ18661;

XX

DT 26-AUG-2004 (first entry)

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1480.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

KW ds.

XX Homo sapiens.

OS

XX WO2004048938-A2.

PN

XX 10-JUN-2004.

PD

XX 26-NOV-2003; 2003WO-US038193.

PF

XX 26-NOV-2002; 2002US-0429739P.

PR

XX (PROT-) PROTEIN DESIGN LABS INC.

PA

XX Aziz N, Ginsburg WM, Zlotnik A;

PI WPI; 2004-441208/41.

XX

XX Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample

PT and comparing the gene expression, also useful in treating soft tissue

PT sarcoma.

XX

XX Example 2; SEQ ID NO 1480; 210pp; English.

XX

XX The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cytosolic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC DNA of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX

SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.47e-71 Length: 3202

Score: 679.00 Matches: 127

Percent Similarity: 84.49% Conservative: 31

Best Local Similarity: 67.91% Mismatches: 29

```

Query Match: 73.41% Indels: 0
DB: 12 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x ADQ18661 (1-3202)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
DB 1890 ATTGACCTGTTGATTTGGCGGACATCAAGCAGCGGATCGTGTGGAGTTTCCTG 1949
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB 1950 CTGCTGCTCTTCCCTGACCCAGTTTCAGCGGTGGAGCGTGTGGCCCTACCTGGCCCTG 2009
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
DB 2010 GCGCAGCTTCAGCCACCATCATCTGTCGATCTCAAGTCTGTGTTTACAGCAGTGCAG 2069
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
DB 2070 AAAACCGAAGGCGCCCTTTCAAGGCTTCTGAGCTTGAGATCACCTTTCTCAG 2129
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
DB 2130 GAGCAGATTTCAGAGTACAGGACTGCCTGCGACTGCTGAGCTTGAGATCACCTTTCTCAG 2189
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
DB 2190 CTGAGGAGGCTCTTCTGTCAGGACCTGCGGATTCCTAAATTTTCAGTCTCGATG 2249
QY 123 TrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
DB 2250 TGGCTCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTGCTGCTGCTG 2309
QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
DB 2310 GTTTCATGTTTACTCTACCTGTAGTGATGTTAAGCACCAGGCACAGATTGACCAATAT 2369
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
DB 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429
QY 183 GlyLeuLysArgLysAlaAsp 189
DB 2430 GCGCTAAGGCGCAGCTGAG 2450

RESULT 55
ID ADR24525
XX ADR24525 standard; DNA; 3202 BP.
XX AC ADR24525;
XX 21-OCT-2004 (first entry)
XX DE Breast cancer prognosis marker #386.
XX XX ds; breast cancer; prognosis; gene expression; diagnosis.
XX OS Homo sapiens.
XX PN WO2004065545-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US001100.
XX PR 15-JAN-2003; 2003US-00342887.
XX PA (ROSE-) ROSETTA INPHARMATICS LLC.
XX PA (NECA-) NETHERLANDS CANCER INST.
XX PI Van't Veer LJ, He Y;
XX WPI; 2004-593473/57.

```

Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.

Disclosure; SEQ ID NO 386; 226pp; English.

The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.

Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.47e-71	Length:	3202
Score:	679.00	Matches:	127
Percent Similarity:	84.4%	Conservative:	31
Best Local Similarity:	67.91%	Mismatches:	29
Query Match:	73.41%	Indels:	0
DB:	13	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADR24525 (1-3202)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22

DB 1890 ATTGACCTGTTGATTTGGCGGACATCAAGCAGCGGATCGTGTGGAGTTTCCTG 1949

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42

DB 1950 CTGCTGCTCTTCCCTGACCCAGTTTCAGCGGTGGAGCGTGTGGCCCTACCTGGCCCTG 2009

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62

DB 2010 GCGCAGCTTCAGCCACCATCATCTGTCGATCTCAAGTCTGTGTTTACAGCAGTGCAG 2069

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82

DB 2070 AAAACCGAAGGCGCCCTTTCAAGGCTTCTGAGCTTGAGATCACCTTTCTCAG 2129

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102

DB 2130 GAGCAGATTTCAGAGTACAGGACTGCCTGCGACTGCTGAGCTTGAGATCACCTTTCTCAG 2189

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122

DB 2190 CTGAGGAGGCTCTTCTGTCAGGACCTGCGGATTCCTAAATTTTCAGTCTCGATG 2249

QY 123 TrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142

DB 2250 TGGCTCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTGCTGCTGCTG 2309

QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162

DB 2310 GTTTCATGTTTACTCTACCTGTAGTGATGTTAAGCACCAGGCACAGATTGACCAATAT 2369

QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182

DB 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429

QY 183 GlyLeuLysArgLysAlaAsp 189

DB 2430 GCGCTAAGGCGCAGCTGAG 2450

RESULT 56

ADR65814

ID ADR65814 standard; DNA; 3202 BP.





CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC DNA of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.

XX  
SQ Sequence 3305 BP; 828 A; 913 C; 843 G; 721 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 4,678-71 Length: 3305  
Score: 679.00 Matches: 127  
Percent Similarity: 84.49% Conservative: 31  
Best Local Similarity: 67.91% Mismatches: 29  
Query Match: 73.41% Indels: 0  
Gaps: 12

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADQ231106 (1-3305)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
DB 1890 ATTGACCTGTTGTTATGCGGACATCAAGCAGCGGCATCGTCTTTGGAGTTTCCTG 1949  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
DB 1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGTGAGCGTCTGCTGCTGCTGCTG 2009  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
DB 2010 GCGGACCTCTCAGCCACCATCAGTTTCGTCATCTACAGTCTGTTTACAGCAGTGGAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
DB 2070 AAAACCGCAGGAGCGCCCTTCAAGCGCTACTTGGAGCTTGAGATCACCTTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
DB 2130 GAGCAGATTCAAGATACAGGACTGCTGTCAGTTCTACGTGAACAGCACACTTAAAGAA 2189  
QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 2190 CTGAGAGGCTCTCTCTGTCAGACCTGCTGGATCTCTTAATTTGCTGCTGCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheArgGlyLeuThrLeuLeuLeuAlaLeu 142  
DB 2250 TGGCTCTGACCTAGCTGGGCTCTCTTCAATGCGCTGACCTGCTGCTGCTGCTGCTG 2309  
QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
DB 2310 GTTTCATGTTTACTCTACCTGATGTATGTTAAGCCAGGCGACGATGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 2370 CTGGACTTGTGAGGACTCACATAATCTGTTGTGGCAAGATTACGCTAATAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaAsp 189  
DB 2430 GCGCGTAAGAGCGAGCTGAG 2450

#### RESULT 59

ADUS99925

ID ADUS99925 standard; cDNA; 3327 BP.

XX

AC ADUS99925;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human reticulon 1 (RTN1), transcript variant 1, cDNA.

XX

KW Human; ss: gene; Bisulphite; metastasis; cancer; cytostatic;

KW DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;

KW electrospray; mass spectrometry; CpG dinucleotide; solid tumour.

XX

OS Homo sapiens.

XX

PN US2003148327-A1.

XX

PD 07-AUG-2003.

XX

PF 21-JAN-2003; 2003US-00240485.

XX

PR 06-APR-2000; 2000DE-01019058.

PR 07-APR-2000; 2000DE-01019173.

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

PR 06-APR-2001; 2001WO-EP003970.

XX (OLEK/) OLEK A.

PA (PIEP/) PIEPENBROCK C.

PA (BERL/) BERLIN K.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-010922/01.

DR GENBANK; NW\_021136.

XX

PT New nucleic acid derived from chemically treated metastasis genes, useful  
PT for diagnosis of cancers by analysis of cytosine methylation, also for  
PT treatment.

XX Claim 2; Page; 9pp; English.

PS

XX

CC The invention relates to a nucleic acid comprising at least 18 bases from  
CC a segment of the chemically pretreated DNA of genes associated with  
CC metastasis, i.e. any of ADS99709-ADS99906 human genomic sequences or any  
CC of the 19 sequences appearing as ADS99911-ADS99929. SEQ ID 2, 4, 6 etc are  
CC the complements of SEQ ID 1, 3, 5, etc. Also included are an oligomer  
CC (particularly an oligonucleotide or peptide nucleic acid) comprising at  
CC least one base sequence of at least 9 bases which hybridises to, or is  
CC identical with, the sequences referred to above, producing an array of  
CC the oligomers on a carrier, obtaining genetic and/or epigenetic  
CC parameters for diagnosis and/or therapy of diseases (or predisposition to  
CC them) by analysis of cytosine methylation and a kit comprising a  
CC bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the  
CC method of above 5-umethylated cytosines in a genomic DNA sample are  
CC converted chemically to uracil, or another base with hybridisation  
CC properties different from those of cytosine, then fragments of the  
CC treated DNA amplified (particularly by polymerase chain reaction) using  
CC the oligomers and a polymerase (preferably heat stable) to produce  
CC labelled amplicons. These are tested for hybridisation to an array of  
CC oligomers and any hybridisation detected. The amplicons are labelled with  
CC fluorescent or radioactive markers, or with a detachable mass marker to  
CC allow their detection by mass spectrometry, specifically using the matrix  
CC -assisted laser desorption/ionisation (MALDI) or electrospray techniques.  
CC To improve detection in the mass spectrometer, fragments formed in the  
CC instrument have only a single net charge (positive or negative). The  
CC genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-  
CC embedded tissue sample. Oligonucleotides or peptide-nucleic acids that  
CC are complementary to (or identical with) parts of the nucleic acids listed  
CC above may be used as primers for amplification of the nucleic acids or  
CC their complements, and for determining cytosine methylation status and/or  
CC single nucleotide polymorphisms in metastasis-related genes. They can be  
CC used for analysis of diseases associated with methylation of CpG  
CC dinucleotides and to determine (epigenetic) parameters for diagnosis  
CC and/or therapy of disease (or predisposition). The genomic DNA sequences  
CC are useful for diagnosis and therapy of solid tumours and cancer. The  
CC present sequence is human gene fragment or cDNA associated with  
CC metastasis. Note: The sequence was not displayed in the specification but  
CC was obtained by the indexer from Genbank.

XX

SQ Sequence 3327 BP; 829 A; 907 C; 877 G; 714 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 4,718-71 Length: 3327

Score: 679.00 Matches: 127

Percent Similarity: 84.49% Conservative: 31

Best Local Similarity: 67.91% Mismatches: 29

Query Match: 73.41% Indels: 0



DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADS99925 (1-3327)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
 DB 1977 ATTGACCTGTTGATTTGGGGGACATCAAGCAGCGGGATGCTGTTTGGGATTCCTG 2036

QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 DB 2037 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGGTGGAGCTGCTGGCTTACCTGGCCCTG 2096

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeu 62  
 DB 2097 GCGGCACTCTGACCCACCATCAGTTTCCGATCTTCAAGTCTGTTTACAAGCAGTGCAG 2156

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 DB 2157 AAACCGACGAGGCCACCTTTCAAGGCTTACTTGGAGCTTGAGATCACCTTCTCTCAG 2216

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 DB 2217 GAGCAGATTGAGAGTACAGGACTGCTGCTGAGTTCTAGTGAACAGCACACTTAAGGAA 2276

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 DB 2277 CTGAGGAGGCTCTCTCTTCTGTCAGGACCTGGTGGATTCCTTAAATTTTCAGTCTCTGATG 2336

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142  
 DB 2337 TGCTCTGACCTACCTGTTGGGCTCTCTTCATGGCTGACCTGCTGCTCTGCTGCTGCTG 2396

QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 DB 2397 GTTTCATGTTTACTCTACTCTGAGTGTATGTTAAGCACCAGCAGATTGACCAATAT 2456

QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 DB 2457 CTGGGACTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTGAGCTAAATCCCA 2516

QY 183 GlyLeuLysArgLysAlaAsp 189  
 DB 2517 GCGCTAAGAGGCACGCTGAG 2537

RESULT 60  
 ID ADB79854  
 AC ADB79854; standard; DNA; 1502 BP.  
 AC ADB79854;

DT 04-DEC-2003 (first entry)  
 DT Rat rS-Rex-s human NSP C homolog coding sequence, SEQ ID 94.  
 XX Analgesic; pain; streptozocin-induced diabetes; rat; gene; ds.  
 XX Rattus norvegicus.  
 XX EP1279744-A2.  
 XX 29-JAN-2003.  
 XX 26-JUL-2002; 2002EP-00255249.  
 XX 27-JUL-2001; 2001GB-00018354.  
 XX 07-FEB-2002; 2002GB-00002910.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;  
 XX WPI; 2003-395407/38.  
 XX P-PSDB; ADB79853.

XX Use of isolated gene sequences and encoded polypeptides that are  
 PT upregulated in the spinal cord in response to streptozocin-induced  
 PT diabetes for screening compounds for the treatment of pain, or for  
 PT diagnosing pain.  
 XX Claim 1; Page 171; 334pp; English.  
 CC The present invention relates to nucleotide sequences which are useful in  
 CC the screening of compounds for the treatment of pain, or for the  
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the  
 CC spinal cord in response to streptozocin-induced diabetes. The present  
 CC sequence is one such nucleotide sequence.  
 XX Sequence 1502 BP; 348 A; 392 C; 363 G; 399 T; 0 U; 0 Other;

Alignment Scores: 2,04e-71 Length: 1502  
 Score: 678.00 Matches: 126  
 Percent Similarity: 84.4% Conservative: 32  
 Best Local Similarity: 67.3% Mismatches: 29  
 Query Match: 73.3% Indels: 0  
 DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADB79854 (1-1502)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
 DB 179 ATTGACCTTCTGCTGCGGACATCAAGCAGCGGGATGCTGTCGGAGCTTCCTG 238

QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 DB 239 CTGCTGCTCTTCTCTGCTGACCGATTCAGCTGTGAGGCTGCTGCTTACCTGGCCCTG 298

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 DB 299 GCTGCCCTCTCTGCCACCATCAGCTTCGCACTTCAAGTCCGTTCTACAAGCTGTGCG 358

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 DB 359 AAACAGATGAGGCTCACCTTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTCTCCAG 418

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 DB 419 GAGCAGATCCCAAGTACACAGACTGCTGCGCTATACGTGAACAGCACTCTGAAGGAG 478

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 DB 479 CTACGGAGGCTCTTCTGCTGCTCAGGACCTGGTGGATTCCTTAAATTTTCAGTCTCTCATG 538

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAlaLeu 142  
 DB 539 TGGCTCTGACCTAGCTTGGCGCACTTCTCAATGGCTGACCTGCTGCTTATGGCTGTG 598

QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 DB 599 GTTTCATGTTTACTCTACTCTGTTGATATGTTAAGCACCAGCAGCAGTGTGACCAATAT 658

QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 DB 659 CTGGGACTGTGAGGACTCACATAACACCGTGTGGCAAGATCCAGCTAAATCCCC 718

QY 183 GlyLeuLysArgLysAlaAsp 189  
 DB 719 GCGCCACAGAGCAGCTGAG 739

RESULT 61  
 ID ADO07889  
 AC ADO07889; standard; cDNA; 2343 BP.  
 XX ADO07889;  
 XX 01-JUL-2004 (first entry)



XX Mouse polynucleotide #58.  
 XX Mouse; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 KW anorectic; antidiabetic.  
 XX Mus sp.  
 XX US2004071700-A1.  
 XX 15-APR-2004.  
 XX 09-OCT-2002; 2002US-00267502.  
 XX 09-OCT-2002; 2002US-00267502.  
 XX (LIFE-) LIFE SCI DEV CORP.  
 XX Kim J, Galant R;  
 XX WPI; 2004-328526/30.  
 XX P-PSDB; ADO08106.  
 XX Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX Claim 1; SEQ ID NO 215; 275pp; English.  
 XX The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC polypeptide or a change in an activity of the polypeptide, treating a  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC mouse cDNA used in the scope of the invention.  
 XX SQ Sequence 2343 BP; 536 A; 710 C; 646 G; 451 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3.8e-71 Length: 2343  
 Score: 678.00 Matches: 126  
 Percent Similarity: 84.49% Conservative: 32  
 Best Local Similarity: 67.38% Mismatches: 29  
 Query Match: 73.30% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADO07889 (1-2343)  
 QY 3 ValAspLeuLeuTyTrpArgAspIleLysThrGlyValPheGlyAlaSerLeu 22  
 Db 1780 ATTGACCTTCTGTTGGGGGACATCAAGCAGCTGGATTGTTGGGAGCTTCTG 1839  
 QY 23 PheLeuLeuLeuSerLeuValPheSerIleValSerValThrAlaTyIleAlaLeu 42  
 Db 1840 CTGCTGCTTCTCTCCCTGACCAGTTTAGCGTTGTGAGCGTGGTTGCTACCTGCGCCTG 1899

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGln 62  
 Db 1900 GCGCCCTCTCTGCCACCATCAGCTTCGCATCTACAAGTCGTTCTACAGCTGCGAG 1959  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyIleuGluSerGluValAlaIleSerGlu 82  
 Db 1960 AAAACAGATGAGGCTCACCTTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTCCAG 2019  
 QY 83 GluLeuValGlnTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 2020 GAGCAGATCCAGAGTACACAGACTGCTGAGCTGTATGTGAACAGCAGCTCTGAAGGAG 2079  
 QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 2080 CTACGGAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2139  
 QY 123 TrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142  
 Db 2140 TGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2199  
 QY 143 IleSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHisTy 162  
 Db 2200 GTTTCGATGTTTACTCTACCTGTTGTGTACCTTAAGCACCAGGCAAGTTGACCAATAT 2259  
 QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 2260 CTGGAGCTTGTGAGGACTCACAATAACACCTGCTGGCAAGATCCAGGCTAATAATCCCC 2319  
 QY 183 GlyLeuLysArgLysAlaAsp 189  
 Db 2320 GCGCCCAAGAGCGCGCTGAG 2340  
 RESULT 62  
 ABX43312 ID ABX43312 standard; cDNA; 422 BP.  
 AC ABX43312;  
 XX 20-FEB-2003 (first entry)  
 XX Bovine EST associated with lactation/muscle/fat deposition #8477.  
 DE Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
 KW muscle deposition; fat deposition; genome mapping; gene identification;  
 KW gene analysis; cattle breeding.  
 XX Bos Taurus.  
 OS US2002137139-A1.  
 XX 26-SEP-2002.  
 XX 24-SEP-2001; 2001US-00960352.  
 XX 12-JAN-1999; 99US-0115707P.  
 PR 11-JAN-2000; 2000US-00480902.  
 XX (BYAT// BYATT J C.  
 PA (MATH// MATHIALAGAN N.  
 PA (TAON// TAO N.  
 PA (WARR// WARREN W C.  
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;  
 XX WPI; 2003-110599/10.  
 DR New nucleic acid associated with lactation, and muscle and fat  
 PT deposition, useful for genome mapping, gene identification and analysis,  
 PT cattle breeding, or for genetically improving cattle.  
 XX Claim 2; SEQ ID NO 8477; 245pp; English.  
 XX The invention relates to a purified nucleic acid molecule associated with

CC lactation or muscle and fat deposition (designated LMPD), derived from  
CC cattle, and the LMPD nucleic acid can specifically hybridize to a second  
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,  
CC appearing as ABX34836-ABX49947, or complements of them. Also included are  
CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic  
CC acid linked to a promoter and a 3' non-translated sequence that  
CC functions in the cell to cause termination of transcription and addition  
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
CC (2) determining a level or pattern of a molecule in a bovine cell or  
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
CC of the 15112 nucleic acid sequences or its complement or fragment) with a  
CC complementary nucleic acid molecule obtained from the bovine cell or  
CC tissue, where hybridization between the marker nucleic acid and the  
CC complementary nucleic acid permits the detection of the molecule; and (b)  
CC detecting the level or pattern of the complementary nucleic acid, where  
CC the detection of the complementary nucleic acid is predictive of the  
CC level or pattern of the molecule. The LMPD nucleic acid is used for  
CC determining a level or pattern of a molecule in a bovine cell or tissue.  
CC It is useful for genome mapping, gene identification and analysis, cattle  
CC breeding, preparation of constructs for use in cattle gene expression, or  
CC for genetically improving cattle. The present sequence is one of the  
CC 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The  
CC present sequence was not shown in the specification but was obtained in  
CC electronic format from the USPTO web site:  
CC seqdata.uspto.gov/sequence.html?DocID=200201371139

XX SQ Sequence 422 BP; 109 A; 79 C; 94 G; 140 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 7,91e-72 Length: 422  
Score: 675.00 Matches: 136  
Percent Similarity: 98.57% Conservative: 2  
Best Local Similarity: 97.14% Mismatches: 2  
Query Match: 72.97% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABX43312 (1-422)

QY 37 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGly 56  
Db 2 ACGGCCTACATTGCCCTTGGCCCTCTCTGTGACTATCAGCTTTAGGATATATAAGGCT 61  
QY 57 ValIleGlnAlaIleGlnIleGlnSerAspGluGlyHisProPheArgIleTyrIleGluSer 76  
Db 62 GTGATCCAGGCTATCAGAAATCTGATGAAGGCCACCCATTGAGGCATATTGGGAATCT 121  
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96  
Db 122 GAAGTTGCTATATCTGAGGAGTTGGTTGAGAGTACAGCAATCTGCTCTTGGTCATGTT 181  
QY 97 AsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeu 116  
Db 182 AACTGCACAATAAAGAACTCAGACGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTG 241  
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThr 136  
Db 242 AAGTTTGCAGTGTGATGGGTATTTACCTATGTTGGTCCCTGTGTCATGCTGCA 301  
QY 137 LeuLeuIleAlaLeuAlaLeuSerLeuPheSerIleProValIleTyrGluArgHisGln 156  
Db 302 CTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGACGGCATCAG 361  
QY 157 ValGlnIleAspHisTyrIleGluGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys 176  
Db 362 GCGCAAAATAGATCATTTATCTGGGACTTGCAAAATAGAAATTTAAAGATGCTATGGCTAAA 421

RESULT 63

ADB85247

ID ADB85247 standard; DNA; 1473 BP.

XX AC

ADB85247;

XX XX

DT 04-DEC-2003 (first entry)

XX DE Rat C1-13 protein neuronal-specific gene SEQ ID NO:128.  
XX KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
KW protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.  
XX OS Rattus norvegicus.

PN EP1284297-A2.

PD 19-FEB-2003.

PF 26-JUL-2002; 2002EP-00255228.

PR 27-JUL-2001; 2001GB-00018354.

PR 07-FEB-2002; 2002GB-00002880.

XX (WARN ) WARNER LAMBERT CO.

PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

XX WPI; 2003-364994/35.

DR P-PSDB; ADB85246.

XX Use of gene sequence that is down-regulated in response to streptozocin-  
PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in  
PT screening of compounds for treating or diagnosing pain.

XX Claim 1; Page 197; 256pp; English.

XX The invention relates to a novel isolated gene sequence that is down-  
CC regulated in the spinal cord in response to streptozocin-induced  
CC diabetes, or comprising, hybridising or having at least 80% sequence  
CC identity to a sequence whose expression products are kinases,  
CC phosphatases, ion channel proteins, receptors, transporters, G-protein  
CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
CC given in the specification. A gene of the invention has analgesic  
CC activity, and may have a use in gene therapy. The gene sequences, vector,  
CC host cell, animal, polypeptide and antibody are useful for screening of  
CC compounds for diagnosing or treating pain. The kits are useful for  
CC simultaneous, separate or sequential detecting and/or quantifying down-  
CC regulation of a gene sequence in the spinal cord of a mammal in response  
CC to streptozocin-induced diabetes. The compound or pharmaceutical  
CC composition is useful as a medicament for treating or diagnosing pain.  
CC The present sequence represents a gene of the invention.

XX SQ Sequence 1473 BP; 357 A; 373 C; 343 G; 400 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,32e-70 Length: 1473  
Score: 665.00 Matches: 126  
Percent Similarity: 84.4% Conservative: 32  
Best Local Similarity: 67.3% Mismatches: 29  
Query Match: 71.8% Indels: 1  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADB85247 (1-1473)

QY 3 ValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 146 ATTGACCTTCTGATCTGCGGACATCAAGACAGCGGATGTGTTCGGAGCTTCCTG 205  
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 206 CTGCTGCTCTTCTCTCCCTGACCCAGTTGTGAGCGTGTGAGCGTGTGAGCGCTG 265  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 266 GCTGCCCTCTCTGCCACCATCATCGCTTCGCAATCAAGTCGCTTCTACAGCTGCGAG 325  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82

Db 326 AAAACAGATGAGGGTCAACCTTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTCCAG 385  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 386 GAGCAGATCCAGAGTACACAGCTCCGCGAGTATACGTGACAGCACTCTGAGGAG 445  
 Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 446 CTACGAGGCTCTCTCTGTCACAGACCTAGTGGATTCCTTAAATTTGACGCTCATG 505  
 Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
 Db 506 TGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565  
 Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 566 GTTTCGATGTTTACTTACTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625  
 Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 626 CTGGGACTTGTGAGGACTCACATAAACACCGTTGTGGCAAGATCCAGGCTAAATCCCC 685  
 Qy 183 GlyLeuLysArgLysAlaAsp 189  
 Db 686 GCGGC-AAAGAGCATGCTGAG 705  
 RESULT 64  
 AAH57558  
 ID AAH57558 standard; cDNA; 3279 BP.  
 XX  
 AC AAH57558;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Human brain cell specific cDNA sequence SEQ ID NO:398.  
 XX  
 KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;  
 KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;  
 KW metabolic disease; developmental disease; cytostatic; immunomodulatory;  
 KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132927-A2.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 02-NOV-2000; 2000WO-US030396.  
 XX  
 PR 04-NOV-1999; 99US-0163508P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Sornassee T, Seilhamer JJ, Watson GA;  
 XX  
 DR WPI; 2001-291057/30.  
 XX  
 PT New cell and tissue specific polynucleotides useful for diagnosis,  
 PT prognosis or monitoring of treatments for disorders where the gene is  
 PT associated with a cancer, immunopathology or neuropathology.  
 XX  
 PS Claim 1; Page 312-313; 327pp; English.  
 XX  
 CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide  
 CC sequences (I). (I) can have cytosolic, immunomodulatory and  
 CC neuroprotective activities, and can be used in gene therapy. (I) and  
 CC proteins (II) encoded by then are used in high throughput screening  
 CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,  
 CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their  
 CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical  
 CC agents. Expression of (I) in a sample indicates the differentiation of  
 CC embryonic stem cells into a tissue selected from brain, heart, kidney,  
 CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used

CC to produce an expression profile that defines a metabolic or  
 CC developmental process, treatment, condition, disease or disorder. The  
 CC gene profile can be used for diagnosis, prognosis or monitoring of  
 CC treatments and for investigating a predisposition to a disorder where the  
 CC gene is associated with a cancer, immunopathology or neuropathology

SQ Sequence 3279 BP; 814 A; 905 C; 850 G; 710 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9e-69 Length: 3279  
 Score: 660.00 Matches: 126  
 Percent Similarity: 83.51% Conservative: 31  
 Best Local Similarity: 67.02% Mismatches: 30  
 Query Match: 71.35% Indels: 1  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAH57558 (1-3279)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 Db 1934 ATTGACCTGTGTATTGGCGGACATCAAGCAGACGGGCATCGTCTTTGGGAGTTTCCTG 1993  
 Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 1994 CTGCTGCTCTTCTCCCTGACCCAGTTCAAGCGTGGTGAGCGTGGCTACCTGCGCCCTG 2053  
 Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 2054 GCGGACTCTCAGCCACCATCAGTTTCGCGATCTACAAGTCTGTTTCAACAGCAGTGCGAG 2113  
 Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 2114 AAAACGACGAGGCGCCACCTTTCAAGGCTTCTTGGAGCTTGAGATCACCTTCTCAG 2173  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 2174 GAGCAGATTCAGAGTACACGCGACTGCGCTGCGAGTTCTACGTGACACAGCACACTTAAGGAA 2233  
 Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 2234 CTGAGGAGGCTCTCTCTTGTCCAGACCTGCTGGATTCCTTAAATTTGACGCTCTGATG 2293  
 Qy 123 TrpValPheThrTyrValGlyAlaLeuPhe-AsnGlyLeuThrLeuLeuIleLeuAlaLe 142  
 Db 2294 TGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2353  
 Qy 142 uIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 2354 GGTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCAGCCAGGCACAGATTGACCAATA 2413  
 Qy 162 rLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 2414 TCTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTCAGGCTAAATCCCC 2473  
 Qy 182 oGlyLeuLysArgLysAlaAsp 189  
 Db 2474 AGGCGCTAAGAGGACCGCTGAG 2495  
 RESULT 65  
 ABX46402  
 ID ABX46402 standard; cDNA; 422 BP.  
 XX  
 AC ABX46402;  
 XX  
 DT 21-FEB-2003 (first entry)  
 XX  
 DE Bovine EST associated with lactation/muscle/fat deposition #11567.  
 XX  
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
 KW muscle deposition; fat deposition; genome mapping; gene identification;  
 KW gene analysis; cattle breeding.  
 XX  
 OS Bos Taurus.



CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,  
CC cytotstatic and tranquiliser activities. This polynucleotide is a full  
CC length human cDNA sequence of the invention. NOTE: This sequence is not  
CC given in the sequence listing of the specification but can be obtained on  
CC CD-ROM from the European Patent Office, Vienna Sub-office.  
XX

SQ Sequence 4607 BP; 1428 A; 944 C; 945 G; 1290 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,098-64 Length: 4607  
Score: 625.50 Matches: 114  
Percent Similarity: 81.05% Conservativity: 40  
Best Local Similarity: 60.00% Mismatches: 35  
Query Match: 67.62% Indels: 1  
DB: 13 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADR06965 (1-4607)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 2353 TCAGTGCAGCATCTGATTCTTGGAGAGATGGAAGAAGACTGGGTTGTCTTTGGCACC 2412  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2413 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCAGTGTGGTTCTTACCTC 2472  
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 2473 ATCTGGCTCTCTCTGTACCATCAGCTTCAGATCTACAACTCGTTCATCCAACTC 2532  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 2533 GTACAGAAGTCAGAAGAAGGCCATCATTTCAAAGCTTACCTGGAGTAGACATTACTCTG 2592  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 2593 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCTGATGATCAACAGAGGCCCTG 2652  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 2653 AAATCATATTTCGTCCTTTCTGGTAGAAGATCGGTGTGACTCTCTGAAGCTGGCTGTC 2712  
Qy 121 LeuMetTrpValPheTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 2713 TTCAATGCTGCTGATGACCTATGTTGCTGCTTTTAAAGGAATCACCTCTTAATCTT 2772  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 2773 GCTGAACCTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTACAGACCCAGATTGAT 2832  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 2833 CACTATGTTGGATCGCCCGAGATCAGACCAAGTCATTTGTTGAAGATCCAAAGCAAA 2892  
Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
Db 2893 CTCCTCGAATGCCCAAAAAGGACAGAA 2922

RESULT 67

AAZ38318

ID AAZ38318 standard; cDNA; 708 BP.

XX AC

XX AAZ38318;

XX 09-FEB-2000 (first entry)

DE Human transmembrane protein cDNA clone HP02061 coding sequence.

XX HP02061; transmembrane domain; Saos-2; homology;

KW neuroendocrine-specific protein C; antibody; assay reagent;

KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

KW antagonist; ligand; therapeutic; ds.

XX

OS Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 1..708  
FT /\*tag= a  
FT /product= "Human transmembrane protein HP02061"  
FT /note= "No stop codon given in the specification"

XX

PN WO9955862-A2.

XX

PD 04-NOV-1999.

XX

PF 27-APR-1999; 99WO-JP002226.

XX

PR 28-APR-1998; 98JP-00119395.

XX

PA (SAGA ) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

PI Kato S, Kimura T;

XX

XX WPI; 2000-023358/02.

DR P-PSDB; AAY52387.

XX

PT Human proteins with transmembrane domains, involved in control of cell

XX proliferation and differentiation, useful for treating e.g. cancer or

PT inflammation.

XX

PS Claim 3; Page 85; 114pp; English.

XX

CC This sequence represents the coding sequence of human cDNA clone HP02061

CC which encodes a 26 kD protein with two putative transmembrane domains.

CC The cDNA was isolated from a Saos-2 (human osteosarcoma cell line) cDNA

CC library. The protein has homology with the human neuroendocrine-specific

CC protein C (PIR Accession No. I60904), and may have a similar function.

CC The protein may be used to raise specific antibodies, as assay reagents,

CC as diagnostic tissue markers, for the isolation of cognate receptors,

CC ligands and binding proteins, and as biologically active agents.

CC Nucleotides encoding the protein may be used as primers and probes or

CC antisense molecules, and in gene therapy. Cells transformed with these

CC nucleotides may be used to screen for agonists and antagonists which are

CC potentially useful therapeutically

XX

SQ Sequence 708 BP; 158 A; 195 C; 169 G; 186 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,48e-65 Length: 708

Score: 622.50 Matches: 113

Percent Similarity: 81.05% Conservativity: 41

Best Local Similarity: 59.47% Mismatches: 35

Query Match: 67.30% Indels: 1

DB: 3 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ38318 (1-708)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20

Db 139 GCGGTGCAGCATCTGATTCTTGGAGAGATGGAAGAAGACTGGGTTGTCTTTGGCACC 198

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 199 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCAGTGTGTTCTTACCTC 258

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 259 ATCTGGCTCTCTCTGTCCATCAGCTTCAGGATCTACAACTCGTTCATCCAACTC 318

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 319 GTACAGAAGTCAGAAGAAGGCCATCATTTCAAAGCTTACCTGGAGTAGACATTACTCTG 378

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

Db

Db 379 TCCTCAGAGCTTTCCATAATTACATGAATGTCGCCATGTCACATCAACAGGCGCTG 438  
 QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAATCATATTTCGCTCTCTTCTGGTAGAAGATCTGGTTGACTCCCTTGAAGCTGGCTGC 498  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCTGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCCCTCTAAATTCCT 558  
 QY 141 AlaLeuLeuSerLeuPheSerLeuProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 559 GCTGAACCTCTCATTTTCAGTGTCCGATGTCTATGAGAAGATCAAGCCAGATTGAT 618  
 QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAAGATCCCAAGCAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 679 CTCCTGGAATCGCCAAAAAAGGCAGAA 708

## RESULT 68

ADK67496

ID ADK67496 standard; cDNA; 711 BP.

XX

AC ADK67496;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human RTN-3 cDNA sequence.

XX

KW ds; neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3;

KW amyloidosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..711

FT FT /\*tag= a

FT FT /product= "RTN-3 protein"

XX

FN WO2003088926-A2.

XX

PD 30-OCT-2003.

XX

PF 08-APR-2003; 2003WO-US008829.

XX

PR 17-APR-2002; 2002US-0373284P.

XX

PA (PHAA ) PHARMACIA &amp; UPJOHN CO.

XX

PI Yan R, Lu Y;

XX

XX WPI; 2003-854033/79.

DR

DR F-PSDB; ADK67497.

XX

PT New polypeptide having BACE1 activity, useful in preparing a composition

PT for treating amyloidosis or Alzheimer's disease.

XX

PS Claim 2; SEQ ID NO 1; 42pp; English.

XX

PS The invention relates to an isolated polypeptide having BACE1 activity.

CC The protein is RTN4 or RTN3 protein. The polypeptide is useful in

CC preparing a composition for treating amyloidosis or Alzheimer's disease.

XX

SQ Sequence 711 BP; 161 A; 196 C; 168 G; 186 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 3.5e-65 Length: 711

Score: 622.50 Matches: 113

Percent Similarity: 81.05% Conservative: 41

Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADK67496 (1-711)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 139 GGGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTGTGTCTTTGGCACC 198  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIle 40  
 Db 199 AGCTGATCATGCTGCTTTCCTGCACGCTTTCAGTGTTCATGTCATGTCGTGTTCTTACCTC 258  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 259 ATCTGGCTCTCTCTCTGTCCATCAGTTCAGGATCTACAGTCTCATCAAGCT 318  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 319 GTACAGAAAGTCAGAAAGAGGCGCATCCATTCAAAGCTTACCTGAGTACATTTACTCTG 378  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 379 TCCTCAGAAAGCTTTCATAATTACATGAATGCTGCGCATGTCACATCAACAGGCGCTG 438  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAATCATATTTCGCTCTCTTCTGTGTAAGATCTGTTGACTCTCTTGAAGCTGGCTGC 498  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCTGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTTCTTAATCTT 558  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 559 GCTGAACCTGCTCATTTTCAGTGTCCGATGTCATGAGAAGTCAAGACCCAGATTGAT 618  
 QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAAGATCCCAAGCAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 679 CTCCTGGAATCGCCAAAAAAGGCAGAA 708

## RESULT 69

AAH34853

ID AAH34853 standard; cDNA; 1330 BP.

XX

AC AAH34853;

XX

DT 03-SEP-2001 (first entry)

XX

DE Human colon cancer antigen encoding cDNA SEQ ID NO:1935.

XX

KW Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW colorectal carcinoma; chromosome 11; ss.

XX

OS Homo sapiens.

XX

PN WO200122920-A2.

XX

PD 05-APR-2001.

XX

XX 28-SEP-2000; 2000WO-US026524.

XX

PR 29-SEP-1999; 99US-0157137P.

XX

PR 03-NOV-1999; 99US-0163280P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Barash SC, Birse CE, Rosen CA;

```
XX WPI; 2001-235357/24.
DR P-PSDB; AAG75448.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
PT
XX
PS Claim 1; Page 3443; 9803pp; English.
PS
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated P, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 1330 BP; 329 A; 334 C; 294 G; 372 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 8,41e-65 Length: 1330
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
Gaps: 4

US-09-830-972-2_COPY_975_1163 (1-189) x AAH34853 (1-1330)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 297 GCGGTGCGACGATCTGATTTCTTGGAGAGATGTGAAGAAGACTGGGTGTCTTGGCACC 356
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 357 AGCTGTATGCTGCTTCTTCCCTGGCAGCTTTCAGTGTATCAGTGTGTGTCTTACCTC 416
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 417 ATCTGTGGCTTCTTCTGTCCATCAGTATCAGTATCAGATCTCAAGTCCGTCATCCAGCT 476
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 477 GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCCTACCTGGAGCTAGACATCTACTG 536
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 537 TCCTCAGAGAGCTTCCATAATACATGATGATGCTGCTGATGATGATGATGATGATGATG 596
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB 597 AAACATCATATTTCGCTCTTCTTCTGTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGC 656
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 657 TTCATGTGCTGATGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 717 GCTGAAGTCTCATTTTTCAGTGTCCGATGTGTATGAGAAAGTCAACAGCCAGCATGAT 776
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaIleGlnAlaLys 180

Db 777 CACTATGTGGCATGCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGCAAAA 836
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 837 CTCCTCGAATGCGCAAAAAGGAGGAGAA 866

RESULT 70
AAH60810
ID AAH60810 standard; DNA; 1656 BP.
XX
XX AC AAH60810;
XX
XX DT 09-AUG-1999 (first entry)
XX
XX DE Human secreted protein encoding DNA (clone yb8-1).
XX
XX KW Secreted protein; kidney; lung; brain; blood; testis; bone marrow;
KW nutritional activity; cytokine; cell proliferation; immune stimulation;
KW hematopoiesis regulation; tissue growth; thrombolytic; gene therapy;
XX anti-inflammatory; tumour invasion; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9926961-A1.
XX
XX PD 03-JUN-1999.
XX
XX PF 24-NOV-1998; 98WO-US025149.
XX
XX PR 26-NOV-1997; 97US-0066804P.
XX
XX PR 23-NOV-1998; 98US-00197886.
XX
XX PA (GEMY ) GENETICS INST INC.
XX
XX PI Jacobs K, McCreay JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Wong GG, Clark HF;
PI Fechtel K;
XX
XX DR WPI; 1999-357809/30.
XX
XX DR P-PSDB; AAH17228.
XX
XX PT New polynucleotides encoding secreted proteins.
XX
XX PS Claim 39; Page 125-126; 133pp; English.
XX
XX CC The invention relates to secreted proteins (AAH17219-228) encoded by
XX polynucleotides obtained from human fetal kidney, adult lung, adult
XX kidney, adult brain, adult blood, adult testes, and fetal brain and
XX murine adult bone marrow cDNA libraries. The secreted protein nucleic acid
XX sequences (X6801-811) correspond to clones bd306-7, gj283-6, fk317-3,
XX k213-2x, na316-1, nf93-20, npl64-1, pe204-1, yal-1 and yb-1, (all clones
XX are deposited as ATCC 98599); The PNs and proteins are predicted to have
XX biological activities which would make them suitable for treating,
XX preventing or ameliorating medical conditions in humans and animals,
XX although no supporting data is given. Suggested activities include
XX nutritional activity, cytokine and cell proliferation/differentiation
XX activity, immune stimulating (e.g. as vaccines) or suppressing activity,
XX hematopoiesis regulating activity, tissue growth activity, activin/
XX inhibin activity, chemotactic/chemokinetic activity, haemostatic and
XX thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, cadherin/tumour invasion suppressor activity, and tumour
XX inhibition activity. The PNs are also stated to be useful for gene
XX therapy
XX
XX SQ Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.14e-64 Length: 1656
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
```









QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 405 TCCTCAGAGCTTCCATAATACATGAATGCTGCCATGCACATCAACAGGCGCCCTG 464  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 465 AAATCATTTATTCGCTCTCTTCGAGAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 524  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 525 TTCTATGCTGCTGATGACCTATGTTGCTGCTGTTTTTAACGGAATCACCTCTTAATTCCT 584  
 QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 585 GCTGAACCTCTCATTTTCAGTCTCCGATGTTCTATGAGAAGTACAAAGCCAGATTGAT 644  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 645 CACTATGTTGGATCCGCCCAAAAAAGGCGAGAA 734  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 DB 705 CTCCTCGGAATGCCCAAAAAAGGCGAGAA 734  
 RESULT 73  
 AAZ36240  
 ID AAZ36240 standard; cDNA; 1668 BP.  
 AC  
 XX  
 XX  
 DT 22-FEB-2000 (first entry)  
 DE  
 XX cDNA encoding a bone marrow secreted protein designated BMS240.  
 DE  
 KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;  
 KW cell proliferation; cell differentiation; hematopoiesis; anaemia;  
 KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;  
 KW erythroid progenitor cell; colony stimulating factor; granulocyte;  
 KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;  
 KW platelet disorder; thrombocytopenia; hematopoietic stem cell;  
 KW stem cell disorder; aplastic anaemia; bone differentiation;  
 KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;  
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;  
 KW bone fracture; cartilage damage; artificial joint; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Location/Qualifiers  
 FT 99..809  
 FT /\*tag= a  
 FT /product= "bone marrow secreted protein"  
 FT poly\_a\_signal  
 FT 1626..1631  
 FT /\*tag= b  
 XX  
 XX W09933979-A2.  
 XX  
 XX 08-JUL-1999.  
 XX  
 XX 18-DEC-1998; 98WO-US027008.  
 XX  
 XX 30-DEC-1997; 97US-0068958P.  
 XX 24-SEP-1998; 98US-0101603P.  
 XX 30-SEP-1998; 98US-0102540P.  
 XX  
 XX (CHIR ) CHIRON CORP.  
 XX  
 XX Lin H, Cao L;  
 XX  
 XX WPI; 2000-038344/03.  
 DR P-PSDB; AAY53634.  
 XX  
 XX New isolated human polynucleotide and secreted proteins can induce

PT production of other cytokines in certain cell populations.

XX Claim 11; Page 98-100; 120pp; English.

XX AAZ36228-49 encode bone marrow secreted proteins of human bone marrow  
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or  
 CC cell differentiation activity (either inducing or inhibiting). They can  
 CC be used to support colony forming cells or factor-dependent cell lines,  
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell  
 CC deficiencies. In addition, they may be used to support the growth and  
 CC proliferation of erythroid progenitor cells, and to treat various  
 CC anaemias. They can have colony stimulating factor (CSF) activity and can  
 CC be used to support the growth and proliferation of myeloid cells such as  
 CC granulocytes, monocytes or macrophages, to prevent or treat myelo-  
 CC suppression, to support the growth and proliferation of megakaryocytes  
 CC and platelets, thereby allowing prevention or treatment of platelet  
 CC disorders such as thrombocytopenia, to support the growth and  
 CC proliferation of hematopoietic stem cells, either in place of or in  
 CC conjunction with platelet transfusions, to treat stem cell disorders,  
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to  
 CC repopulate the stem cell compartment after irradiation or chemotherapy.  
 CC They can be used for growth or differentiation of bone, cartilage,  
 CC tendon, ligament, or nerve tissue, as well as for wound healing and  
 CC tissue repair and replacement, and in the treatment of burns, incisions  
 CC and ulcers, to induce cartilage and/or bone growth in circumstances where  
 CC bone is not normally formed and thus have an application in healing bone  
 CC fractures and cartilage damage or defects, prophylactic use in fracture  
 CC reduction and also in the improved fixation of artificial joints  
 XX  
 SQ Sequence 1668 BP; 435 A; 414 C; 349 G; 470 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 1.16e-64 Length: 1668  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 3 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ36240 (1-1668)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 237 GCGGTGCGAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGTGTCTTTGGCACC 296  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 297 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTAGTGTGTTCTTACCTC 356  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 357 ATCTGGGCTTCTCTCTGTCCATCAGCTTCAGATCTACAGATCCGTCCGTATCCAGCT 416  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 417 GTACAGAGTCAAGAGAGGCCATCCATTCAAAGCTACCTGGACGTAGACTACTCTG 476  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 477 TCCTCAGAAGCTTTCATAAATTACATGAATGTGTCATGTGCACATCAACAGGCGCCCTG 536  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 537 AAATCATTTATTCGCTCTCTTCGAGAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 596  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 597 TTCTATGCTGCTGATGACCTATGTTGCTGCTGTTTTTAACGGAATCACCTCTTAATTCCT 656  
 QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 657 GCTGAACCTGCTCATTTTCAGTGTCCCGATTTGTTCTATGAGAAGTACAAAGCCAGATTGAT 716

QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTTGGCATGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 776  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 777 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 806

RESULT 74  
 AAZ38319  
 ID AAZ38319 standard; cDNA; 1759 BP.  
 AC AAZ38319;  
 XX  
 DT 09-FEB-2000 (first entry)  
 XX  
 DE Human transmembrane protein cDNA clone HP02061.  
 XX  
 KW HP02061; transmembrane domain; Saos-2; homology;  
 KW neuroendocrine-specific protein C; antibody; assay reagent;  
 KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;  
 KW antagonist; ligand; therapeutic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT Location/Qualifiers  
 FT 142..852  
 FT /\*tag= a  
 FT /product= "Human transmembrane protein HP02061"  
 FT  
 FT  
 XX  
 XX WO9955862-A2.  
 XX  
 XX 04-NOV-1999.  
 XX  
 XX 27-APR-1999; 99WO-JP002226.  
 XX  
 XX 28-APR-1998; 98JP-00119395.  
 XX  
 XX (SAGA ) SAGAMI CHEM RES CENT.  
 XX (PROT-) PROTEGENE INC.  
 XX  
 XX Kato S, Kimura T;  
 XX  
 XX WPI; 2000-023358/02.  
 XX P-PSDB; AAY52387.  
 XX  
 XX Human proteins with transmembrane domains, involved in control of cell  
 PT proliferation and differentiation, useful for treating e.g. cancer or  
 PT inflammation.  
 XX  
 PS Claim 4; Page 92-94; 114pp; English.  
 XX  
 CC This sequence represents the human cDNA clone HP02061 which encodes a 26  
 CC kD protein with two putative transmembrane domains. The cDNA was isolated  
 CC from a Saos-2 (human osteosarcoma cell line) cDNA library. The protein  
 CC has homology with the human neuroendocrine-specific protein C (PIR  
 CC Accession No. I60904), and may have a similar function. The protein may  
 CC be used to raise specific antibodies, as assay reagents, as diagnostic  
 CC tissue markers, for the isolation of cognate receptors, ligands and  
 CC binding proteins, and as biologically active agents. Nucleotides encoding  
 CC the protein may be used as primers and probes or antisense molecules, and  
 CC in gene therapy. Cells transformed with these nucleotides may be used to  
 CC screen for agonists and antagonists which are potentially useful  
 CC therapeutically  
 XX  
 SQ Sequence 1759 BP; 454 A; 433 C; 376 G; 496 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.25e-64 Length: 1759  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1

Db US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ38319 (1-1759)  
 Gaps: 1  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 280 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTGTTGCTTGGCCACC 339  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaThrIle 40  
 Db 340 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCATCAGTGGTTCCTTACCTC 399  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 400 ATCTGGCTCTTCTCTCTGTCAACCATCAGCTTCAAGATCTACAGTCGTCATCCAAGCT 459  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 460 GTACAGAAGTCAGAGAAGGCCATCCATTCAAGCCTACCTGGAGCTAGACATTACTCTG 519  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 520 TCCTCAGAAGCTTCCATAATTACATGAATCTGCCATGTGGTGCAATCAACAGGCCCTG 579  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 580 AAACCTATTATTCGCTCTTCTCTGTAGAGATCTGGTGTGACTCTTGAAGCTGGCTGTC 639  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 640 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCTTCTTAATTCCT 699  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 700 GCTGAACCTGCTCATTTTCAGTGTCCCGATTCATGAGAGATGCAAGACCCAGATTGAT 759  
 QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 760 CACTATGTTGGCATGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 819  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 820 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 849

RESULT 75  
 AAZ59748  
 ID AAZ59748 standard; DNA; 1766 BP.  
 XX  
 AC AAZ59748;  
 XX  
 DT 19-JAN-1999 (first entry)  
 XX  
 DE Human secreted protein gene 92 clone HAUBL57.  
 XX  
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9839448-A2.  
 XX  
 XX 11-SEP-1998.  
 XX  
 XX 06-MAR-1998; 98WO-US004493.  
 XX  
 XX 07-MAR-1997; 97US-0038621P.  
 XX 07-MAR-1997; 97US-0040161P.

PR 07-MAR-1997; 97US-0040162P.  
PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040626P.  
PR 11-APR-1997; 97US-0043311P.  
PR 11-APR-1997; 97US-0043312P.  
PR 11-APR-1997; 97US-0043313P.  
PR 11-APR-1997; 97US-0043314P.  
PR 11-APR-1997; 97US-0043315P.  
PR 11-APR-1997; 97US-0043568P.  
PR 11-APR-1997; 97US-0043569P.  
PR 11-APR-1997; 97US-0043576P.  
PR 11-APR-1997; 97US-0043578P.  
PR 11-APR-1997; 97US-0043669P.  
PR 11-APR-1997; 97US-0043670P.  
PR 11-APR-1997; 97US-0043671P.  
PR 11-APR-1997; 97US-0043672P.  
PR 11-APR-1997; 97US-0043674P.  
PR 23-MAY-1997; 97US-0047582P.  
PR 23-MAY-1997; 97US-0047583P.  
PR 23-MAY-1997; 97US-0047584P.  
PR 23-MAY-1997; 97US-0047585P.  
PR 23-MAY-1997; 97US-0047586P.  
PR 23-MAY-1997; 97US-0047587P.  
PR 23-MAY-1997; 97US-0047588P.  
PR 23-MAY-1997; 97US-0047589P.  
PR 23-MAY-1997; 97US-0047590P.  
PR 23-MAY-1997; 97US-0047592P.  
PR 23-MAY-1997; 97US-0047593P.  
PR 23-MAY-1997; 97US-0047594P.  
PR 23-MAY-1997; 97US-0047595P.  
PR 23-MAY-1997; 97US-0047596P.  
PR 23-MAY-1997; 97US-0047597P.  
PR 23-MAY-1997; 97US-0047598P.  
PR 23-MAY-1997; 97US-0047599P.  
PR 23-MAY-1997; 97US-0047600P.  
PR 23-MAY-1997; 97US-0047601P.  
PR 23-MAY-1997; 97US-0047612P.  
PR 23-MAY-1997; 97US-0047613P.  
PR 23-MAY-1997; 97US-0047614P.  
PR 23-MAY-1997; 97US-0047615P.  
PR 23-MAY-1997; 97US-0047617P.  
PR 23-MAY-1997; 97US-0047618P.  
PR 23-MAY-1997; 97US-0047632P.  
PR 23-MAY-1997; 97US-0047633P.  
PR 06-JUN-1997; 97US-0048646P.  
PR 06-JUN-1997; 97US-0048974P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 16-JUL-1997; 97US-0051926P.  
PR 18-AUG-1997; 97US-0052874P.  
PR 22-AUG-1997; 97US-0055724P.  
PR 22-AUG-1997; 97US-0056630P.  
PR 22-AUG-1997; 97US-0056631P.  
PR 22-AUG-1997; 97US-0056632P.  
PR 22-AUG-1997; 97US-0056636P.  
PR 22-AUG-1997; 97US-0056637P.  
PR 22-AUG-1997; 97US-0056662P.  
PR 22-AUG-1997; 97US-0056664P.  
PR 22-AUG-1997; 97US-0056845P.  
PR 22-AUG-1997; 97US-0056862P.  
PR 22-AUG-1997; 97US-0056864P.  
PR 22-AUG-1997; 97US-0056872P.  
PR 22-AUG-1997; 97US-0056874P.  
PR 22-AUG-1997; 97US-0056875P.

PR 22-AUG-1997; 97US-0056876P.  
PR 22-AUG-1997; 97US-0056877P.  
PR 22-AUG-1997; 97US-0056878P.  
PR 22-AUG-1997; 97US-0056879P.  
PR 22-AUG-1997; 97US-0056880P.  
PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
PR 22-AUG-1997; 97US-0056886P.  
PR 22-AUG-1997; 97US-0056887P.  
PR 22-AUG-1997; 97US-0056888P.  
PR 22-AUG-1997; 97US-0056889P.  
PR 22-AUG-1997; 97US-0056892P.  
PR 22-AUG-1997; 97US-0056893P.  
PR 22-AUG-1997; 97US-0056894P.  
PR 22-AUG-1997; 97US-0056903P.  
PR 22-AUG-1997; 97US-0056908P.  
PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 22-AUG-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057669P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 02-OCT-1997; 97US-0061060P.

# (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;  
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PB, Greene JM;  
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
PI Moore PA, Shi Y, Iaffeur DW, Li Y, Zeng Z, Kyaw H;  
XX WPI; 1998-506364/43.  
DR P-PSDB; AAW74963.

PT New isolated human genes and the secreted polypeptide(s) they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.

PS Claim 1; Page 473-474; 721pp; English.

XX This sequence represents a nucleic acid molecule designated Gene 92 from  
CC the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC  
CC 209043) which encodes a secreted human protein. The gene can be used to  
CC generate fusion proteins by linking to the gene to a human immunoglobulin  
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused  
CC protein as compared to the human protein only. The invention relates to  
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-  
CC V59812; amino acid sequences AAW74731-W5026) which are useful for  
CC preventing, treating or ameliorating medical conditions e.g. by protein  
CC or gene therapy. Also, pathological conditions can be diagnosed by  
CC determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new polynucleotides.  
CC Specific uses are described for each of the 186 polynucleotides, based on  
CC which tissues they are most highly expressed in (see AAV59511 for  
CC described uses)

XX Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

## Alignment Scores:

Pred. No.:	1.25e-64	Length:	1766
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	2	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAV59748 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 287 GCGGTGCACGATCTGATTTCTTCTGGAGAGATGTGAAGAGACTGGGTTTCTTTGGCACC 346

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 347 ACCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATGAGTGGTTCCTACCTC 406
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 407 ATCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCAAGCT 466
QY 61 IleGlnIleSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 467 GTACAGAGTCAGAGAGGCCATTCATTCAAGGCTACCTCGAGCTAGACATTACTCTG 526
QY 81 SerGluGluLeuValGlnIleTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100
Db 527 TCCTCAGAGCTTCCATAATATACATGATGCTGCCATGTCACATCAACAGGCCCTG 586
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 587 AAACCTCATATTTCGCTCTCTTCTGGTAGAAGATCTGTTGACTCCTTGAAGCTGGCTGTC 646
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140
Db 647 TTCATGTGCTGATGACCTATGTTGGTGTCTTTTAACGGATCACCTTCTTAATCTT 706
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 707 GCTGAAGTCTCATTTTCAGTGTCCGATGTCTATGAGTAGTACAAACCCAGATTGAT 766
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 767 CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCAAGCAAAA 826
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189
Db 827 CTCCTGGAATGCCCAAAAAAGGAGAA 856

RESULT 76
ABS73741
ID ABS73741 standard; cDNA; 1766 BP.
XX
AC ABS73741;
XX
DT 15-JAN-2003 (first entry)
XX
DE Human cDNA #2 for novel secreted protein gene 92.
XX
KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
OS Homo sapiens.
XX
PN US6420526-B1.
XX
PD 16-JUL-2002.
XX
PF 08-SEP-1998; 98US-00149476.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
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PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
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PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
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PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 13-JUN-1997; 97US-0048974P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
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PR 22-AUG-1997; 97US-0056884P.  
 PR 22-AUG-1997; 97US-0056886P.  
 PR 22-AUG-1997; 97US-0056887P.  
 PR 22-AUG-1997; 97US-0056888P.  
 PR 22-AUG-1997; 97US-0056889P.  
 PR 22-AUG-1997; 97US-0056892P.  
 PR 22-AUG-1997; 97US-0056893P.  
 PR 22-AUG-1997; 97US-0056894P.  
 PR 22-AUG-1997; 97US-0056903P.  
 PR 22-AUG-1997; 97US-0056908P.  
 PR 22-AUG-1997; 97US-0056910P.  
 PR 22-AUG-1997; 97US-0056911P.  
 PR 05-SEP-1997; 97US-0057650P.  
 PR 05-SEP-1997; 97US-0057669P.  
 PR 12-SEP-1997; 97US-0057761P.  
 PR 12-SEP-1997; 97US-0058785P.  
 PR 02-OCT-1997; 97US-0061060P.  
 PR 06-MAR-1998; 98WO-US004493.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;  
 PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;  
 PI Perrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX  
 DR WPI; 2002-634796/68.  
 DR P-PSDB; ABG95423.  
 XX

PT New isolated human secreted protein for diagnosing, preventing, treating  
 PT or ameliorating medical conditions and used as a food additive or  
 PT preservative.

PS Example 1; SEQ ID NO 254; 129pp; English.

XX The invention relates to an isolated protein that is one of 186 human  
 CC secreted proteins, given in the specification, encoded by one of 309 cDNA  
 CC sequences also given in the specification. The protein is used in a  
 CC pharmaceutical composition used to prevent, treat or ameliorate a medical  
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. The present sequence represents a cDNA derived from a gene  
 CC encoding one of the novel human secreted proteins of the invention. Note:  
 CC This sequence did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=642052681  
 XX

SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 1.25e-64 Length: 1766  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABS73741 (1-1766)

QY 1-SerValValAspLeuLeuTyrTrpArgAspIleLysIleThrGlyValValPheGlyAla 20

Db 287 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTGTCTTTGGACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 347 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 407 ATCCTGGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAAGCT 466  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 467 GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCTACCTGGAGCTAGACATTACTCTG 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 527 TCCTCAGAAGCTTTTCCATAATTACATGAATGCTGCGCATGCACATCAACAGGCCCTG 586  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAATCATATTATTCGTCTCTTTCTGTGAAGATCTGGTTGACTCCTTGAAGCTGCTGTC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 647 TTCATGTGCTGATGACCTATGTTGCTGCTGTTTAAACGGATCACCCTTCTAATCTT 706  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 707 GCTGAACCTGCTCATTTTCAGTGTCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGCAAA 826  
 QY 181 lleProGlyLeu--LysArgLysAlaAsp 189  
 Db 827 CTCCTTGAATCGCCCAAAAAGGAGCAAA 856  
 RESULT 77  
 ID ACD82884 standard; CDNA; 1766 BP.  
 XX ACD82884;  
 AC ACD82884;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE cDNA sequence #244 containing coding region of a human secreted protein.  
 XX  
 KW Human; secreted protein; hyperproliferative disorder; leukaemia;  
 KW breast cancer; wound; reproductive disorder; blood-related disorder;  
 KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;  
 KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;  
 KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;  
 KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;  
 KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;  
 KW angina pectoris; cerebral ischaemia; congenital heart defect;  
 KW respiratory disorder; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;  
 KW immunosuppressive; antibacterial; haemostatic; thrombolytic;  
 KW anticoagulant; neuroprotective; thyromimetic; antiallergic;  
 KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antiangiinal;  
 KW cerebroprotective; cardiac; nootropic; antiparkinsonian;  
 KW antiinflammatory; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003049618-A1.  
 PN  
 XX 13-MAR-2003.  
 PD  
 XX  
 XX 16-MAR-2001; 2001US-00809391.  
 PF  
 XX

PR 07-MAR-1997; 97US-0038621P.  
 PR 07-MAR-1997; 97US-0040162P.  
 PR 07-MAR-1997; 97US-0040163P.  
 PR 07-MAR-1997; 97US-0040333P.  
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 PR 23-MAY-1997; 97US-0047586P.  
 PR 23-MAY-1997; 97US-0047587P.  
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 PR 06-JUN-1997; 97US-0048964P.  
 PR 06-JUN-1997; 97US-0048974P.  
 PR 08-JUL-1997; 97US-0051928P.  
 PR 16-JUL-1997; 97US-0052874P.  
 PR 18-AUG-1997; 97US-0055724P.  
 PR 22-AUG-1997; 97US-0056630P.  
 PR 22-AUG-1997; 97US-0056631P.  
 PR 22-AUG-1997; 97US-0056632P.  
 PR 22-AUG-1997; 97US-0056636P.  
 PR 22-AUG-1997; 97US-0056637P.  
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 PR 22-AUG-1997; 97US-0056862P.  
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 PR 22-AUG-1997; 97US-0056880P.  
 PR 22-AUG-1997; 97US-0056881P.  
 PR 22-AUG-1997; 97US-0056882P.  
 PR 22-AUG-1997; 97US-0056884P.  
 PR 22-AUG-1997; 97US-0056886P.  
 PR 22-AUG-1997; 97US-0056887P.  
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 PR 22-AUG-1997; 97US-0056889P.  
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 PR 22-AUG-1997; 97US-0056909P.  
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 PR 22-AUG-1997; 97US-0056911P.  
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 PR 05-SEP-1997; 97US-0057669P.  
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 PR 12-SEP-1997; 97US-0058785P.  
 PR 09-OCT-1997; 97US-0061660P.  
 PR 06-MAR-1998; 98MO-US004493.  
 PR 08-SEP-1998; 98US-00149476.  
 PR 17-MAR-2000; 2000US-0190068P.  
 XX  
 PA (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (CART/) CARTER K C.  
 PA (BEDN/) BEDNARIK D P.  
 PA (ENDR/) ENDRESS G A.  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (FENG/) FENG P.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (DUAN/) DUAN D R.  
 PA (HUJJ/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (FISC/) FISCHER C L.  
 PA (EBNE/) EENER R.  
 PA (BREW/) BREWER L A.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (LAPL/) LAPLEUR D W.  
 PA (LIYY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (KYAW/) KYAW H.  
 XX  
 PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednariak DP;  
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
 PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
 PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX WPI: 2003-521800/49.  
 DR P-PSDB; ABO34617.  
 XX  
 PT New genes and its encoded prostate cancer antigen proteins, useful for  
 PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
 PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
 PT ischemia.  
 XX Claim 4; SEQ ID NO 254; 260pp; English.  
 PS The present invention relates to the isolation of novel human secreted  
 XX proteins and the polynucleotide sequences encoding them. The invention  
 CC

CC also discloses vectors, host cells, antibodies, and recombinant methods  
 CC for producing human secreted proteins. The polypeptide and polynucleotide  
 CC sequences for the secreted proteins are useful for preventing, treating,  
 CC ameliorating or diagnosing medical conditions such as hyperproliferative  
 CC disorders (e.g. leukemia or breast cancers), wounds, reproductive  
 CC disorders, blood-related disorders (e.g. haemophilia or  
 CC thrombocytopenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
 CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,  
 CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),  
 CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
 CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
 CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
 CC disorders, neurological disorders (e.g. Alzheimer's disease or  
 CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
 CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
 CC ACD82641-ACD82950 encode human secreted proteins or their fragments.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC USPTO web site at [seqdata.uspto.gov/psipndbentry.html](http://seqdata.uspto.gov/psipndbentry.html)

XX SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 1-25e-64 Length: 1766  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ACD82884 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 287 GCGGTGCACGATCTGATTTCTGAGAGATTCAGACAGCTGGGTTCTTCTTGGCACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 347 AGCGTCAATGCTGCTTCCCTGGCAGCTTTCAGTGTCTCAGTGTGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGlnAla 60  
 Db 407 ATCTGCGCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCACCAAGCT 466  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 467 GTACAGAAGTCAGAGAAGGCCATCCATTCAGAGCCCTACCTGGCAGCTAGACATTA 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 527 TCCTCAGAAGCTTTCATTAATACATGATGCTGCATCATCAACAGGCGCCCTG 586  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AACTCATATTGCTCTCTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 647 TTCATGCTGCTGATGACCTATGTTGCTGCTGTTTAAAGGAATCACCTTCTAATTC 706  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 707 GCTGAACCTGCTCATTTTCTAGTGCCGATGTTCTATGAGAAGTACAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTTGGCATCCCGCAGATCAGACCAAGTCAATGTTCAAAAGATCCAGCAAAA 826  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 827 CTCCTTGAATCGCCAAAAAAGGAGGAGAA 856

RESULT 78

AD122969  
 ID AD122969 standard; cDNA; 1766 BP.  
 XX AC AD122969;  
 DT 22-APR-2004 (first entry)  
 XX DE cDNA encoding novel human secreted protein seq id 254.  
 XX KW cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.  
 XX OS Homo sapiens.  
 XX PN US2003175858-A1.  
 XX PD 18-SEP-2003.  
 XX PF 18-JUN-2001; 2001US-00882171.  
 XX PR 07-MAR-1997; 97US-0038621P.  
 PR 07-MAR-1997; 97US-0040162P.  
 PR 07-MAR-1997; 97US-0040163P.  
 PR 07-MAR-1997; 97US-0040333P.  
 PR 07-MAR-1997; 97US-0040334P.  
 PR 07-MAR-1997; 97US-0040336P.  
 PR 07-MAR-1997; 97US-0040628P.  
 PR 11-APR-1997; 97US-0043311P.  
 PR 11-APR-1997; 97US-0043312P.  
 PR 11-APR-1997; 97US-0043313P.  
 PR 11-APR-1997; 97US-0043314P.  
 PR 11-APR-1997; 97US-0043315P.  
 PR 11-APR-1997; 97US-0043568P.  
 PR 11-APR-1997; 97US-0043569P.  
 PR 11-APR-1997; 97US-0043576P.  
 PR 11-APR-1997; 97US-0043578P.  
 PR 11-APR-1997; 97US-0043580P.  
 PR 11-APR-1997; 97US-0043669P.  
 PR 11-APR-1997; 97US-0043670P.  
 PR 11-APR-1997; 97US-0043671P.  
 PR 11-APR-1997; 97US-0043672P.  
 PR 11-APR-1997; 97US-0043674P.  
 PR 23-MAY-1997; 97US-0047492P.  
 PR 23-MAY-1997; 97US-0047500P.  
 PR 23-MAY-1997; 97US-0047501P.  
 PR 23-MAY-1997; 97US-0047502P.  
 PR 23-MAY-1997; 97US-0047503P.  
 PR 23-MAY-1997; 97US-0047581P.  
 PR 23-MAY-1997; 97US-0047582P.  
 PR 23-MAY-1997; 97US-0047583P.  
 PR 23-MAY-1997; 97US-0047584P.  
 PR 23-MAY-1997; 97US-0047585P.  
 PR 23-MAY-1997; 97US-0047586P.  
 PR 23-MAY-1997; 97US-0047587P.  
 PR 23-MAY-1997; 97US-0047588P.  
 PR 23-MAY-1997; 97US-0047589P.  
 PR 23-MAY-1997; 97US-0047590P.  
 PR 23-MAY-1997; 97US-0047592P.  
 PR 23-MAY-1997; 97US-0047593P.  
 PR 23-MAY-1997; 97US-0047594P.  
 PR 23-MAY-1997; 97US-0047595P.  
 PR 23-MAY-1997; 97US-0047596P.  
 PR 23-MAY-1997; 97US-0047597P.  
 PR 23-MAY-1997; 97US-0047598P.  
 PR 23-MAY-1997; 97US-0047599P.  
 PR 23-MAY-1997; 97US-0047600P.  
 PR 23-MAY-1997; 97US-0047601P.  
 PR 23-MAY-1997; 97US-0047612P.  
 PR 23-MAY-1997; 97US-0047613P.  
 PR 23-MAY-1997; 97US-0047614P.  
 PR 23-MAY-1997; 97US-0047615P.  
 PR 23-MAY-1997; 97US-0047617P.  
 PR 23-MAY-1997; 97US-0047618P.  
 PR 23-MAY-1997; 97US-0047632P.



PR	23-MAY-1997;	97US-0047633P.
PR	06-JUN-1997;	97US-0048964P.
PR	06-JUN-1997;	97US-0048974P.
PR	13-JUN-1997;	97US-0049610P.
PR	08-JUL-1997;	97US-0051926P.
PR	16-JUL-1997;	97US-0052874P.
PR	18-AUG-1997;	97US-0055724P.
PR	22-AUG-1997;	97US-0056630P.
PR	22-AUG-1997;	97US-0056631P.
PR	22-AUG-1997;	97US-0056632P.
PR	22-AUG-1997;	97US-0056633P.
PR	22-AUG-1997;	97US-0056637P.
PR	22-AUG-1997;	97US-0056662P.
PR	22-AUG-1997;	97US-0056664P.
PR	22-AUG-1997;	97US-0056845P.
PR	22-AUG-1997;	97US-0056862P.
PR	22-AUG-1997;	97US-0056864P.
PR	22-AUG-1997;	97US-0056872P.
PR	22-AUG-1997;	97US-0056874P.
PR	22-AUG-1997;	97US-0056875P.
PR	22-AUG-1997;	97US-0056876P.
PR	22-AUG-1997;	97US-0056877P.
PR	22-AUG-1997;	97US-0056878P.
PR	22-AUG-1997;	97US-0056879P.
PR	22-AUG-1997;	97US-0056880P.
PR	22-AUG-1997;	97US-0056881P.
PR	22-AUG-1997;	97US-0056882P.
PR	22-AUG-1997;	97US-0056884P.
PR	22-AUG-1997;	97US-0056886P.
PR	22-AUG-1997;	97US-0056887P.
PR	22-AUG-1997;	97US-0056888P.
PR	22-AUG-1997;	97US-0056889P.
PR	22-AUG-1997;	97US-0056892P.
PR	22-AUG-1997;	97US-0056893P.
PR	22-AUG-1997;	97US-0056894P.
PR	22-AUG-1997;	97US-0056903P.
PR	22-AUG-1997;	97US-0056908P.
PR	22-AUG-1997;	97US-0056909P.
PR	22-AUG-1997;	97US-0056910P.
PR	22-AUG-1997;	97US-0056911P.
PR	05-SEP-1997;	97US-0057650P.
PR	05-SEP-1997;	97US-0057669P.
PR	05-SEP-1997;	97US-0057761P.
PR	12-SEP-1997;	97US-0058785P.
PR	09-OCT-1997;	97US-0061660P.
PR	06-MAR-1998;	98WO-US004493.
PR	08-SEP-1998;	98US-00149476.
PR	17-MAR-2000;	2000US-0190068P.
PR	16-MAR-2001;	2001US-00809391.
XX	(RUBE/) RUBEN S M.	
PA	(ROSE/) ROSEN C A.	
PA	(SOPE/) SOPPET D R.	
PA	(CART/) CARTER K C.	
PA	(BEDN/) BEDNARIK D P.	
PA	(ENDR/) ENDRESS G A.	
PA	(YUGG/) YU G.	
PA	(NIJJ/) NI J.	
PA	(FENG/) FENG P.	
PA	(YOUN/) YOUNG P E.	
PA	(GREE/) GREENE J M.	
PA	(FERR/) FERRIE A M.	
PA	(DUAN/) DUAN D R.	
PA	(HUIJ/) HU J.	
PA	(FLOR/) FLORENCE K A.	
PA	(OLSE/) OLSEN H S.	
PA	(FISC/) FISCHER C L.	
PA	(EBNE/) EBNER R.	
PA	(BREW/) BREWER L A.	
PA	(MOOR/) MOORE P A.	
PA	(SHIY/) SHI Y.	
PA	(LAFI/) LAFLEUR D W.	
PA	(LIYY/) LI Y.	
PA	(ZENG/) ZENG Z.	
PA	(KYAW/) KYAW H.	
XX	Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP,	
PI	Duanas GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;	
PI	Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;	
PI	Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;	
XX	WPI; 2003-898535/82.	
DR	P-PSDB; ADI23278.	
XX	New nucleic acid molecule, useful for preparing a medicament for	
PT	diagnosing, preventing, treating or ameliorating a medical condition	
PT	e.g., cancer.	
XX	Claim 1; SEQ ID NO 254; 256bp; English.	
XX	The invention describes an isolated nucleic acid comprising a sequence	
CC	having 95 % identity with: a polynucleotide fragment of a sequence not	
CC	given in the specification, or its allelic variant; a polynucleotide	
CC	fragment of the cDNA sequence; a polynucleotide sequence encoding a	
CC	polypeptide, or its fragment, domain, epitope or species homologue; or a	
CC	polynucleotide that hybridises under stringent conditions to any one of	
CC	the sequences of (a)-(c). The nucleic acid is useful for preparing a	
CC	medicament for diagnosing, preventing, treating or ameliorating a medical	
CC	condition e.g., cancer. The sequence encodes a novel human secreted	
CC	protein of the invention.	
XX	Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;	
SQ		
Alignment Scores:		
Pred. No.:	1.25e-64	Length: 1766
Score:	622.50	Matches: 113
Percent Similarity:	81.05%	Conservative: 41
Best Local Similarity:	59.47%	Mismatches: 35
Query Match:	67.30%	Indels: 1
DB:	10	Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x ADI22969 (1-1766)		
Oy	1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20	
Db	287 GCGGTGCACCATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCAC 346	
Oy	21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40	
Db	347 ACGCTGATCATGCTGCTTCCTCGGACGCTTCAGTGTCATCATGCTGGTTCTTACCCTC 406	
Oy	41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60	
Db	407 ATCTGGCTCTTCTCTGTGCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 466	
Oy	61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80	
Db		



PS Claim 3; SEQ ID NO 254; 142pp; English.

XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and its complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)). The present sequence  
CC represents a human secreted protein cDNA.

SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

#### Alignment Scores:

Pred. No.:	1.25e-64	Length:	1766
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADH73971 (1-1766)

QY	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
DB	287	CGGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC	346
QY	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
DB	347	ACGCTGATCATGCTGCTTCCCTGGCAGCTTTACGTGTCATCAGTGTGGTTCCTTACCTC	406
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
DB	407	ATCTGGCTCTTCTCTGTCCATCAGCTTTCAGGATCTCAAGTCGCTCATCCAGCT	466
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
DB	467	GTACAGAAGTCAGAAGAAGGCCCATCCATTCAAAGCTTACCTGGAGCTAGACATTA	526
QY	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
DB	527	TCTTCAGAGCTTTCATTAATACATGATGTCGCTGATGTCATCAACAGGCGCTG	586
QY	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
DB	587	AAATCATTTATTCGCTCTCTCTGCTAGAGATCTGTTGACTCTTGAAGCTGCTGTC	646
QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
DB	647	TTATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTTCTTAATCTT	706
QY	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
DB	707	GCTGAACGTCTCATTTTACGTCTCCGATTTGTATGAGAGATGATCAACAGCCAGATTGAT	766
QY	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
DB	767	CACATATGTTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAA	826
QY	181	IleProGlyLeu---LysArgLysAlaAsp	189
DB	827	CTCCCTGGAATCGCCAAAAAAGGCAGAA	856

#### RESULT 80

ID	ADM36177	standard; DNA; 1911 BP.
AC	ADM36177;	
DT	03-JUN-2004	(first entry)
DE	Human RTN3 isoform VI coding sequence, SEQ ID 60.	
KW	Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;	
XX	amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	124..834
FT		/*tag= a
FT		/product= "RTN3 isoform VI"
XX	WO2004001069-A2.	
XX	31-DEC-2003.	
XX	20-JUN-2003; 2003WO-FR001910.	
PR	25-JUN-2002; 2002FR-00007846.	
XX	(UWPA-) UNIV PASTEUR LOUIS.	
PI	Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;	
PI	Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;	
DR	WPI; 2004-071743/07.	
XX	P-PSDB; ADM36178.	
PT	Diagnosing, prognosing and monitoring neuromuscular disease, particularly	
PT	amyotrophic lateral sclerosis, comprises detecting modulation of the	
PT	reticulon 3 gene.	
PS	Claim 17; SEQ ID NO 60; 116pp; French.	
XX	The present invention relates to a method for diagnosing, or evaluating	
CC	progression of, a neuromuscular disease. The method comprises detecting	
CC	modulation of the expression of a product (I) of the RTN (reticulon)3	
CC	gene. Differential expression of RTN3 is a specific marker of	
CC	neuromuscular disease, allowing early diagnosis from readily available	
CC	muscle biopsies. The method is also useful for determining the efficacy	
CC	of treatment. The method is used to diagnose (also to evaluate	
CC	progression or therapy of) neuromuscular disorders, specifically	
CC	amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies	
CC	specific for isoforms of RTN3 or oligonucleotides (antisense sequences or	
CC	small interfering RNA) that can block/reduce expression of these isoforms	
CC	are useful for treating neuromuscular diseases and (ii) cells that	
CC	express RTN3 are useful in screening for therapeutic agents. The present	
CC	sequence is a RTN3 DNA sequence used to illustrate the invention.	
XX	Sequence 1911 BP; 488 A; 463 C; 406 G; 554 T; 0 U; 0 Other;	

#### Alignment Scores:

Pred. No.:	1.4e-64	Length:	1911
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36177 (1-1911)

QY	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
DB	262	CGGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC	321

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 AGCGTCATGCTGCTTCCCTCCGCGAGCTTTTCAGTGTCTCATGCTGCTTTTACCTC 381
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 382 ATCTCTGGCTCTCTCTCTGTCACCATCAGCTTCAGGATCTACAGGTCCTGTCACAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 442 GTACAGAACTCAGAGAAGCGCCATCCATTCAAGGCTACTCGACGTAGACATTACTCTG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 502 TCTCAGAAAGCTTTCATTAATACATGAATGCTGCTGATGTCACATCAACAGGGCCCTG 561
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAsp 120
Db 562 AAATCATATTGCTGCTCTCTCTGTTGGTGAAGATCTGTTGATCTCTTGAAGCTGGCTGC 621
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 622 TTCATGTGCTGATGACCTATGTTGTGCTGTTTAAACGAATCACCTCTCAATCTT 681
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 682 GTGAATCTCTATTTTCAGTGTCCGATGTTCTATGATGAGATCAAGACCCAGATTGAT 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 742 CACTATGTTGGATCCCGAGATCAGACAGATCAATGTTGTAAGAAGATCCAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 802 CTCCTCGGAATCGCCAAAAGGAGGAGCA 831
RESULT 81
ABA09204
ID ABA09204 standard; cDNA; 1915 BP.
XX
AC ABA09204;
XX
XX 11-JAN-2002 (first entry)
XX
DE Human neuroendocrine-specific protein-like homologue cDNA, SEQ ID NO:980.
XX
KW Human; cytokine; cell proliferation; tissue growth; immunomodulation; growth factor;
KW haematopoiesis regulation; tumour growth; tumour growth; tumour growth; tumour growth;
KW inhibin; chemotaxis; chemokinesis; thrombolytic; thrombolytic; thrombolytic;
KW proliferation; metastasis; cancer; tumour; tumour; tumour; tumour; tumour;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; anti-inflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytosolic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.
XX
OS Homo sapiens.
XX
XX WO200157188-A2.
XX
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US003800.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-FEB-2000; 2000US-00560875.
XX
XX (HYSE-) HYSEQ INC.
```

```
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
DR P-PSDB; ABB11960.
XX
XX Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
XX Claim 1; Page 838; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX
SQ Sequence 1915 BP; 492 A; 463 C; 411 G; 549 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 1.4e-64 Length: 1915
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: Gaps: 4
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABA09204 (1-1915)

```
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 287 GCGGTGCACGATCTGATTTCTTGAGAGATGTGAAGAGACTGGGTTTCTTTGGCACC 346
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 347 AGCTGATCATCTGCTTCTTCCCTGCGAGCTTTCAGTGTATCAGTGTGGTGTCTTACCTC 406
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 407 ATCTCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCAAGCT 466
```

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla11e 80  
 Db 467 GTACAGAGTCAAGAGAGCCATCCATTCAAGGCTACCTGGAGTACATTAAGTCTG 526  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100  
 Db 527 TCCTCAGAGCTTTCCATATAATACATGAATGCTGCTGCTGCTGCTGCTGCTG 586  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAATCATATTGCTGCTCTTCTGAGAGATCTGCTGCTGCTGCTGCTGCTGCTG 646  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 647 TTCATGTGCTGATGACCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 706  
 Qy 141 AlaLeuLeuSerLeuPheSerIleProValleTyrGluArgHisGlnValGlnLeuAsp 160  
 Db 707 GCTGAAGTCTCATTTTTCAGTGTCCGATTTGCTATGAGAGATGACAGACCCAGATTGAT 766  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysLeuGlnAlaLys 180  
 Db 767 CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 826  
 Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 827 CTCCTGGAATGCCCAAAAAGGAGCAAA 856

RESULT 82  
 AAF93902  
 ID AAF93902 standard; cDNA; 2530 BP.  
 AC AAF93902;  
 XX  
 XX 23-MAY-2001 (first entry)  
 XX  
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0103.  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1067182-A2.  
 PD 10-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114090.  
 PR 08-JUL-1999; 95JP-00194179.  
 PR 11-JAN-2000; 2000JP-00118775.  
 PR 02-MAY-2000; 2000JP-00183766.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 XX WPI; 2001-093989/11.  
 DR P-PSDB; AAB88475.  
 XX  
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.  
 XX  
 PS Claim 1; SEQ ID NO 317; 609pp + Sequence Listing; English.  
 XX  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene

CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes

XX SQ Sequence 2530 BP; 665 A; 577 C; 534 G; 754 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 2,07e-64 Length: 2530  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 5 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF93902 (1-2530)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 276 GCGGTGCACGATCTGATTTCTCGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 335  
 Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 336 ACGCTGATCATCTGCTGCTTCCCTGGCAGCTTTCAGTGTCTCATCGTGTGGTTTCTTACCTC 395  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 396 ATCTGTGCTCTTCTCTCTGTCACCATCAGCTTCAGATCTACAAAGTCCGTCATCCAGCT 455  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla11e 80  
 Db 456 GTACAGAGTCAAGAGAGCCATCCATTCAAGGCTACCTGGAGTACATTAAGTCTG 515  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100  
 Db 516 TCCTCAGAGCTTTCCATATAATACATGAATGCTGCCATGTCACATCAAGAGGCGCTG 575  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 576 AAATCATATTGCTGCTCTTCTGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 635  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 636 TTCATGTGCTGATGACCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695  
 Qy 141 AlaLeuLeuSerLeuPheSerIleProValleTyrGluArgHisGlnValGlnLeuAsp 160  
 Db 696 GCTGAAGTCTCATTTTTCAGTGTCCGATTTGCTATGAGAGATGACAGACCCAGATTGAT 755  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysLeuGlnAlaLys 180  
 Db 756 CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 815  
 Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 816 CTCCTGGAATGCCCAAAAAGGAGCAAA 845

RESULT 83  
 ADL02184  
 ID ADL02184 standard; cDNA; 2559 BP.  
 XX

AC ADL02184;  
 XX 06-MAY-2004 (first entry)  
 XX Human neuroendocrine specific protein linked gene, hNSPL1, cDNA.  
 DE ss; gene; human; neuroendocrine specific protein linked gene; hNSPL1;  
 KW glia cell; tumour; nervous system disease.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 137..847  
 FT /\*tag= a  
 FT /product= "hNSPL1"  
 XX  
 XX CN1408868-A.  
 XX 09-APR-2003.  
 XX 25-SEP-2001; 2001CN-00141445.  
 XX 25-SEP-2001; 2001CN-00141445.  
 XX (PREC-) PRECLINICAL MEDICINE INST CHINESE ACAD.  
 XX Yuan J, Qiang B, Peng X;  
 XX WPI; 2003-713650/68.  
 DR P-PSDB; ADL02185.  
 XX  
 XX Gene NSPL1 with expression difference in human normal neuroglia cell and  
 PT neuroglia cell tumor.  
 XX  
 XX Disclosure; Page 7-8; 34pp; Chinese.  
 XX The present invention relates to human neuroendocrine specific protein  
 CC linked gene, hNSPL1, highly expressed in human nerve system. The protein  
 CC is located in the endoplasmic reticulum membrane of cell, is highly  
 CC expressed in normal nerve cell and has obvious difference in expression  
 CC inside glia cell and inside glia cell tumour. It may have important  
 CC effect in maintaining the physiological function of nerve system and in  
 CC some nerve system disease occurrence. The present sequence represents  
 CC human neuroendocrine specific protein linked gene, hNSPL1, cDNA.  
 XX  
 XX Sequence 2559 BP; 694 A; 577 C; 533 G; 755 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 2,11e-64 Length: 2559  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADL02184 (1-2559)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 275 GCGGTGCACGATCTGATTCTTCGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGCACC 334  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 335 ACGCTGATCATGTGCTTCTCCCTGGCAGCTTTCAGTGTTCATCATGTGTTCTTACCTC 394  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 395 ATCTGGCTTCTTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 454  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 455 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACTGTCAGCTAGACATTACTCTG 514

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 515 TCCTCAGAGCTTTCCATAATTACATGATGCTGCCATGGTGCCATCAACAGGGCCCTG 574  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 575 AAACATATATTCGTCCTCTTCTGCTAGAGATCTGGTGTGACTCTTGAAGCTGGCTGC 634  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 635 TTCATGTGGCTGATGACCTATCTTGGTGTGCTTTTAAACGGAATCACCTTCTTAATCTT 694  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 695 GCTGAACGTCTCAATTTTCAGTGTCCGATTTGTATGAGAAGTACAAAGACCCAGATTGAT 754  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 755 CACTATGTGGCATCGCCGAGATCAGACCAAGTCAATTTGTTGAAAAGATCCACAGCAAA 814  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 815 CTCCTGGAATGCCCAAAAAAAGGCAGAA 844  
 RESULT 84  
 AAV59749  
 ID AAV59749 standard; DNA; 2664 BP.  
 XX  
 AC AAV59749;  
 XX  
 XX 19-JAN-1999 (first entry)  
 XX Human secreted protein gene 92 clone HAUBL57.  
 DE  
 XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9839448-A2.  
 XX  
 XX 11-SEP-1998.  
 XX 06-MAR-1998; 98WO-US004493.  
 PF 07-MAR-1997; 97US-0038621P.  
 PR 07-MAR-1997; 97US-0040161P.  
 PR 07-MAR-1997; 97US-0040162P.  
 PR 07-MAR-1997; 97US-0040163P.  
 PR 07-MAR-1997; 97US-0040333P.  
 PR 07-MAR-1997; 97US-0040334P.  
 PR 07-MAR-1997; 97US-0040336P.  
 PR 07-MAR-1997; 97US-0040626P.  
 PR 11-APR-1997; 97US-0043311P.  
 PR 11-APR-1997; 97US-0043312P.  
 PR 11-APR-1997; 97US-0043313P.  
 PR 11-APR-1997; 97US-0043314P.  
 PR 11-APR-1997; 97US-0043315P.  
 PR 11-APR-1997; 97US-0043568P.  
 PR 11-APR-1997; 97US-0043569P.  
 PR 11-APR-1997; 97US-0043576P.  
 PR 11-APR-1997; 97US-0043578P.  
 PR 11-APR-1997; 97US-0043580P.  
 PR 11-APR-1997; 97US-0043669P.  
 PR 11-APR-1997; 97US-0043670P.  
 PR 11-APR-1997; 97US-0043671P.  
 PR 11-APR-1997; 97US-0043672P.

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PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.

PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC,
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM,
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA,
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI: 1998-506364/43.
XX P-PSDB; AAW74964.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 475-476; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 92 from
CC the human cDNA clone HAU5L57 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused to
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W75026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)
XX
XX SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

Alignment Scores:
Pred. No.: 2.23e-64 Length: 2664
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 2 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x AAV59749 (1-2664)

QY 1 SerValValAspLeuLeuTy-TrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 262 GCGGTGCAGATCTGATTCTTGGAGAGATGTGAAGAAGACTGGGTGTCTTGGACC 321
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 322 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTCCTACCTC 381
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 382 ATCTGGGCTCTCTCTGTCCATCAGTTCAGGATCTACAGATCCGCTCATCAAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 442 GTACAGAAAGTCAGAGAAGGCCATCCATTCAAAGCCTACCTGGAGTACATTAATCTCTG 501
QY 81 SerGluGluLeuValGlnLysTy-SerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 502 TCCTCAGAAAGCTTCCATAATTACATGATGCTGCCATGCTGTCATCAACAGGGCCCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaVal 120
DB 562 AAACATATTTCGTCTCTTTCTGTGTAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 621
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QY      121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db      622 TTCAATGGCTGATGACCTATGTTGCTGCTGTTTTTAACGAATCACCTTCTAATTCCT 681
QY      141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db      682 GCTGAACCTGCTATTTCATGTCGCGATTGTCATGAGAAGTACCAAGACCCAGATTGAT 741
QY      161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db      742 CACTATGTTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 801
QY      181 IleProGlyLeu---LysArgIysAlaAsp 189
Db      802 CTCCTTGAATGCCCAAAAAAAGGCAGAA 831

RESULT 85
ABS73742
ID ABS73742 standard; cDNA; 2664 BP.
XX
AC ABS73742;
XX
DT 15-JAN-2003 (first entry)
XX
DE Human cDNA #3 for novel secreted protein gene 92.
XX
KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
XX
XX preservative; nutritional.
XX
OS Homo sapiens.
XX
PN US6420526-B1.
XX
PD 16-JUL-2002.
XX
PF 08-SEP-1998; 98US-00149476.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
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PR 23-MAY-1997; 97US-0047598P.
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PR 05-SEP-1997; 97US-0057669P.
PR 12-SEP-1997; 97US-0057761P.
PR 02-OCT-1997; 97US-0058785P.
PR 06-MAR-1998; 97US-0061060P.
XX 98WO-US004493.
XX
```



## (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;  
 PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;  
 PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX

DR WPI; 2002-634796/68.  
 DR P-PSDB; ABG95424.

XX New isolated human secreted protein for diagnosing, preventing, treating  
 PT or ameliorating medical conditions and used as a food additive or  
 PT preservative.

PS Example 1; SEQ ID NO 255; 129pp; English.

XX The invention relates to an isolated protein that is one of 186 human  
 CC secreted proteins, given in the specification, encoded by one of 309 cDNA  
 CC sequences also given in the specification. The protein is used in a  
 CC pharmaceutical composition used to prevent, treat or ameliorate a medical  
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angioneuromatosis, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. The present sequence represents a cDNA derived from a gene  
 CC encoding one of the novel human secreted proteins of the invention. Note:  
 CC This sequence did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=642052681

SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

## Alignment Scores:

Pred. No.: 2,236-64 Length: 2664  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 6 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABS73742 (1-2664)

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 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrIle 40  
 DB 322 AGCTGATCATCTCTCTCTGTCACCATCAGTTTCAGTGTCATCAGTGTTCTTACCTC 381  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 382 ATCTGGCTCTTCTCTGTCTGTCACCATCAGTTTCAGATCTCAAGTCGTCATCCAGCT 441  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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 QY 81 SerGluGluLeuValGlnLysTyrSerLeuSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 502 TCTTCAGAAAGCTTTCCATAATTTACATGATGCTGTCATGCTGTCATCAACAGGCGCCCTC 561  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLeuPheAlaVal 120

DB 562 AAACCTATTATTCTGTCCTCTTCTGGTAGAAGACTCTGGTGTGACTCTCTGAAGCTGGCTGTC 621  
 QY 121 LeuMetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 622 TTCATGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 682 GCTGAACCTGCTCATTTTTCAGTGTCCGATTTGTCATGATGATGATGATGATGATGATGAT 741  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 742 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCAACAGCAAAA 801  
 QY 181 IleProGlyLeu--LysArgLysAlaAsp 189  
 DB 802 CTCCTGGAATCGCCAAAAGGAGCAAA 831

## RESULT 86

ACD82885

ID ACD82885 standard; cDNA, 2664 BP.

XX ACD82885;

XX 22-SEP-2003 (first entry)

DE cDNA sequence #245 containing coding region of a human secreted protein.

XX Human; secreted protein; hyperproliferative disorder; leukaemia;  
 KW breast cancer; wound; reproductive disorder; blood-related disorder;  
 KW haemophilia; thrombocytopenia; immunodeficiency; thymic hypoplasia;  
 KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;  
 KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;  
 KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;  
 KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;  
 KW angina pectoris; cerebral ischaemia; congenital heart defect;  
 KW respiratory disorder; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;  
 KW immunosuppressive; antibacterial; haemostatic; thrombolytic;  
 KW anticoagulant; neuroprotective; thymomimetic; antiallergic;  
 KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;  
 KW cerebroprotective; cardiant; nootropic; antiparkinsonian;  
 KW antinflammatory; gene; ss.

XX Homo sapiens.

XX US2003049618-A1.

XX 13-MAR-2003.

XX 16-MAR-2001; 2001US-00809391.

XX 07-MAR-1997; 97US-0038621P.

XX 07-MAR-1997; 97US-0040162P.

XX 07-MAR-1997; 97US-0040163P.

XX 07-MAR-1997; 97US-0040333P.

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PR 12-SEP-1997; 97US-0058785P.  
PR 09-OCT-1997; 97US-0061660P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
PR 17-MAR-2000; 2000US-0190068P.  
XX  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHLY/) SHI Y.  
PA (LAFLE/) LAFLEUR D W.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
XX  
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX WPI: 2003-521800/49.  
DR P-PSDB; ABO34618.  
XX  
PT New genes and its encoded prostate cancer antigen proteins, useful for  
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
PT ischemia.  
XX  
PS Claim 4; SEQ ID NO 255; 260pp; English.  
XX  
CC The present invention relates to the isolation of novel human secreted  
CC proteins and the polynucleotide sequences encoding them. The invention  
CC also discloses vectors, host cells, antibodies, and recombinant methods  
CC for producing human secreted proteins. The polypeptide and polynucleotide  
CC sequences for the secreted proteins are useful for preventing, treating,  
CC ameliorating or diagnosing medical conditions such as hyperproliferative  
CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive  
CC disorders, blood-related disorders (e.g. haemophilia or  
CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,  
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),  
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
CC disorders, neurological disorders (e.g. Alzheimer's disease or  
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
CC ACD2641-ACD82950 encode human secreted proteins or their fragments.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/paipaDIDEntry.html](http://seqdata.uspto.gov/paipaDIDEntry.html)  
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 PR 22-AUG-1997; 97US-0056879P.  
 PR 22-AUG-1997; 97US-0056880P.  
 PR 22-AUG-1997; 97US-0056881P.  
 PR 22-AUG-1997; 97US-0056882P.  
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 PR 22-AUG-1997; 97US-0056911P.  
 PR 05-SEP-1997; 97US-0057650P.  
 PR 05-SEP-1997; 97US-0057669P.  
 PR 12-SEP-1997; 97US-0057761P.  
 PR 09-OCT-1997; 97US-0058785P.  
 PR 06-MAR-1998; 98WO-US004493.  
 PR 08-SEP-1998; 98US-00149476.  
 PR 17-MAR-2000; 2000US-0190068P.  
 PR 16-MAR-2001; 2001US-00809391.  
 XX  
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 PA (NIJU/) NI J.  
 PA (FENG/) FENG P.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERE/) FERRIE A M.  
 PA (DUAN/) DUAN D R.  
 PA (HUJU/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (FISC/) FISCHER C L.  
 PA (EBNE/) EBNER R.  
 PA (BREW/) BREWER L A.  
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 PA (SHIY/) SHI Y.  
 PA (LAFLE/) LAFLEUR D W.  
 PA (LIYY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (KYAW/) KYAW H.  
 XX  
 PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednariak DP;  
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
 PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
 PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX WPI; 2003-898535/82.  
 DR P-PSDB; ADI23279.  
 XX  
 PT New nucleic acid molecule, useful for preparing a medicament for  
 PT diagnosing, preventing, treating or ameliorating a medical condition  
 PT e.g., cancer.  
 XX  
 PS Claim 1; SEQ ID NO 255; 256pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid comprising a sequence  
 CC having 95 % identity with: a polynucleotide fragment of a sequence not  
 CC given in the specification, or its allelic variant; a polynucleotide

CC fragment of the cDNA sequence; a polynucleotide sequence encoding a  
 CC polypeptide, or its fragment, domain, epitope or species homologue; or a  
 CC polynucleotide that hybridises under stringent conditions to any one of  
 CC the sequences of (a)-(c). The nucleic acid is useful for preparing a  
 CC medicament for diagnosing, preventing, treating or ameliorating a medical  
 CC condition e.g., cancer. The sequence encodes a novel human secreted  
 CC protein of the invention.  
 XX  
 SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;  
 Alignment Scores:  
 Pred. No.: 2,23e-64 Length: 2664  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADI22970 (1-2664)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 262 GGGGTGCACGATCTGATTTCTCGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 321  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 322 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTGCATCAGTGTGGTTCTTACCTC 381  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 382 ATCTGGGCTCTCTCTCTGTCCACATCAGTTCAGATCTACAACTCGTCATCCAGCT 441  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 442 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 501  
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 Db 502 TCCTCAGAAGCTTTCCATAATTTACATGAATGTCCTGTCATCAACACAGGCCCTG 561  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 562 AAACATCATTTATTCGTCCTCTCTGTGAGAGATCTGGTTGACTCTCTGAAGCTGCTGTC 621  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 622 TTCATGTGGTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTCTCTAATTCCT 681  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 682 GCTGAACGTCTCATTTTCAGTGTCCGATGTGTATGAGAAGTACACAGCCAGATTGAT 741  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 742 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTAGTCAATTTGTGAAAAGATCCACGAAA 801  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 802 CTCCTCGGAATCGCAAAAAAAGGCAGAA 831  
 RESULT 88  
 ADH73972  
 ID ADH73972 standard; cDNA; 2664 BP.  
 XX  
 AC ADH73972;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Human secreted protein cDNA #245.  
 XX  
 KW human; secreted protein; cancer; haematopoietic disorder;  
 KW endocrine disorder; immune system disease; inflammatory disorder; es;  
 KW gene.

XX OS Homo sapiens.  
XX PN US2003225248-A1.  
XX PD 04-DEC-2003.  
XX PF 10-JUN-2002; 2002US-00164861.  
XX XX 07-MAR-1997; 97US-0038621P.  
PR 07-MAR-1997; 97US-0040161P.  
PR 07-MAR-1997; 97US-0040162P.  
PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040626P.  
PR 11-APR-1997; 97US-0043311P.  
PR 11-APR-1997; 97US-0043312P.  
PR 11-APR-1997; 97US-0043313P.  
PR 11-APR-1997; 97US-0043314P.  
PR 11-APR-1997; 97US-0043315P.  
PR 11-APR-1997; 97US-0043568P.  
PR 11-APR-1997; 97US-0043569P.  
PR 11-APR-1997; 97US-0043576P.  
PR 11-APR-1997; 97US-0043578P.  
PR 11-APR-1997; 97US-0043580P.  
PR 11-APR-1997; 97US-0043669P.  
PR 11-APR-1997; 97US-0043670P.  
PR 11-APR-1997; 97US-0043671P.  
PR 11-APR-1997; 97US-0043672P.  
PR 11-APR-1997; 97US-0043674P.  
PR 23-MAY-1997; 97US-0047492P.  
PR 23-MAY-1997; 97US-0047500P.  
PR 23-MAY-1997; 97US-0047501P.  
PR 23-MAY-1997; 97US-0047502P.  
PR 23-MAY-1997; 97US-0047503P.  
PR 23-MAY-1997; 97US-0047581P.  
PR 23-MAY-1997; 97US-0047582P.  
PR 23-MAY-1997; 97US-0047583P.  
PR 23-MAY-1997; 97US-0047584P.  
PR 23-MAY-1997; 97US-0047585P.  
PR 23-MAY-1997; 97US-0047586P.  
PR 23-MAY-1997; 97US-0047587P.  
PR 23-MAY-1997; 97US-0047588P.  
PR 23-MAY-1997; 97US-0047589P.  
PR 23-MAY-1997; 97US-0047590P.  
PR 23-MAY-1997; 97US-0047592P.  
PR 23-MAY-1997; 97US-0047593P.  
PR 23-MAY-1997; 97US-0047594P.  
PR 23-MAY-1997; 97US-0047595P.  
PR 23-MAY-1997; 97US-0047596P.  
PR 23-MAY-1997; 97US-0047597P.  
PR 23-MAY-1997; 97US-0047598P.  
PR 23-MAY-1997; 97US-0047599P.  
PR 23-MAY-1997; 97US-0047600P.  
PR 23-MAY-1997; 97US-0047601P.  
PR 23-MAY-1997; 97US-0047612P.  
PR 23-MAY-1997; 97US-0047613P.  
PR 23-MAY-1997; 97US-0047614P.  
PR 23-MAY-1997; 97US-0047615P.  
PR 23-MAY-1997; 97US-0047617P.  
PR 23-MAY-1997; 97US-0047618P.  
PR 23-MAY-1997; 97US-0047632P.  
PR 23-MAY-1997; 97US-0047633P.  
PR 06-JUN-1997; 97US-0048964P.  
PR 06-JUN-1997; 97US-0048974P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 08-JUL-1997; 97US-0051926P.  
PR 16-JUL-1997; 97US-0052874P.  
PR 18-AUG-1997; 97US-0055724P.  
PR 22-AUG-1997; 97US-0056630P.  
PR 22-AUG-1997; 97US-0056631P.  
PR 22-AUG-1997; 97US-0056632P.  
PR 22-AUG-1997; 97US-0056636P.  
PR 22-AUG-1997; 97US-0056637P.  
PR 22-AUG-1997; 97US-0056662P.  
PR 22-AUG-1997; 97US-0056664P.  
PR 22-AUG-1997; 97US-0056845P.  
PR 22-AUG-1997; 97US-0056862P.  
PR 22-AUG-1997; 97US-0056864P.  
PR 22-AUG-1997; 97US-0056872P.  
PR 22-AUG-1997; 97US-0056874P.  
PR 22-AUG-1997; 97US-0056875P.  
PR 22-AUG-1997; 97US-0056876P.  
PR 22-AUG-1997; 97US-0056877P.  
PR 22-AUG-1997; 97US-0056878P.  
PR 22-AUG-1997; 97US-0056879P.  
PR 22-AUG-1997; 97US-0056880P.  
PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
PR 22-AUG-1997; 97US-0056886P.  
PR 22-AUG-1997; 97US-0056887P.  
PR 22-AUG-1997; 97US-0056888P.  
PR 22-AUG-1997; 97US-0056889P.  
PR 22-AUG-1997; 97US-0056892P.  
PR 22-AUG-1997; 97US-0056893P.  
PR 22-AUG-1997; 97US-0056894P.  
PR 22-AUG-1997; 97US-0056903P.  
PR 22-AUG-1997; 97US-0056908P.  
PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 22-AUG-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057669P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 02-OCT-1997; 97US-0061060P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DM, Li Y, Zeng Z, Kyaw H;  
XX WPI; 2004-131264/13.  
DR P-PSDB; ADH74281.  
XX Isolated nucleic acid molecules encoding human secreted proteins, useful  
PT for preventing, diagnosing and treating disorders associated with  
PT aberrant expression and activity.  
XX Claim 3; SEQ ID NO 255; 142pp; English.  
XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and its complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)). The present sequence



Db 740 GCTGAAGTCTCATTTTCAGTGTCCGATGTGTATGAGAGTACAGACCCAGATTGAT 799  
 QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 800 CACTATGTTGGATCCCGAGATCAGACCAATGTTGTAAGATCCAGCAAA 859  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 860 CTCCTGGAATCCCAAAAAAGGCAGAA 889

RESULT 90  
 ID ADB58889 standard; DNA; 2773 BP.  
 XX  
 AC ADB58889;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Toxicity-related gene, SEQ ID 3915.  
 XX  
 KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
 KW drug screening; toxicity assay; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003064624-A2.  
 XX  
 PD 07-AUG-2003.  
 XX  
 PF 31-JAN-2003; 2003WO-US003194.  
 XX  
 PR 31-JAN-2002; 2002US-00060087.  
 PR 15-MAR-2002; 2002US-0364045P.  
 PR 15-MAR-2002; 2002US-0364055P.  
 PR 30-DEC-2002; 2002US-0436643P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
 XX  
 DR WPI; 2003-689530/65.  
 XX  
 PT Predicting a toxic effect of a compound, useful in identifying toxicity  
 PT markers in liver tissues or cells for drug screening and toxicity assays,  
 PT comprises preparing gene expression profile of tissue or cells exposed to  
 PT the compound.  
 XX  
 PS Claim 1; SEQ ID NO 3915; 1156pp; English.  
 XX  
 CC The present invention relates to a method for predicting a toxic effect  
 CC of a compound. The method comprises preparing a gene expression profile  
 CC of a tissue or cell sample exposed to the compound, and comparing the  
 CC gene expression profile to a database comprising SEQ ID 1-4925, where  
 CC differential expression of the gene indicates at least one toxic effect.  
 CC The method is useful for predicting at least one toxic effect of a  
 CC compound, predicting hepatotoxicity or the progression of a toxic effect  
 CC of a compound, identifying an agent that modulates the onset or  
 CC progression of a toxic response, predicting the cellular pathways that a  
 CC compound modulates in a cell, and identifying an agent that modulates at  
 CC least one activity of a protein. The method and compositions of the  
 CC present invention using a database of genes having liver toxin-induced  
 CC differential expression, are useful in identifying toxicity markers in  
 CC liver tissues or cells for drug screening and toxicity assays. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 2773 BP; 699 A; 653 C; 632 G; 789 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,366-64 Length: 2773  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41

Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADB58889 (1-2773)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 267 GCGGTGCATGATCTGATTTCTGGCGAGATGTGAAGAGACTGGTGTCTTTGGCACC 326  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 327 ACGCTGATCATGCTGCTCTCTGCGAGCTTTTCAGTGTATCAGTGTGCTCTTACCTC 386  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 387 ATCTGGGTCTACTCTCTGTCCATCAGCTTCAGAGTCTACAGTCTGTGTCTATCCAGCT 446  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 447 GTGCAGAGTTCAGAGAGAGGACATCCATTCAAGGCTTACCTGGATGTGGACATTACACTG 506  
 QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100  
 Db 507 TCCTCAGAAGCTTTCCACAGCTACATGAATGCTGCAATGGTGCATGTCAACAAGGCCCTC 566  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaVal 120  
 Db 567 AAATCATTTATTCGTCTCTTCTGTGTAAGACTTGGTTGACTCTCTTGAAGCTGGCTGTC 626  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 627 TTCAATGTCGTGATGATCACCCTAGCTCGTCTGCTGTTTAAAGGAAATTACCTCTTGATTCTC 686  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 687 GCCAGCTGCTGGTGTTCAGGCTCCCAATGCTATGAGAAGTATAAGACACAGATTGAC 746  
 QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 747 CACTATGTTGGGATTTGCCCGGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAG 806  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 807 CTTCCTGGAATCCCAAAAAAGGCAGAA 836

RESULT 91  
 ADM36171  
 ID ADM36171 standard; DNA; 1968 BP.  
 XX  
 AC ADM36171;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human RTN3 isoform III coding sequence, SEQ ID 54.  
 XX  
 KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulum 3;  
 KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 124..891  
 FT /\*tag= a  
 FT /product= "RTN3 isoform III"  
 XX  
 PN WO2004001069-A2.  
 XX  
 PD 31-DEC-2003.  
 XX  
 PF 20-JUN-2003; 2003WO-FR001910.  
 XX  
 PR 25-JUN-2002; 2002FR-00007846.

XX (UYPA-) UNIV PASTEUR LOUIS.  
PA Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX WPI; 2004-071743/07.  
DR F-PSDB; ADM36172.  
XX  
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX Claim 35; SEQ ID NO 54; 116pp; French.  
XX  
CC The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
SQ Sequence 1968 BP; 496 A; 482 C; 411 G; 579 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,92e-64 Length: 1968  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservative: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36171 (1-1968)

QY 2 ValValAspLeuLeuTyrrArgAspIleLeuLeuThrGlyValValPheGlyAlaSer 21  
DB 322 GTGCAGATCTGATTTCTGGAGATGTGAAGACCTGGTTCTTGGCCACCG 381  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 382 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCTCATGTTGGTTCTTACCTCATC 441  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
DB 442 CTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGCTCATCCAAGCTGA 501  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 502 CAGAAGTCAGAGAGGACCATCATTCAGGCTCTCTGAGCTAGACATCTCTGTCTCC 561  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 562 TCAGAGCTTTCATTAATACATGATGTGCGCATGTGCACATCAACAGGCGCTGAAA 621  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 622 CTCATTATTCTCTCTCTGGTAGAGATCTGTGTGACTCTCTGAGCTGGGTGCTCTTC 681  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuLeuIleLeuAla 141  
DB 682 ATGTGCTGATGACCTATGTGTGTCTGTTTAAACGGAATACCTCTCTTAATCTTGTCT 741  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 742 GAACCTGCTCATTTTCAGTGTGCCGATTGTCTATGAGAAGTACAAGACCCAGATTGATCAC 801

QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysPheAlaMetAlaLysIleGlnAlaLysIle 181  
DB 802 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAACTC 861  
QY 182 ProGlyLeu--LysArgLysAlaAsp 189  
DB 862 CCTGGAATCGCCCAAAAAAAGGCAGAA 888  
RESULT 92  
ADQ84465  
ID ADQ84465 standard; cDNA; 2250 BP.  
XX AC ADQ84465;  
XX  
DT 07-OCT-2004 (first entry)  
XX Human tumour-associated antigenic target (TAT) cDNA sequence #1279.  
DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
KW cancer; cell proliferative disorder; gene; ss.  
XX Homo sapiens.  
OS WO2004060270-A2.  
PN 22-JUL-2004.  
XX 15-OCT-2003; 2003WO-US029126.  
XX 18-OCT-2002; 2002US-0418988P.  
XX (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
XX Wu TD, Zhou Y;  
XX WPI; 2004-534300/51.  
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
PT preventing or treating cell proliferative disorders such as cancer.  
PT Claim 1; SEQ ID NO 1279; 5504pp; English.  
XX  
CC The present invention describes an isolated tumour-associated antigenic  
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
CC (c). Also described: (1) an expression vector comprising the above  
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
CC a process for producing a polypeptide; (4) an isolated polypeptide  
CC comprising: (a) an amino acid sequence encoded by any of the above  
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
CC length coding region of the above nucleotide sequences; or (c) a sequence  
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
CC an isolated antibody that binds to the above polypeptide; (7) a process  
CC for producing the antibody; (8) an isolated oligopeptide that binds to  
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
CC binding organic molecule that binds to the above polypeptide; (10) a  
CC composition of matter comprising the above (chimeric) polypeptide,  
CC antibody, oligopeptide or TAT binding organic molecule, in combination  
CC with a carrier; (11) an article of manufacture comprising a container and  
CC the composition of matter contained within the container; (12) methods of  
CC inhibiting the growth of a cell that expresses the above protein, where  
CC the growth of the cell is at least in part dependent upon a growth  
CC potentiating effect of the above protein; (13) a method of  
CC therapeutically treating a mammal having a cancerous tumour comprising  
CC cells that express the above protein; (14) a method of determining the  
CC presence of a protein in a sample suspected of containing the protein  
CC described above; (15) methods of diagnosing the presence of a tumour in a



CC mammal; (16) a method for treating or preventing a cell proliferative  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.

XX  
 SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,32e-64 Length: 2250  
 Score: 621.50 Matches: 113  
 Percent Similarity: 80.95% Conservatives: 40  
 Best Local Similarity: 59.79% Mismatches: 35  
 Query Match: 67.19% Indels: 1  
 DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADQ84465 (1-2250)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
 DB 1 GTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTGTCTTTGGCACCACG 60  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 61 CTGATCATGCTGCTTTCCTGGCAGCTTTTCAGTGTGCATCAGTGGTGTCTTACCTATC 120  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 121 CTGGCTCTCTCTGTACCATCAGCTTCAGATCTACAGTCCGTCTATCCAGCTGTA 180  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 181 CAGAAAGTCAGAAAGAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTAATCTGTCC 240  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 241 TCAGAAAGCTTTCCATAATACATGATGATGCTGCTGATGATGATGATGATGATGATG 300  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 301 CTCATATTGCTCTCTCTCTGAGAGATCTGTTGACTCTTGAAGCTGGCTGCTTC 360  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 361 ATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTTCTAATCTTGTCT 420  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 DB 421 GAACGTGCTCATTTTCAGTGTCCGATTTGTATGAGAAGTACAGACCCAGCATGATCAC 480  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 481 TATGTTGGATGCTCCGAGATCAGACCAAGTCAATTGTTGAAGATCCAGCAAACTC 540  
 QY 182 ProGlyLeu---LysArgLysAlaAsp 189  
 DB 541 CCTGGAATCGCCCAAAAAGAGGACAG 567

RESULT 93

ADQ86409

ID ADQ86409 standard; cDNA; 2250 BP.

XX AC ADQ86409;

XX DT 07-OCT-2004 (first entry)

XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #3281.

XX

KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
 KW cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (GETH ) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
 XX preventing or treating cell proliferative disorders such as cancer.

XX Claim 1; SEQ ID NO 3281; 5504pp; English.

CC The present invention describes an isolated tumour-associated antigenic  
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
 CC sequence identity to (a)-(c); or (e) a sequence that hybridizes to (a)-  
 CC (c). Also described: (1) an expression vector comprising the above  
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
 CC a process for producing a polypeptide; (4) an isolated polypeptide  
 CC comprising: (a) an amino acid sequence encoded by any of the above  
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
 CC length coding region of the above nucleotide sequences; or (c) a sequence  
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
 CC an isolated antibody that binds to the above polypeptide; (7) a process  
 CC for producing the antibody; (8) an isolated oligopeptide that binds to  
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
 CC binding organic molecule that binds to the above polypeptide; (10) a  
 CC composition of matter comprising the above (chimeric) polypeptide,  
 CC antibody, oligopeptide or TAT binding organic molecule, in combination  
 CC with a carrier; (11) an article of manufacture comprising a container and  
 CC the composition of matter contained within the container; (12) methods of  
 CC inhibiting the growth of a cell that expresses the above protein, where  
 CC the growth of the cell is at least in part dependent upon a growth  
 CC potentiating effect of the above protein; (13) a method of  
 CC therapeutically treating a mammal having a cancerous tumour comprising  
 CC cells that express the above protein; (14) a method of determining the  
 CC presence of a protein in a sample suspected of containing the protein  
 CC described above; (15) methods of diagnosing the presence of a tumour in a  
 CC mammal; (16) a method for treating or preventing a cell proliferative  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.

XX SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,32e-64 Length: 2250  
 Score: 621.50 Matches: 113  
 Percent Similarity: 80.95% Conservatives: 40  
 Best Local Similarity: 59.79% Mismatches: 35  
 Query Match: 67.19% Indels: 1

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DB: 12 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x ADQ86409 (1-2250)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB 1 GTGCAGATCTGATTTCTGGAGAGATGTGAGAGACTGGTGTCTTTGGCACCAG 60
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 61 CTGATCATGCTGTTTCCCTGCAGCTTTTCAGTGTCTCATGCTGCTGTTCTTACCTCATC 120
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 121 CTGGCTCTTCTCTCTCACCATCAGCTTCAAGATCTACAAGTCCGTCTCATCAAGCTGA 180
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 181 CAGAAGTCAGAGAAGGCCATCCATTCAAAGCTACTCTGAGCTAGACATTACTCTGTCC 240
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 241 TCAGAAGCTTTCATTAATACATGAATGCTGCATGCTGCATCAACAGGGCCCTGAAA 300
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121
DB 301 CTCATTATTGCTCTCTCTCTGAGAGATCTGGTTGACTCTTGAAGCTGGCTGTCTTC 360
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 361 ATGTGCTGATGACCTATGTTGTGTCTGTTTAAAGGATCACTCTTCTAATCTTGTCT 420
QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 421 GAACTGCTCATTTTCAGTGTCCGATGTCTATGAGAGATCAACAGACCCAGATTGATCAC 480
QY 162 TyrLeuGluLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 481 TAGTTGGATGCCCGAGATCAGACCAAGTCAATTTGTTGAAAAGATCCAGCAAAATC 540
QY 182 ProGlyLeu---LysArgLysAlaAsp 189
DB 541 CCTGGATGCCCAAAAAGGACAGAA 567
RESULT 94
ADQ85262
ID ADQ85262 standard; cDNA; 2250 BP.
XX
AC ADQ85262;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2076.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN W02004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH ) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
```

```
DR XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PS preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 2076; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 2,328-64 Length: 2250
Score: 621.50 Matches: 113
Percent Similarity: 80.95% Conservative: 40
Best Local Similarity: 59.79% Mismatches: 35
Query Match: 67.19% Indels: 1
DB: 13 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x ADQ85262 (1-2250)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB 1 GTGCAGATCTGATTTCTGGAGAGATGTGAGAGACTGGTGTCTTTGGCACCAG 60
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 61 CTGATCATGCTGCTTCTCCCTGCAGCTTTTCAGTGTCTCATGCTGCTGTTCTTACCTCATC 120
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 121 CTGGCTCTTCTCTCTCACCATCAGCTTCAAGATCTACAAGTCCGTCTCATCAAGCTGA 180
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 181 CAGAAGTCAGAGAAGGCCATCCATTCAAAGCTACTCTGAGCTAGACATTACTCTGTCC 240
```

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 241 TCAGAGCTTCCATAATACATGATGCTGCCATGGTCACATCAACAGGGCCCTGAAA 300  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 301 CTCATTATTCGTCTCTTCTGCTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGCTTC 360  
 Qy 122 MetTrpValPheThrValGlnAlaLeuPheGlnGlyLeuThrLeuLeuLeuAla 141  
 Db 361 ATGTGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCCCTCTAATTTCTGCT 420  
 Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 421 GAACGTCTCATTTTCAGTGTCCGATGCTCTATGAGAAGTACAGACCCAGATTGATCAC 480  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 481 TATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 540  
 Qy 182 ProGlyLeu---LysArgLysAlaAsp 189  
 Db 541 CTGGAATCGCCAAAAGGACAGAA 567

## RESULT 95

ID ADQ83313 standard; cDNA; 2250 BP.  
 AC ADQ83313;

DT 07-OCT-2004 (first entry)

DE Human tumour-associated antigenic target (TAT) cDNA sequence #127.

XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
 KW cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (GETH ) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
 PT preventing or treating cell proliferative disorders such as cancer.

XX Claim 1; SEQ ID NO 127; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic  
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
 CC (c). Also described: (1) an expression vector comprising the above  
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
 CC a process for producing a polypeptide; (4) an isolated polypeptide  
 CC comprising: (a) an amino acid sequence encoded by any of the above  
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
 CC length coding region of the above nucleotide sequences; or (c) a sequence  
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide

CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
 CC an isolated antibody that binds to the above polypeptide; (7) a process  
 CC for producing the antibody; (8) an isolated oligopeptide that binds to  
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
 CC binding organic molecule that binds to the above polypeptide; (10) a  
 CC composition of matter comprising the above (chimeric) polypeptide,  
 CC antibody, oligopeptide or TAT binding organic molecule, in combination  
 CC with a carrier; (11) an article of manufacture comprising a container and  
 CC the composition of matter contained within the container; (12) methods of  
 CC inhibiting the growth of a cell that expresses the above protein, where  
 CC the growth of the cell is at least in part dependent upon a growth  
 CC potentiating effect of the above protein; (13) a method of  
 CC therapeutically treating a mammal having a cancerous tumour comprising  
 CC cells that express the above protein; (14) a method of determining the  
 CC presence of a protein in a sample suspected of containing the protein  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.

XX SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2.32e-64	Length:	2250
Score:	621.50	Matches:	113
Percent Similarity:	80.95%	Conservative:	40
Best Local Similarity:	59.79%	Mismatches:	35
Query Match:	67.19%	Indels:	1
DB:	13	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADQ83313 (1-2250)

Qy	2	valValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21
Db	1	GTGCACGATCTGATTTTCTGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCCACG	60
Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	61	CTGATCATGCTGCTTTCCCTGGCAGCTTCAGTGTCTATCAGTGTGTTCTTACTCTATC	120
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	121	CTGGCTCTCTCTCTGTCCACCATCAGCTTCAGGATCTACAAAGTCGGTCATCCAGCTGA	180
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	181	CAGAAGTCAGAAGAAGGCCCATCCATTCAAAGCTTACCTGGAGCTAGAGATCTCTGTCC	240
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
Db	241	TCAGAAGCTTTCATATTAATACATGATGCTGCCATGGTGCACATCAACAGGGCCCTGAAA	300
Qy	102	GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	301	CTCATTTATTCGTCTCTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGCTTC	360
Qy	122	MetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla	141
Db	361	ATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCCCTCTAATTTCTGCT	420
Qy	142	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
Db	421	GAACGTCTCATTTTCAGTGTCCCGATGCTCTATGAGAAGTACAAAGCCAGATTGATCAC	480
Qy	162	TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	181

Db 481 TATGTTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAATCTC 540

Qy 182 ProGlyLeu---LysArgLysAlaAsp 189  
|||||:::|||||:::|||||:::  
Db 541 CCTGGAATCGCCCAAAAAAAGGCAGAA 567

## RESULT 96

ADM36175  
ID ADM36175 standard; DNA; 3231 BP.

XX

AC

ADM36175;

XX DT 03-JUN-2004 (first entry)

XX DE Human RTN3 isoform V coding sequence, SEQ ID 58.

XX KW Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;

XX KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

XX FT 124..2154

XX FT /\*tag= a

XX FT /product= "RTN3 isoform V"

XX PN WO2004001069-A2.

XX PD 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX PX (UYPA-) UNIV PASTEUR LOUIS.

XX PI Dupuis L, Di Scala F, De Tapia M, Larnet Y, Loeffler J;

XX PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;

XX DR WPI; 2004-071743/07.

XX DR P-PSDB; ADM36176.

XX PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
XX PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
XX PT reticulon 3 gene.

XX PS Claim 35; SEQ ID NO 58; 116pp; French.

XX CC The present invention relates to a method for diagnosing, or evaluating  
XX CC progression of, a neuromuscular disease. The method comprises detecting  
XX CC modulation of the expression of a product (I) of the RTN (reticulon)3  
XX CC gene. Differential expression of RTN3 is a specific marker of  
XX CC neuromuscular disease, allowing early diagnosis from readily available  
XX CC muscle biopsies. The method is also useful for determining the efficacy  
XX CC of treatment. The method is used to diagnose (also to evaluate  
XX CC progression or therapy of) neuromuscular disorders, specifically  
XX CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
XX CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
XX CC small interfering RNA) that can block/reduce expression of these isoforms  
XX CC are useful for treating neuromuscular diseases and (ii) cells that  
XX CC express RTN3 are useful in screening for therapeutic agents. The present  
XX CC sequence is a RTN3 DNA sequence used to illustrate the invention.

XX SQ Sequence 3231 BP; 947 A; 717 C; 690 G; 877 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	3 85e-64	Length:	3231
Score:	621.50	Matches:	113
Percent Similarity:	80.95%	Conservative:	40
Best Local Similarity:	59.79%	Mismatches:	35
Query Match:	67.19%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36175 (1-3231)

Qy 2 ValValAspLeuLeuTyrTriArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
|||||:::|||||:::|||||:::  
Db 1585 GTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACG 1644Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
|||||:::|||||:::|||||:::  
Db 1645 CTGATCATGCTGCTTTCCCTGCACGCTTTCAGTGTGCATCAGTGTGGTTCCTTACCTCATC 1704Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
|||||:::|||||:::|||||:::  
Db 1705 CTGGCTCTCTCTCTGTCCATCAGCTTCAGATCTACAAGTCGTCATCCAGCTGTA 1764Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
|||||:::|||||:::|||||:::  
Db 1765 CAGAAGTCAGAAGAAGGCCATCCATTCAAGGCTACCTGGACGTAGACATTACTCTGTCC 1824Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
|||||:::|||||:::|||||:::  
Db 1825 TCAGAAAGCTTTCCATAATTACATGATGCTGCCATGTCATCAACAGGCCCTGAAA 1884Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
|||||:::|||||:::|||||:::  
Db 1885 CTCATTATTCGTCTCTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTCTC 1944Qy 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
|||||:::|||||:::|||||:::  
Db 1945 ATGTGGCTGATGACCTATGTTGCTGCTTTTAAACGGAATCACCTCTTCTTAATTCTTGT 2004Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
|||||:::|||||:::|||||:::  
Db 2005 GAACTGGCTCATTTTCAGTGTCCGATGCTATGAGAAGTACACAGCCAGATTGATCAC 2064Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
|||||:::|||||:::|||||:::  
Db 2065 TATGTTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAATCTC 2124

Qy 182 ProGlyLeu---LysArgLysAlaAsp 189

Db 2125 CCTGGAATCGCCCAAAAAAAGGCAGAA 2151

## RESULT 97

ADM36169

ID ADM36169 standard; DNA; 3288 BP.

XX AC

XX ADM36169;

XX DT 03-JUN-2004 (first entry)

XX DE Human RTN3 isoform II coding sequence, SEQ ID 52.

XX KW Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
XX KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

XX FT 124..2211

XX FT /\*tag= a

XX FT /product= "RTN3 isoform II"

XX PN WO2004001069-A2.

XX PD 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX PA (UYPA-) UNIV PASTEUR LOUIS.

XX PI Dupuis L, Di Scala F, De Tapia M, Larnet Y, Loeffler J;

PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX WPI; 2004-071743/07.  
DR P-PSDB; ADM36170.  
XX  
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX  
PS Claim 35; SEQ ID NO 52; 116pp; French.  
XX  
CC The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
SQ Sequence 3288 BP; 955 A; 736 C; 695 G; 902 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 3.95e-64 Length: 3288  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservative: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1  
DB: 12 Gaps: 1  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36169 (1-3288)  
  
QY 2 ValValAspLeuLeuTyrTTPArgAspIleValSerThrGlyValValPheGlyAlaSer 21  
DB 1642 GTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGTTTGTCTTTGGCACCACG 1701  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAla 41  
DB 1702 CTGATCATGCTGCTTCTCCCTGCAGCTTTCAGTGTCTCATGTTGGTTTCTTACCTCATC 1761  
  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 1762 CTGGCTCTTCTCTGTCCACCATCATGCTTCAAGATCTCAAGTCCGTCCATCAAGCTGA 1821  
  
QY 62 GlnYsSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 1822 CAGAAGTCAGAAAGGCCCATCCATTCAAGGCTTACCTGGAGCTAGACATTACTCTGTCC 1881  
  
QY 82 GluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1882 TCAGAAGCTCTCCATAATATCATGATCTGCCATGGTGACATCAACAGGGCCCTGAA 1941  
  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1942 CTCATTATTCTGCTCTTTCTGTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTTC 2001  
  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuIleAla 141  
DB 2002 ATGGCGCTGATGACCTATGTGGTGCTGTTTTTAACGGAATCACCCCTTCTAATCTTGCT 2061  
  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 2062 GAACGTCTCTATTTTCAGTGTCCGATGCTCTATGAGAAGTACAGACCCAGATTGATC 2121  
  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 2122 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCAAGCAAGCAAACT 2181

QY 182 ProGlyLeu---LysArgLysAlaAsp 189  
DB 2182 CCTGGATCGCCAAAGAAAGGAGCA 2208  
  
RESULT 98  
ADM36179  
ID ADM36179 standard; DNA; 4092 BP.  
XX AC ADM36179;  
XX  
XX 03-JUN-2004 (first entry)  
XX Human RTN3 isoform VII coding sequence, SEQ ID 62.  
XX Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;  
KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 163..3015  
CDS /\*tag= a  
FT /product= "RTN3 isoform VII"  
XX  
XX WO2004001069-A2.  
XX  
XX 31-DEC-2003.  
XX  
XX 20-JUN-2003; 2003WO-FR001910.  
XX  
XX 25-JUN-2002; 2002FR-00007846..  
XX  
XX (UYPA-) UNIV PASTEUR LOUIS.  
XX  
XX Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX  
XX WPI; 2004-071743/07.  
DR P-PSDB; ADM36180.  
XX  
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX  
XX Claim 35; SEQ ID NO 62; 116pp; French.  
XX  
XX The present invention relates to a method for diagnosing, or evaluating  
XX progression of, a neuromuscular disease. The method comprises detecting  
XX modulation of the expression of a product (I) of the RTN (reticulon)3  
XX gene. Differential expression of RTN3 is a specific marker of  
XX neuromuscular disease, allowing early diagnosis from readily available  
XX muscle biopsies. The method is also useful for determining the efficacy  
XX of treatment. The method is used to diagnose (also to evaluate  
XX progression or therapy of) neuromuscular disorders, specifically  
XX amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
XX specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
XX small interfering RNA) that can block/reduce expression of these isoforms  
XX are useful for treating neuromuscular diseases and (ii) cells that  
XX express RTN3 are useful in screening for therapeutic agents. The present  
XX sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
SQ Sequence 4092 BP; 1286 A; 834 C; 836 G; 1136 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 5.37e-64 Length: 4092  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservative: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1  
DB: 12 Gaps: 1  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36179 (1-4092)



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QY 182 ProGlyLeu---LysArgLysAlaLeu 189
Db 3133 CCTGGAATCGCCCAAAAAAAGGCAGAA 3159

RESULT 100
ADM36167
ID ADM36167 standard; DNA; 4296 BP.
XX
AC ADM36167;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human RTN3 isoform I coding sequence, SEQ ID 50.
XX
KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;
KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 124..3219
FT FT /*tag= a
FT ET /product= "RTN3 isoform I"
XX
PN WO2004001069-A2.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-FR001910.
XX
PR 25-JUN-2002; 2002FR-00007846.
XX
PA (UYPA-) UNIV PASTEUR LOUIS.
XX
PI Dupuis L, Di Scala F, De Tapia M, Larnet Y, Loeffler J;
PI Gonzales De Aguilar J, Bouillier AL, Gaidon C, Rene F;
XX
DR WPI; 2004-071743/07.
DR P-PSDB; ADM36168.
XX
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly
PT amyotrophic lateral sclerosis, comprises detecting modulation of the
PT reticulon 3 gene.
XX
PS Claim 35; SEQ ID NO 50; 116pp; French.
XX
CC The present invention relates to a method for diagnosing, or evaluating
CC progression of, a neuromuscular disease. The method comprises detecting
CC modulation of the expression of a product (i) of the RTN (reticulon)3
CC gene. Differential expression of RTN3 is a specific marker of
CC neuromuscular disease, allowing early diagnosis from readily available
CC muscle biopsies. The method is also useful for determining the efficacy
CC of treatment. The method is used to diagnose (also to evaluate
CC progression or therapy of) neuromuscular disorders, specifically
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or
CC small interfering RNA) that can block/reduce expression of these isoforms
CC are useful for treating neuromuscular diseases and (ii) cells that
CC express RTN3 are useful in screening for therapeutic agents. The present
CC sequence is a RTN3 DNA sequence used to illustrate the invention.
XX
SQ Sequence 4296 BP; 1290 A; 944 C; 895 G; 1167 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 5,75e-64 Length: 4296
Score: 621.50 Matches: 113
Percent Similarity: 80.95% Conservative: 40
Best Local Similarity: 59.79% Mismatches: 35
Query Match: 67.19% Indels: 1
DB: 12 Gaps: 1

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US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36167 (1-4296)

Search completed: June 19, 2005, 07:20:15  
Job time : 417 secs

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Db 2650 GTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACATGGGTGTTGCTTTGGCACCACG 2709
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 2710 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTGCATCAGTGTGGTTTCTTACCTCATC 2769
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 2770 CTGGCTCTCTCTCTGTCCATCAGCTTCCAGATCTCAAGTCCGTCCGTATCCAGCTGTA 2829
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 2830 CAGAAGTCAGAAGAAGGCCATCCATTCAAGGCTTACCTGGACGTAGACATTACTCTGTCC 2889
QY 82 GluGluLeuValGlnLysTyrSerHisSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 2890 TCAGAAGCTTTCCATTAATTACATGAATGCTGCCATGTGTCATCAACAGGCGCCCTGAAA 2949
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 2950 CTCATTATTCGTCTCTTCTGTGTAAGATCTGGTTGACTCTCTGAAGCTGGCTGCTTC 3009
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 3010 ATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTTCTTAATTTCTTGT 3069
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 3070 GAACGTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAAGTACAGACCCAGATTGATCAC 3129
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 3130 TATGTGGCATCGCCCGAGATCAGACCAAGTCAATTGTGTGAAAAGATCCAGCAAAATTC 3189
QY 182 ProGlyLeu---LysArgLysAlaAsp 189
Db 3190 CCTGGAATCGCCCAAAAAAAGGCAGAA 3216

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 18, 2005, 20:51:35 ; Search time 125.5 Seconds  
(without alignments)

2464.194 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRAD 189

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlp

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-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908	98.2	4822	3	US-09-484-970B-106
2	904	97.7	799	2	US-08-700-607-2
3	904	97.7	1669	4	US-09-949-016-3253
4	891	96.3	2610	4	US-09-023-655-382
5	679	73.4	2069	4	US-09-949-016-3309
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7	625.5	67.6	2262	4	US-09-949-016-2988
8	622.5	67.3	1766	3	US-09-149-476-254
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11	524.5	56.7	1095	2	US-08-700-607-4
12	518	56.0	2014	4	US-09-270-767-13561

13	509.5	55.1	794	3	US-09-149-476-102	Sequence 102, App
14	475	51.4	2181	4	US-09-949-016-1419	Sequence 1419, Ap
c 15	341	36.9	601	4	US-09-949-016-117588	Sequence 117588,
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17	341	36.9	42075	4	US-09-949-016-14995	Sequence 14995, A
18	286	30.9	443	4	US-09-513-999C-3784	Sequence 3784, Ap
19	282.5	30.5	135667	4	US-09-949-016-15051	Sequence 15051, A
20	282.5	30.5	152486	4	US-09-949-016-12869	Sequence 12869, A
c 21	278.5	30.1	601	4	US-09-949-016-40169	Sequence 40169, A
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c 30	114	12.3	601	4	US-09-949-016-117609	Sequence 117609,
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33	100	10.8	425	3	US-08-905-223-178	Sequence 178, App
34	95	10.3	1828	3	US-08-487-596-7	Sequence 7, Appli
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c 36	94	10.2	1273	4	US-09-949-016-5725	Sequence 5725, Ap
c 37	94	10.2	1722	4	US-08-956-171E-407	Sequence 407, App
c 38	94	10.2	1722	4	US-08-781-986A-407	Sequence 407, App
39	92.5	10.0	12566	3	US-08-961-527-149	Sequence 149, App
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42	88.5	9.6	4673	4	US-09-814-915A-100	Sequence 100, App
43	86.5	9.4	296	4	US-09-313-294A-81	Sequence 81, Appl
44	86.5	9.4	1779	4	US-09-134-000C-2072	Sequence 2072, Ap
45	86	9.3	1302	4	US-08-956-171E-322	Sequence 322, App

ALIGNMENTS

RESULT 1

US-09-484-970B-106

Sequence 106, Application US/09484970B

Patent No. 6426186

GENERAL INFORMATION:

APPLICANT: Jones, Karen A.

APPLICANT: Volkmut, Wayne

APPLICANT: Walker, Michael G.

TITLE OF INVENTION: BONE REMODELING GENES

FILE REFERENCE: PB-0014 US

CURRENT APPLICATION NUMBER: US/09/484,970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PERL Program

SEQ ID NO 106

LENGTH: 4822

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1

NAME/KEY: unsure

LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,

OTHER INFORMATION: a, t, c, g, or other

Alignment Scores:	3.32e-116	Length:	4822
Pred. No.:	908.00	Matches:	184
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.35%	Mismatches:	2
Query Match:	98.16%	Indels:	0
DB:	3	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-484-970B-106 (1-4822)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3265 TCAGTTGTTGACCTCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGC 3324  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3325 AGCCTATTCCTGCTGCTTTCATGACAGATTCAGCATTTGTGAGCGTAACACGCTACAT 3384  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3385 GCCTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAAAGGTGTGATCCAAGCT 3444  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3445 ATCCAGAAATCAGATGAAGCCACCCATTCAGGCAATATCTGGAATCTGAAGTTGCTATA 3504  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3505 TCTGAGGAGTTGTTTCTGAGAGTACAGTAATTCCTGCTTGGTCATGTGAAGTGCAGATA 3564  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3565 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 3624  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3625 TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAAATGGTCTGCACACTACTGATTTG 3684  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3685 GCTCTCATTTTCACTCTTCACTGTTTCACTGTTTCACTGTTTATTAAGACGTCATCAGCAGATAGAT 3744  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3745 CATATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 3804  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3805 ATCCCTGGATTGAAGCGCAAGCTGAA 3831

## RESULT 2

US-08-700-607-2  
; Sequence 2, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 799 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
; US-08-700-607-2

Alignment Scores:  
Pred. No.: 6.66e-117 Length: 799  
Score: 904.00 Matches: 193  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 2 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-700-607-2 (1-799)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 168 CTATTCCTGCTGCTTTCATTCAGCATTCAGCATTTGAGCGTAACAGCCTACATTTGCC 227  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCAAGCTATC 287  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 288 CAGAAATCAGATGAAGCCACCCATTCAGGCAATATCTGGAATCTGGAAGTTGCTATATCT 347  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 348 GAGGAGTTGGTTTCAAGATACAGTAATTCCTGCTTGTGTCATGTGAACCTGCACGATAAG 407  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 408 GAACCTCAGCGCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAAGTTTCAGTGTG 467  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 468 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATGTTGCTGACACTACTGATTTTGGCT 527  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
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QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 648 CTGGATTGAAGCGCAAGCTGAA 671

## RESULT 3

US-09-949-016-3253  
; Sequence 3253, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3253  
;; LENGTH: 1669  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-3253

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Score: 504.00 Matches: 183  
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Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-3253 (1-1669)

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Db CTATTCCTGCTGCTTTCATTCAGCATTTAGCATTTGTGAGCGTAACAGCCTACATTGCC 367
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAGCTATC 427
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db CAGAAATCAGATGAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAATGCTATATCT 487
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db GAGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTTGTGTCATGTGAACTGCACGATAAG 547
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 607
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db ATGTGGGTATTTACTATGTTGGTGCCTTGTATTAATGCTGACACTACTGATTTGGCT 667
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 727
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIle 181
Db TATCTAGACTTGCAAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 787
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db CTGTGATGAAGCGCAAGCTGAA 811
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## RESULT 4

US-09-023-655-382  
; Sequence 382, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

;; TITLE OF INVENTION: EXPRESSION  
;; NUMBER OF SEQUENCES: 1508  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;; STREET: 3174 PORTER DRIVE  
;; CITY: PALO ALTO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/023,655  
;; FILING DATE: HEREWITH  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Zeller, Karen J.  
;; REGISTRATION NUMBER: 37,071  
;; REFERENCE/DOCKET NUMBER: PA-0001 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (650) 855-0555  
;; TELEFAX: (650) 845-4166  
;; INFORMATION FOR SEQ ID NO: 382:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2610 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: LUNGN0T14  
;; CLONE: 1508778  
US-09-023-655-382

Alignment Scores:  
Pred. No.: 3e-114 Length: 2610  
Score: 891.00 Matches: 183  
Percent Similarity: 98.41% Conservativity: 3  
Best Local Similarity: 96.83% Mismatches: 2  
Query Match: 96.32% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-023-655-382 (1-2610)

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Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db GTTGTGACCTCCTGCTACTGGAGACATTAAGAGACTGGAGTGTGTTGGTGCCAGC 1370
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41
Db CTATTCCTGCTGCTTTCATTCAGCATTTAGCATTTGTGAGCGTAACAGCCTACAAATGC 1430
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db CTTCGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGCTAT 1490
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db CCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAATGCTATATC 1550
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db TGAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGGTCTATGTGAACTGCACGATAA 1610
Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 121
Db GGAACCTCAGGCGCCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGT 1670
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QY 121 uMetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141  
Db 1671 GATGGGGTATTACCTATGTGGTCCCTGTGTTAATGCTCTGACACTACTGATTGGC 1730  
QY 141 aleuileSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHi 161  
Db 1731 TCTCATTTCCACTCTTCAGTGTTCCTGTTATTTATGACCGCATCAGGCACATAGATCA 1790  
QY 161 sTyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 1791 TTATCTAGGACTTGCAATAAGAAATGTTAAGATGCTATGGCTAAATCCAGCAAAAT 1850  
QY 181 eProGlyLeuLysArgLysAlaAsp 189  
Db 1851 CCCTGGGTTGAAGCGCAAGCTGAA 1875  
RESULT 5  
US-09-949-016-3309  
; Sequence 3309, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3309  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-3309  
Alignment Scores:  
Pred. No.: 1,17e-84 Length: 2069  
Score: 679.00 Matches: 127  
Percent Similarity: 84.49% Conservative: 31  
Best Local Similarity: 67.91% Mismatches: 29  
Query Match: 73.41% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-3309 (1-2069)  
QY 3 ValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 757 ATTGACTCTGTGTTATGGCGGCATCAGCAGCGGCATCGTGTTCGGAGTTTCCTG 816  
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAlaLeu 42  
Db 817 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGTCGCTACCTGGCCCTG 876  
QY 43 AlaLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGln 62  
Db 877 GCGGCACTCTCAGCCACCATCATGTTCCGCATCTACAAGTCTGTTTACAGCAGTGCAG 936  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSerGlu 82  
Db 937 AAACCGACGAGCCACCCCTTTCAGGCTACTTCGAGCTTGAGATCACCCCTTCTCAG 996  
QY 83 GluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
Db 997 GAGCAGATTGAGAAGTACAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056  
QY 103 LeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122

Db 1057 CTGAGAGGCTCTTCTTGTTCAGGACCTGGTGGATTCTTAAATTTGCACTCTCTGATG 1116  
QY 123 TrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
Db 1117 TGGCTCCTGACCTACGCTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTG 1176  
QY 143 IleSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHisTy 162  
Db 1177 GTTTCATATGTTTACTTCTACTCTGATGATGTTAAGCACCAGGCACAGATTCACCAAT 1236  
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 1237 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 1296  
QY 183 GlyLeuLysArgLysAlaAsp 189  
Db 1297 GCGGCTAAGAGGCACGCTGAG 1317  
RESULT 6  
US-09-949-016-1127  
; Sequence 1127, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1127  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1127  
Alignment Scores:  
Pred. No.: 2,37e-84 Length: 3202  
Score: 679.00 Matches: 127  
Percent Similarity: 84.49% Conservative: 31  
Best Local Similarity: 67.91% Mismatches: 29  
Query Match: 73.41% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-1127 (1-3202)  
QY 3 ValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACTCTGTGTTATGGCGGCATCAGCAGCGGCATCGTGTTCGGAGTTTCCTG 1949  
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAlaLeu 42  
Db 1950 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGTCGCTACCTGGCCCTG 2009  
QY 43 AlaLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCGGCACTCTCAGCCACCATCATGTTCCGCATCTACAAGTCTGTTTACAGCAGTGCAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAACCGACGAGCCACCCCTTTCAGGCTACTTCAGGCTTGAGATCACCCCTTCTCAG 2129  
QY 83 GluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
Db 2130 GAGCAGATTGAGAAGTACAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2189

QY 103 LeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGGTGATTCCTTAATTTGCGATCTCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAlaLeuLeuThrLeuLeuLeuAlaLeu 142  
Db 2250 TGGCTCCTGACCTACGCTGCTCTCTCAATGGCTGACCTGCTCTGCTCATGGCTGTG 2309  
QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
Db 2310 GTTTCATGTTTACTCTACCTGTAGTGATGTAAAGCAGCAGCAGCAGCAGCAGATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaAsp 189  
Db 2430 GCGCTAAGAGGACGCTGAG 2450  
RESULT 7  
US-09-949-016-2988  
; Sequence 2988, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 2988  
; LENGTH: 2262  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2988  
Alignment Scores:  
Pred. No.: 4,368-77 Length: 2262  
Score: 625.50 Matches: 114  
Percent Similarity: 81.05% Conservative: 40  
Best Local Similarity: 60.00% Mismatches: 35  
Query Match: 67.62% Indels: 1  
Gaps: 4  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-2988 (1-2262)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysValThrGlyValPheGlyAla 20  
Db 7 TCAGTGCAGATCTGATTTCTGGAGAGATGAAGAAGACTGGGTTGTCTTTGGCACC 66  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 67 AGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGTTCTTACCTC 126  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 127 ATCTCGGCTCTCTCTGTCCACCATCAGCTTCAGGATCTCAAGATCGCTCATCCAGCT 186  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 187 GTACAGAAGTCAGAAGAGGCCATCCATTTCAAGGCTTACCTGGACGACGACATTACTCTG 246  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

Db 247 TCCTCAGAAGCTTTCATAATATACATGAATGCTGCCATGTCATCAACAGGCGCCCTG 306  
QY 101 LysGluLeuArgGlyLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaVal 120  
Db 307 AAACCTATTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTG 366  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 367 TTCATGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCTTCTTAATCTT 426  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 427 GCTCAACTGCTCAATTTTCAGTGTCCGATTCCTATGAGAAGTACAGACCCAGATTCAT 486  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 487 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCATTTGTAAGATCCACAGCAAA 546  
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189  
Db 547 CTCCTGGAATCGCCAAAAGGCGAGAA 576

## RESULT 8

US-09-149-476-254  
; Sequence 254, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,334  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,336  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,600  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,615  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,597  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,502  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,633  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,583  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,617  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,618  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,503  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,592  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,581  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,584  
; PRIOR FILING DATE: 1997-05-23

[illegible]

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; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Alignment Scores:
Pred. No.:          7,72e-77      Length:      1766
Score:             622.50         Matches:    113
Percent Similarity: 81.05%        Conservative: 41
Best Local Similarity: 59.47%      Mismatches:  35
Query Match:       67.30%         Indels:      1
DB:                3              Gaps:          1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-149-476-254 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 287 GCGGTGCACGATCTGATTTCTCGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC 346
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 347 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGTTTCTTACCTC 406
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 407 ATCTGGCTCTCTCTCTGTCAACATCAGCTTCAGGATCTCAAGTCGTCATCCAGCT 466
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 467 GTACAGAAGTCAGAAGAGGCCATCCATTCAAAGCTACCTGCAGTAGACATTACTCTG 526
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 527 TCTTCAGAAGCTTTCATTAATACATGATGCTGTCATGTCATCAACAGGCCCTG 586
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 587 AAATCATATTTCGCTCTCTCTGTCAGAGATCTGGTGTACTCTTGAAGCTGCTGTC 646
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140
DB 647 TTCATGTGCTGATGACCTATGTTGGTGTGTTTAAACGAATCACCTTCTTAATCTT 706
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 707 GCTGAAGTCTCATTTTCAGTGTCCCGATTGTCTATGAGAGTCAACAGCCAGATTGAT 766
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 767 CACTATGTGGATGCCCGAGATCAGACCAGTCAATTGTTGAAGAAGATCCAGCAAA 826
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189
DB 827 CTCCTCGAATGCCCAAAAAAAGCAGAA 856

RESULT 9
US-09-149-476-255
; Sequence 255, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002PI
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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## Alignment Scores:

Pred. No.:	1,5e-76	Length:	2664
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	3	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-149-476-255 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	262	GGGTGACGATCTGATTTCTGGAGAGATGTGAAGACATGGGTTTCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCAGTGTGGTTTCTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCCTGGCTCTTCTCTCTGACCATCAGTTTCAGGATCTACAGTCCGTCATCCAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAAGTCAGAGAGCCCATCCATTCAAAGCTTACCTGACGATAGCATTAATCTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	502	TCTCAGAAGCTTTCCATTAATTACATGAATGTGCATGTGTCATCAACAGGCGCCCTG	561
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120





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; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
US-08-700-607-4

Alignment Scores:
Pred. No.: 2,03e-63 Length: 1095
Score: 524.50 Matches: 102
Percent Similarity: 72.77% Conservative: 37
Best Local Similarity: 53.40% Mismatches: 30
Query Match: 56.70% Indels: 22
DB: 2 Gaps: 2

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-700-607-4 (1-1095)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
329 GCGGTGCAGATCTGATTTTGGAGAGATGTGAAGACACTGGGTTTCTTTGGCACC 388
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
389 AGCGTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTCTCAGTGTGTGGTTTCTTACCTC 448
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
449 ATCTGGCTCTCTCTCTGTACCATCAGCTTTCAGATCTACAGTCCGCTCATCCAGCT 508
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
509 GTACAGAAGTCAGAAAGGCCATCCATTCAAAGCTACCTGGACGTACAGCTTACTCTG 568
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
569 TCTCAGAAAGCTTTCATTAATACATGAATGTGCGCATCAACAGGGCCCTG 628
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
629 AAATCATTAATTCGCTCTCTCTGAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 688
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
689 TTCATGTGCTGATGACCTATGTTGTGTGTTTAAACGGAATCACCCTTCTAATTCCT 748
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
749 GCTGAAGTCTCATTTTNAAGTGTCCCGATTGTTNATNAGAAGTAC----- 793
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
794 -----AAGTTCCAGCAAA 808

QY 180 sileProGlyLeu---LysArgLysAlaAsp 189
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
809 ACTCCCTGGAATCGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839

RESULT 12
US-09-270-767-13561
; Sequence 13561, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13561

; LENGTH: 2014
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13561

Alignment Scores:
Pred. No.: 4.43e-62 Length: 2014
Score: 518.00 Matches: 93
Percent Similarity: 75.28% Conservative: 41
Best Local Similarity: 52.25% Mismatches: 44
Query Match: 56.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-270-767-13561 (1-2014)
QY 5 LeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeu 24
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
164 CTTATCTACTGGCGGATGTGAAGAAATCCGGCATTTGTTCCGCTACTTGTGCTCCTACCA 223
QY 25 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
224 CTGGCGGCATCTCCAGCTTCTCGGTGATCAGCGTGTTCGCTACTTGTGCTCCTAACCC 283
QY 45 LeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSer 64
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
284 CTCCTCGGCACCGTCCGCTTCAGAAATCTACAAATCTGTGACACAGCCGCTGCAAAAGACA 343
QY 65 AspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeu 84
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
344 AACGAGGTGTCACCCCTTTAAGGATTTACCTGGAGCTGGATCTGACGCTGTGCGCAGAAAG 403
QY 85 ValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 104
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
404 GTACAGAACATTTGCCGGCTGCTGTGCACATATCAATGGCTTCATCTCCGAGCTGAGG 463
QY 105 ArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
464 CCGCTGTTCTTGTGTGAGATATCATCGATTTCGATTCGATTCGATCTTGGCCCTTGTCTCG 523
QY 125 PheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSer 144
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
524 TTCACCTACGTGGTGGCTGGTTCAATGGCATGACTCTGGTTCATCTTGGCCCTTGTCTCG 583
QY 145 LeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGly 164
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
584 CTGTTTACCTGCCCAAGCTCTACGAGAACACAAAGCAATCGATCGACACTCCTTGGAT 643
QY 165 LeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
644 CTGGTGGCAGCAAAATTCAGAAATACCCGCAAGATCCGAGTGGCCATCCCC 697

RESULT 13
US-09-149-476-102
; Sequence 102, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
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EARLIER APPLICATION NUMBER: 60/056,909  
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EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
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EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Alignment Scores:  
Pred. No.: 1,54e-61 Length: 794  
Score: 509.50 Matches: 101  
Percent Similarity: 76.37% Conservative: 38  
Best Local Similarity: 55.49% Mismatches: 41  
Query Match: 55.08% Indels: 3  
DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-149-476-102 (1-794)

1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
254 GCGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGAC-- 311  
21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIl 40  
312 ACCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCATGTGGGTTTCTTAMCT 371  
40 eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
372 CATCTGGCTCTTCTCTGTCCACCATCARTTTCAGATCTACAGTCCGTCATCCACAGC 431  
60 alleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80  
432 GTGTCAGARTCAGAAAGGCCATCAWTCACAGCCCTACCTGGACGTAGACATTACTC 491  
80 leSerGluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAnsSerThri 100  
492 TGTCTCTCAGAAGCTTTCCCAATTTACATGAATGTCGCCATGTGGTCACATCAACAGGCC 551  
100 leLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
552 TGAATCATATTATCTCTCTTCTGTGAGAGATCTGGTGTACTCTTGAAGCTGGCTG 611  
120 alleuMetTrpValPheThrTyrValGlyAlaLeuPheAnsGlyLeuThrLeuLeuIleL 140  
612 TCTTCATGTGGCTGATGACCTATGTTGGTCTGTTTTTAACGGAATCACCCCTCTTAATC 671

140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160  
672 TTGCTGAACCTGCTCATTTTCAGTCCCGATTTGTATGAGAAGTACAGACCCAGATTG 731  
160 spHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180  
732 ATCATATGTTGGCATGCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCCAAGCA 791  
180 ys 180  
792 AA 793

## RESULT 14

US-09-949-016-1419  
Sequence 1419, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1419  
LENGTH: 2181  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1419

Alignment Scores:  
Pred. No.: 5,46e-56 Length: 2181  
Score: 475.00 Matches: 92  
Percent Similarity: 70.33% Conservative: 36  
Best Local Similarity: 50.55% Mismatches: 54  
Query Match: 51.35% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-1419 (1-2181)

2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
1162 GTGGCGGACCTGCTGTACTGTGAAGACAGCAGGACGTTCAGGAGTGGTCTTCACAGCCCTG 1221  
22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
1222 ATGGTCTCCCTCTCTGCTGCTGCTAGCATCGTTCGCTGGCCGCGCACTTGGCT 1281  
42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
1282 CTGTTGCTGCTCTGGCGGACCATCTCTCTCAGGGTTTACCGAAAGTGTCTGAGGCCGCTG 1341  
62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
1342 CACCGGGGGGATGGAGCCCAACCTTTCAGGCTTACCTGGATGTGGACCTCACCTGACT 1401  
82 GluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAnsSerThrIleLys 101  
1402 CGGAGACAGACGGAACGTTTGTCCACCATGATCACCTCCCGCTGGTCTCGCGGCCACG 1461  
102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
1462 CAGCTGCGGACATTTCTTCTGTGAGAGACCTCGTGGATTCCTCAAGCTGGCCCTCCTC 1521  
122 MetTrpValPheThrTyrValGlyAlaLeuPheAnsGlyLeuThrLeuLeuIleLeuAla 141

Db 1522 TTCTACATCTTGACCTTCTGGTGCCATCTTCAATGGTTTGACCTCTCTCATCTTGGGA 1581

Qy 142 LeulleSerLeuPheSerileProValilleTyrgluArgHisGlnValGlnleAspHis 161

Db 1582 GTGATGGTCTATTACCATCCCTCTGTACCGGAGCACCAGCTCAGATCGACCA 1641

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysleGlnAlaLysle 181

Db 1642 TATGTGGGGTGTGTGACCAATCAGTTGAGCCACATCAAAGCTAAGATCGAGCTAAATC 1701

Qy 182 ProGly 183

Db 1702 CAGGG 1707

RESULT 15

US-09-949-016-117588/c

; Sequence 117588, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 117588

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-117588

Alignment Scores:

Pred. No.: 4.38e-38 Length: 601

Score: 341.00 Matches: 70

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 36.86% Indels: 0

DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-117588 (1-601)

Qy 2 ValValAspLeuLeuTyrrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

Db 518 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 459

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAla 41

Db 458 CTATCTCTGCTGCTTTTCAATGACAGTATTGACGATTGTGACGCTAACAGCTTACATTGCC 399

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIle 61

Db 398 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGTATCCAAAGCTATC 339

Qy 62 GlnLysSerAspGluGlyHisPropheArg 71

Db 338 CAGAAATCAGATGAAGGCCACCCATTGAG 309

RESULT 17

US-09-949-016-14995

; Sequence 14995, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14995

; LENGTH: 42075

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14995

Alignment Scores:

Pred. No.: 4.13e-35 Length: 42075

Score: 341.00 Matches: 70

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 117589

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-117589

Alignment Scores:

Pred. No.: 4.38e-38 Length: 601

Score: 341.00 Matches: 70

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 36.86% Indels: 0

DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-117589 (1-601)

Qy 2 ValValAspLeuLeuTyrrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

Db 518 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 459

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAla 41

Db 458 CTATCTCTGCTGCTTTTCAATGACAGTATTGACGATTGTGACGCTAACAGCTTACATTGCC 399

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIle 61

Db 398 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGTATCCAAAGCTATC 339

Qy 62 GlnLysSerAspGluGlyHisPropheArg 71

Db 338 CAGAAATCAGATGAAGGCCACCCATTGAG 309

RESULT 17

US-09-949-016-14995

; Sequence 14995, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14995

; LENGTH: 42075

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14995

Alignment Scores:

Pred. No.: 4.13e-35 Length: 42075

Score: 341.00 Matches: 70

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

```
Query Match: 36.86% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-14995 (1-42075)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 24648 GTTGTGACCTCTGTACTGGAGACATTAGAGACTGGAGTGGTGTGGTGGCCAGC 24707
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 24708 CTATTCTGCTGCTTTCATTGACAGTATTGACGATTGTCAGCGTAACAGCCATACATTGCC 24767
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61
DB 24768 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGTATCAAGCTATC 24827
QY 62 GlnLysSerAspGluGlyHisProPheArg 71
DB 24828 CAGAAATCAGATGAGGCCACCCATTTCAGG 24857

RESULT 18
US-09-513-999C-3784
; Sequence 3784, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: Patent.pm
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3784
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 96..437
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 96..239
; OTHER INFORMATION: score 4.6
; OTHER INFORMATION: seq VFGSFLILLFSLT/QF
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 305
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 323
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 335
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 360
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 22
; OTHER INFORMATION: Xaa=Phe or Leu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 41
```

```
; OTHER INFORMATION: Xaa= * or Gly or Arg
US-09-513-999C-3784
```

## Alignment Scores:

```
Pred. No.: 1.4e-30 Length: 443
Score: 286.00 Matches: 59
Percent Similarity: 80.00% Conservative: 17
Best Local Similarity: 62.11% Mismatches: 19
Query Match: 30.92% Indels: 1
DB: 4 Gaps: 0
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-513-999C-3784 (1-443)

```
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
DB 159 ATTGACCTGTTGTATTTGGCGGACATCAAGCAGCGGCATCGTGTGGGAGTTTCCTG 218
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB 219 CTGCTGCTCTCTCTCCCTGACCATTCAGCTTCAGGTGGTGGTGGCTGCTGCTGCTG 278
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
DB 279 GCGGCACCTCTCAGCCACCATCAGTTTTCGTCATCTACAAGTCTGTGTTTACAGCAGTSCAG 338
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIleSerGlu 82
DB 339 ATACCGCAGCAGGCCACCG-TNGAAGGCTTACTTTGGAGCTTGAGATCACCCCTTTCTCAG 397
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 97
DB 398 GAGCAGATTTCAGAGTACAGGACTGCTGCTGAGCTTCTACGTGAC 442
```

## RESULT 19

```
US-09-949-016-15051
; Sequence 15051, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15051
; LENGTH: 135667
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15051
```

## Alignment Scores:

```
Pred. No.: 4.43e-26 Length: 135667
Score: 282.50 Matches: 73
Percent Similarity: 50.52% Conservative: 24
Best Local Similarity: 38.02% Mismatches: 51
Query Match: 30.54% Indels: 44
DB: 4 Gaps: 4
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-15051 (1-135667)

```
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 122176 GCAGCTATTGACCTGTGTATTGGCGGACATCAAGCAGACGCGCATCGTTGGAGT 122235
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
```

```
Db 122236 TTCTGCTGCTCTCTCTCCCTGACCCAGTTACGGTGGTGGAGCGTGGTGGCTTACCTG 122295
Qy 41 AlalaLeuLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 122296 GCCCTGGCGGCGACTCTCAGCCACCATCATAGTTTCGCCATCTACAAGTCTGTTTACAAGCA 122355
Qy 61 IleGlnLysSerAspGluGlyHisProPheArg----- 71
Db 122356 GTGCAGAAAACCGACGAGGCCACCTTTCAAGTCAGTGGCTCAGCTGAGGAGCCCTCAC 122415
Qy 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 122416 CCACTGACGAGGGCTTTTACCTCACCCTGATTTTCAGTCTCAGATGCATCTGAGTCAT 122475
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99
Db 122476 -----GTTTCTCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTTAACACCTGCTTTTG 122529
Qy 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 122530 AATATCTAACATTCTCTGGTGAATTTCTGAAACAACCTCGATTATTTTATTCATATCTT 122589
Qy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 122590 ATTGCTTTGTTGAGTTTTCATATGTAT----- 122616
Qy 133 AsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSer-IleProValIleTyr 152
Db 122617 -----TTACTATTAAACAGTAATCATATAATCAACAATTAATTAATCTCTCAGCAATATC 122670
Qy 152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db 122671 AGAAGGCACACGAGGCATTTTGTCCCTATTATA 122704
```

## RESULT 20

```
US-09-949-016-12869
; Sequence 12869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12869
; LENGTH: 152486
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12869
```

```
Alignment Scores:
Pred. No.: 5,35e-26 Length: 152486
Score: 282.50 Matches: 73
Percent Similarity: 50.52% Conservative: 24
Best Local Similarity: 38.02% Mismatches: 51
Query Match: 30.54% Indels: 44
DB: 4 Gaps: 4
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-12869 (1-152486)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 90995 GCAGCTATTGACCTGTTGTTGGCGGACATCAAGCAGCGGATCGTGTGGGAGT 91054
```

```
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 91055 TTCTGCTGCTGCTCTCTCTCCCTGACCCAGTTACGGTGGTGGAGCGTGGTGGCTTACCTG 91114
Qy 41 AlalaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 91115 GCCCTGGCGGCGACTCTCAGCCACCATCATAGTTTCGCCATCTACAAGTCTGTTTACAAGCA 91174
Qy 61 IleGlnLysSerAspGluGlyHisProPheArg----- 71
Db 91175 GTGCAGAAAACCGACGAGGCCACCTTTCAAGTCAGTGGCTCAGCTGAGGAGCCCTCAC 91234
Qy 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 91235 CCACTGACGAGGGCTTTTACCTCACCCTGATTTTCAGTCTCAGATGCATCTGAGTCAT 91294
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99
Db 91295 -----GTTTCTCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTTAACACCTGCTTTTG 91348
Qy 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 91349 AATATCTAACATTCTCTGGTGAATTTCTGAAACAACCTCGATTATTTTATTCATATCTT 91408
Qy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 91409 ATTGCTTTGTTGAGTTTTCATATGTAT----- 91435
Qy 133 AsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSer-IleProValIleTyr 152
Db 91436 -----TTACTATTAAACAGTAATCATATAATCAACAATTAATTAATCTCTCAGCAATATC 91489
Qy 152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db 91490 AGAAGGCACACGAGGCATTTTGTCCCTATTATA 91523
```

## RESULT 21

```
US-09-949-016-40169/c
; Sequence 40169, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40169
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40169
```

```
Alignment Scores:
Pred. No.: 2.59e-29 Length: 601
Score: 278.50 Matches: 72
Percent Similarity: 50.00% Conservative: 24
Best Local Similarity: 37.50% Mismatches: 52
Query Match: 30.11% Indels: 44
DB: 4 Gaps: 4
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-40169 (1-601)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
```

Db 580 GCAGCTATTGACCTGTTGATTTGGCGGACATCAAGCAGACGGGCATCGTTGGGAGT 521  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 520 TTCCTGCTGCTCTCTCTCCCTGACCCAGTTCAGCGTGTGAGCGTCTGCGCTACCTG 461  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 460 GGCCTGGCGGCACTCTCAGCCACCATCAGTTCCGCATCTACAAGTCTGTTTACAAGCA 401  
QY 61 IleGlnLysSerAspGluGlyHisProPheArg----- 71  
Db 400 GTGCAGAAAACCGAAGGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341  
QY 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 340 CCAGTACACAGGGGCTTTTACCTCAGCTGATTTTCAGCYCACAGATGCACTGATCAT 281  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99  
Db 280 -----GTTTCTCTGAGACCCACAGACCTCTTAGAGTCTCCCTAACACCTGCTTTG 227  
QY 100 -----IleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 226 AATATCTAACAATTCTGCTGGAATTTCTGAACAACTCGATTAATTTTCAATACATCT 167  
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132  
Db 166 ATTGCTTTGAGTTTCATATGAT----- 140  
QY 133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSer-IleProValIleTyr 152  
Db 139 -----TTACTATTACAGTAATCAATAATCAACAACTTACTTAATCTCTCAGCAATATC 86  
QY 152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163  
Db 85 AGAAAGGCACAGCAGGCAATTTTGTCCCTATTATTA 52

## RESULT 22

US-09-949-016-119335/c  
; Sequence 119335, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119335  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-119335

Alignment Scores:  
Pred. No.: 2,59e-29 Length: 601  
Score: 278.50 Matches: 72  
Percent Similarity: 50.00% Conservative: 24  
Best Local Similarity: 37.50% Mismatches: 52  
Query Match: 30.11% Indels: 44  
DB: 4 Gaps: 4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-119335 (1-601)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 580 GCAGCTATTGACCTGTTGATTTGGCGGACATCAAGCAGACGGGCATCGTTGGGAGT 521  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 520 TTCCTGCTGCTCTCTCTCCCTGACCCAGTTCAGCGTGTGAGCGTCTGCGCTACCTG 461  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 460 GGCCTGGCGGCACTCTCAGCCACCATCAGTTCCGCATCTACAAGTCTGTTTACAAGCA 401  
QY 61 IleGlnLysSerAspGluGlyHisProPheArg----- 71  
Db 400 GTGCAGAAAACCGAAGGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341  
QY 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 340 CCAGTACACAGGGGCTTTTACCTCAGCTGATTTTCAGCYCACAGATGCACTGATCAT 281  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99  
Db 280 -----GTTTCTCTGAGACCCACAGACCTCTTAGAGTCTCCCTAACACCTGCTTTG 227  
QY 100 -----IleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 226 AATATCTAACAATTCTGCTGGAATTTCTGAACAACTCGATTAATTTTCAATACATCT 167  
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132  
Db 166 ATTGCTTTGAGTTTCATATGAT----- 140  
QY 133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSer-IleProValIleTyr 152  
Db 139 -----TTACTATTACAGTAATCAATAATCAACAACTTACTTAATCTCTCAGCAATATC 86  
QY 152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163  
Db 85 AGAAAGGCACAGCAGGCAATTTTGTCCCTATTATTA 52

RESULT 23  
US-08-700-607-9  
; Sequence 9, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555



TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

LIBRARY: SPLNFET01

CLONE: 28742

US-08-700-607-9

## Alignment Scores:

Pred. No.:	1.51e-29	Length:	261
Score:	276.00	Matches:	59
Percent Similarity:	89.71%	Conservative:	2
Best Local Similarity:	86.78%	Mismatches:	7
Query Match:	29.84%	Indels:	0
DB:	2	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-700-607-9 (1-261)

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 2 CTATNCCNGCTGCTTTCATTCAGCATTTTCAGCATTTGAGCGTAACAGCCTACATTGCC 61

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 62 TTNGCCCTGCGNCTCTGTGACCATCAGCTNTAGGCTATACAAAGGGGTGATCCAGCTATC 121

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 122 CAGAAATCAGATGAAGNCACCCATTCAGGCGATATCTGGANTCTGAAGTTGCTATATCT 181

Qy 82 GluGluLeuValGlnLysTyrSer 89

Db 182 GAGGAGTTGNTTCAGAGTACACG 205

## RESULT 24

US-09-949-016-14730

; Sequence 14730, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14730

; LENGTH: 13906

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14730

## Alignment Scores:

Pred. No.:	4.63e-26	Length:	13906
Score:	271.00	Matches:	50
Percent Similarity:	87.32%	Conservative:	12
Best Local Similarity:	70.42%	Mismatches:	9
Query Match:	29.30%	Indels:	0
DB:	4	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-14730 (1-13906)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 2007 TCAGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC 2066  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 2067 ACGTGATCATGCTGCTTTCCCTGCGACGTTTCAGTGTTCATCAGTGTGTTTCTTACCTC 2126  
 Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 2127 ATCCTGGCTCTTCTCTGTGTCACCATCAGCTTCAGGATCTCAAGTCCGTCATCAAGCT 2186  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArg 71  
 Db 2187 GTACAGAAGTCAGAAGAGGCGCATCCATTCAG 2219

## RESULT 25

US-09-949-016-13161

; Sequence 13161, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13161

; LENGTH: 15661

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-13161

## Alignment Scores:

Pred. No.:	9.48e-23	Length:	15661
Score:	248.00	Matches:	86
Percent Similarity:	30.69%	Conservative:	34
Best Local Similarity:	21.99%	Mismatches:	53
Query Match:	26.81%	Indels:	220
DB:	4	Gaps:	4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-13161 (1-15661)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

Db 9398 ACAGTGGCGGACCTGCTGTACTGGAAGACACGAGGAGCTCAGGAGTGTCTTCACAGGC 9457

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 9458 CTGATGTCCTCCCTCTGCTCTGCTGCTTTAGCATTCGTCGTCGCGCGGCACTTG 9517

Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 9518 GCTCTGTTGCTGCTCTGCGGACCATCTCTCTCAGGGTTTACCGCAAGTGTCTCAGGCC 9577

Qy 61 IleGlnLysSerAspGluGlyHisProPhe 70

Db 9578 GTGCACCGGGGGATGG-AGCCAAACCTTTCCAGTGAGAACCCCGGCCCTGACCTGAG 9636

Qy 70 70

Db 9637 CCCCTGTCTGACCCCTAAAGCATGACCCACGACCTCAATCAGGACCGCATCCACCCG 9696

Qy 70 70

```
Db 9697 GACCCGACTCATCTTGATCATTTTTCATCCGATCCCTAACTACCCCTTCAATCCTTAA 9756
Qy 70 ----- 70
Db 9757 TCTCTGATCCTAACTGGTACCTTTCATCTCGATCCCTTCCCTGACCTGACCTGAC 9816
Qy 70 ----- 70
Db 9817 CCCAGCCCTTACATGTGATCTCTGAGTGCCCTCAGTCTAACTCTGTCTTCTCC 9876
Qy 70 ----- 70
Db 9877 CACCCGCAATCTCTCCCTTGTTCAGCTGCCCCGACAGCTGAGCTGGTCAACCA 9936
Qy 71 ----- 80
Db 9937 CTGAGTCGCCACACACTCTTTGTCGCCGCGAGGCGCTACCTGGATGTGGACCTCACCTG 9996
Qy 81 SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrlle 100
Db 9997 ACTCGGAGCAGACGGAAGCTTTGTCGCCACAGATCACCTCCCGCGTGTCTCGCGGCC 10056
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLys----- 117
Db 10057 ACGAGCTCGGCACCTTCTTCTGTGTAGAAGACCTCGTGATTCCTCAAGGTGGCTGG 10116
Qy 117 ----- 117
Db 10117 AGTCTCAGCCCTCCTCGGTTCGCCCAATTCACCTCTGCATGGCTAGGGGGTGGAGGCG 10176
Qy 117 ----- 117
Db 10177 GACTGTGGTAAATTCACAGATGAGAGGAATTCCTCGGTGGCTCTCTGACCTGAC 10236
Qy 118 -----PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsn 133
Db 10237 CTTACCCCCAGTGGCCCTCTCTCTACATCTTGACCTTGTGGTGCCCATCTTCAT 10296
Qy 134 GlyLeuThrLeuLeuLeuAla----- 141
Db 10297 GGTTTGACTCTTCTCATTTCTGGG-TGAGTGGAGGCGGTAAAGGGCAATGGGACTT 10355
Qy 141 ----- 141
Db 10356 GGAGTCTGTGGGGGACAGGGCTCCAGATGGAACCTTTCATCTCTTTGGGAACACCTGAC 10415
Qy 142 -----LeuIleSerLeuPheSerIleProValIleTyrGlu 153
Db 10416 GCCCCCATCTGTACCCACAGAGTGATGGTCTATTACCATCCCTCTGTGTACCGG 10475
Qy 154 ArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173
Db 10476 CAGCACCGGTG-----AGTGTGACACCTCA 10502
Qy 174 MetAlaLysIleGlnAlaLysIleProGlyLeu 184
Db 10503 GTTGTGACGACCCCACTGATAACATGGGGGTCTG 10535
RESULT 26
US-09-513-999C-11198
; Sequence 11198, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11198
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-11198

Alignment Scores:
Pred. No.: 4.22e-25 Length: 200
Score: 243.00 Matches: 48
Percent Similarity: 98.08% Conservatve: 3
Best Local Similarity: 92.31% Mismatches: 1
Query Match: 26.21% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-513-999C-11198 (1-200)

Qy 138 LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnVal 157
Db 2 CTGATTTTGGGCTCTCATTTCACTTCTCAGTGTCTCTGTTATTATGAACGGCATCAGCA 61
Qy 158 GlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIle 177
Db 62 CAGATAGATCATATCTAGGACTTCGCAATATGAATGTTAAAGATGCTATGGCTAAATC 121
Qy 178 GlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
Db 122 CAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 157

RESULT 27
US-09-949-016-40170/c
; Sequence 40170, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40170
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40170

Alignment Scores:
Pred. No.: 1.02e-10 Length: 601
Score: 146.00 Matches: 29
Percent Similarity: 82.22% Conservatve: 8
Best Local Similarity: 64.44% Mismatches: 8
Query Match: 15.78% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-40170 (1-601)

Qy 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 136 AGGGCTACTTGGAGCTTGAGATCACCTTCTCAGGACAGATTCAGAGTACAGGAC 77
Qy 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db 76 TGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAACCTGAGGAGGCTCTTCTTGTCCAG 17
```

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Qy 111 AspLeuValAspSer 115
Db 16 GACCTGGTGGATTCC 2

RESULT 28
US-09-949-016-119336/c
; Sequence 119336, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119336
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-119336

Alignment Scores:
Pred. No.: 1,02e-10 Length: 601
Score: 146.00 Matches: 29
Percent Similarity: 82.22% Conservative: 8
Best Local Similarity: 64.44% Mismatches: 8
Query Match: 15.78% Indels: 0
Gaps: 4
DB:

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-119336 (1-601)

Qy 71 ArgAlaThrLeuGluSerGluValAlaLeuSerGluGluLeuValGlnLysTyrSerAsn 90
Db 136 AGGCCTACTTTGGAGCTTGGATCATCCCTTCTCAGGAGCAGATTTCAGAAAGTACACGGAC 77

Qy 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgAcqLeuPheLeuValAsp 110
Db 76 TGCCTGCAGTTCTCAGTGAACAGCACCTTAAGGAACCTGAGAGGCTCTCTCTTGTCCAG 17

Qy 111 AspLeuValAspSer 115
Db 16 GACCTGGTGGATTCC 2

RESULT 29
US-09-248-796A-1905
; Sequence 1905, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; SENSITIVITY FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1905
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1905
```

```
Alignment Scores:
Pred. No.: 1,02e-09 Length: 1125
Score: 142.00 Matches: 50
Percent Similarity: 48.40% Conservative: 41
Best Local Similarity: 26.60% Mismatches: 75
Query Match: 15.35% Indels: 22
Gaps: 7
DB:

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-248-796A-1905 (1-1125)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 187 TCAACCACTGATTTTTCACCTTGAAGAACCAATCAAACTGGTAAAGTTTGGTTCC 246

Qy 21 SerLeuPhe-----LeuLeuLeuSerLeuThrValPheSerIleValSerValThr 37
Db 247 CTGTGTTTGGTTTGAATGCTCTGAAACTGTCAATTTATTCAATATCTTTTCCATTTA 306

Qy 38 AlaTyrIleAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyVal 57
Db 307 GCTTACATTTGGTTTA---TTGATCTCTGCTGCTGCTGAA-----TATTCCTGGT--- 351

Qy 58 IleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGlu 77
Db 352 -----AAATTGATTACTGCTAAAGGGTTTCCTTGCTAATTTCAACCA--- 393

Qy 78 ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer-----AlaLeu 93
Db 394 -----ACTGGTAAATTTGACGCTAAAGAGATTCAATGATGAAGTATTGCCAGAAITG 444

Qy 94 GlyHisValAsnSerThrIleLysGlu---LeuArgArgLeuPheLeuValAspLeu 112
Db 445 CCCAACTTAAATGTCATTTCGAGAAAGAGTTTAAATAAATTTCTATTTCACATGACATT 504

Qy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 505 GAAACCACTTTGAAAGCTGCTGGTATTCTTATATATATATATAAATTCACATTCATGGTTT 564

Qy 133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSerIleProValIleTyr 152
Db 565 TCATTGTACACTTGAATTTTCATTTCTGTTGTTGATTTTCCACGTTTCTGTCATTATAC 624

Qy 153 GluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp 172
Db 625 AAAACTTCAAGAAAGAAATTTGATGCTGCTGCTGCGGATATTACCAAGACCATTAACACC 684

Qy 173 AlaMetAlaLysIleGlnAlaLys 180
Db 685 AAGTCTGCTGAATTTACTGAAAG 708

RESULT 30
US-09-949-016-117609/c
; Sequence 117609, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117609
; LENGTH: 601
; TYPE: DNA
```

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; ORGANISM: Human
US-09-949-016-117609

Alignment Scores:
Pred. No.: 3,17e-06 Length: 601
Score: 114.00 Matches: 36
Percent Similarity: 35.19% Conservative: 2
Best Local Similarity: 33.33% Mismatches: 3
Query Match: 12.32% Indels: 67
DB: 4 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-117609 (1-601)

QY 141 AlaLeuileSerLeuPheSerIleProValIleTyrGluArgHisGlnVal----- 157
Db 505 GCTCTCATTTCACTTTCAGTGTCTCTGTTATTTATGAACGCATCAGGTAATTTCCCTAA 446
QY 157 ----- 157
Db 445 CTAAGTGTGACTTCAGAAATAGAGCACTCACTTATTACATGGGATTTACGGATGTATTA 386
QY 157 ----- 157
Db 385 GTGCCATTTTCAATGCTCTTACAAAATGAGAGTGTGATGTTCTTAAAGCCTTAGCT 326
QY 157 ----- 157
Db 325 TGACACATAGTAGTGGTTAATAAGMTTCTTTAGCAACGGTAATAATTCCTTTATACCTCT 266
QY 158 -----GlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValIleAspAlaMe 174
Db 265 CTTTCAGGCACAGATAGATCATATCTAGGACTTGCAAAATAGAATGTTTAAAGATGCTAT 206
QY 174 tAlaLysIleGlnAlaLysIle 181
Db 205 GCGTAAGTAAGTATTAAATC 184

RESULT 31
US-09-313-294A-703
; Sequence 703, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 703
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549677H1
US-09-313-294A-703

Alignment Scores:
Pred. No.: 4.29e-06 Length: 266
Score: 109.00 Matches: 21
Percent Similarity: 65.08% Conservative: 20
Best Local Similarity: 33.33% Mismatches: 20
Query Match: 11.78% Indels: 2
DB: 4 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-313-294A-703 (1-266)

QY 106 LeuPheLeuValAspLeuValAspSerLeu-----LysPheAlaValLeuMetTrp 123
Db 71 CTTCTAATTATATGCTCTTATCCCTGTTCTTGGTGCAAAAGGTGATATGATTTTGTGG 130

QY 124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuLeuLeu 143
Db 131 GTGGTTTCATTTCGAATGCTCTTCAATTTTCTAGCTTATTACATTTGGTGTAAATG 190
QY 144 SerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db 191 CTTTCTCTGTTGGTTCCCACTCTATGAGAAGTAGTACCAGGACCGAGTTGATGAGAAGGTT 250
QY 164 GlyLeuAla 166
Db 251 GGTGTAGCG 259

RESULT 32
US-09-949-016-48087/c
; Sequence 48087, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 48087
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-48087

Alignment Scores:
Pred. No.: 0.000153 Length: 601
Score: 102.00 Matches: 21
Percent Similarity: 70.00% Conservative: 7
Best Local Similarity: 52.50% Mismatches: 12
Query Match: 11.03% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-48087 (1-601)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 120 ACAGTGGCGGACCTGCTGACTGGAAGGACACGAGGACGCTCAGGAGTGTCTTCACAGGC 61
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 60 CTGATGGTCTCCCTCTCTGCTCTGACATTAGCATGCTGCTCCGCGGCACTTG 1

RESULT 33
US-08-905-223-178
; Sequence 178, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelt, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Win95  
SOFTWARE: Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 178:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: DOUBLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: other  
LOCATION: 73..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 97  
OTHER INFORMATION: region 1..245  
OTHER INFORMATION: id HUM506F10B  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..376  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 98  
OTHER INFORMATION: region 243..305  
OTHER INFORMATION: id HUM506F10B  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 63..193  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 99  
OTHER INFORMATION: region 1..131  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 95  
OTHER INFORMATION: region 254..341  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 277..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 97  
OTHER INFORMATION: region 216..256  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 397..426  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 338..367  
OTHER INFORMATION: id AA056148

OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 88..189  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 98  
OTHER INFORMATION: region 1..102  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 230..317  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 187..271  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 95  
OTHER INFORMATION: region 101..185  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 269..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 93  
OTHER INFORMATION: region 184..232  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 397..426  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 314..343  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 87..200  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 92  
OTHER INFORMATION: region 1..114  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 231..318  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 199..275  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 94  
OTHER INFORMATION: region 114..190  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 269..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 91  
OTHER INFORMATION: region 185..233  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est

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FEATURE:
NAME/KEY: other
LOCATION: 397..426
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 96
OTHER INFORMATION: region 315..344
OTHER INFORMATION: id HSC16E081
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 85..186
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 99
OTHER INFORMATION: region 24..125
OTHER INFORMATION: id AA157365
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 183..263
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 90
OTHER INFORMATION: region 123..203
OTHER INFORMATION: id AA157365
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 337..401
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 95
OTHER INFORMATION: region 278..342
OTHER INFORMATION: id AA157365
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 273..326
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 90
OTHER INFORMATION: region 213..266
OTHER INFORMATION: id AA157365
OTHER INFORMATION: est
Alignment Scores:
Pred. No.: 0.000167 Length: 425
Score: 100.00 Matches: 20
Percent Similarity: 80.00% Conservative: 8
Best Local Similarity: 57.14% Mismatches: 7
Query Match: 10.81% Indels: 1
DB: 3 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-08-905-223-178 (1-425)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAla 20
Db 321 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAGAGAGACTGGGTTTGTCTTGGCACC 380
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35
Db 381 ACGCTGATCATGCTGCTTTC-CTGGCAGCTTTCAGTGTGCATCAGT 424
RESULT 34
US-08-487-596-7
Sequence 7, Application US/08487596
Patent No. 6440681
GENERAL INFORMATION:
APPLICANT: Eliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
FEATURE:
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 155..1561
OTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"
US-08-487-596-7
Alignment Scores:
Pred. No.: 0.00884 Length: 1828
Score: 95.00 Matches: 41
Percent Similarity: 38.74% Conservative: 33
Best Local Similarity: 21.47% Mismatches: 56
Query Match: 10.27% Indels: 56
DB: 3 Gaps: 7
US-09-830-972-2_COPY_975_1163 (1-189) x US-08-487-596-7 (1-1828)
QY 24 LeuLeuLeuSerLeuThrValPheSerIleVal----- 34
Db 1016 GTACTTGTGCTTTTGCATGCTCTTCCTGTTATTGAAGAGATCATCATCTTCA 1075
QY 35 -----SerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50
Db 1076 AAAGTCATACCTCTTAATGGAGATGATCTGTATTACCATGATTTTGTGACACTGTCA 1135
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro--- 69
Db 1136 ATTATGGTAACCGCTCTTCCTATCAACATTCATCATCGTTCCTCTCAACACATAATGCC 1195
QY 70 -----PheArg 71
Db 1196 ATGGGCGCTTTGGTCCGCAAGATATTTCTTCACAGCTTCCCAAACTGCTTTTGCATGAGA 1255
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Qy 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGln-----Lys 87  
: : : : :  
Db 1256 AGTCATGTAGACAGCTACTTCACACAGAAAGAGAAAACCTGAGAGTGCTAGTGACCACAAA 1315  
  
Qy 88 TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPhe 107  
: : : : :  
Db 1316 TCITCTAGAACAACATTGGAGCGCTCAATTCATTCCGTACATTACAGACACATC 1375  
  
Qy 108 Leu-----ValAspAspLeuValAspSerLeuLysPhe----- 118  
: : : : :  
Db 1376 ATGAAGAAATAATGATGTCGCGTAGGTTGTTGAAGATTGGAAATTCATAGCCAGGTTCTT 1435  
  
Qy 119 ---AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 137  
: : : : :  
Db 1436 GATCGGATGTTCTGTGGACTTTTCTTTTCGTTTCA----- 1471  
  
Qy 138 LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnVal 157  
: : : : :  
Db 1472 ---ATTGTGGATCTCTGGGCCTTTT---GTTCTGTATTATATAAATGGGCAAATATA 1525  
  
Qy 158 GlnIleAspHisTyrLeuGlyLeuAlaAsnLys 168  
: : : : :  
Db 1526 TTAATACCAGTTCATATGGAAATGCCAAATAAG 1558  
  
RESULT 35  
US-08-660-451A-7  
; Sequence 7, Application US/08660451A  
; Patent No. 6524789  
; GENERAL INFORMATION:  
; APPLICANT: Elliott, Kathryn J.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE  
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME.  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,451A  
; FILING DATE: June 7, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,722  
; FILING DATE: 06/07/95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-9370B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1828 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5725
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-5725

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; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2072
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2072

Alignment Scores:
Pred. No.: 0.132 Length: 1779
Score: 86.50 Matches: 49
Percent Similarity: 38.46% Conservative: 41
Best Local Similarity: 20.94% Mismatches: 61
Query Match: 9.35% Indels: 83
DB: 4 Gaps: 12

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-134-000C-2072 (1-1779)
QY 7 TyrTrpArgAspIleuValSerLeuPheGlyAlaSerLeuPheLeuLeu 26
Db 133 TTCTGGAACAGTGAACGT-----TTATTGATACATG 168
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSer 46
Db 169 TCTAAACGAATGCTGCAATTATTGCTGTC-----TTAGTATTAGCAATTGCGGCC 219
QY 47 ValThrIleSerPheArg-----IleTyrIle 55
Db 220 GTCTGTTTCCAAATTCACACCAACAAAGTATTAGGACGCGCAACACTGAATTTTAA 279
QY 56 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla----- 72
Db 280 GCGTCATGAAGGCGCTGCTGAATGAACACAGGCTTAAATAACATCTTTTCCAATT 339
QY 73 -----TyrLeuGluSerGlu 77
Db 340 GATTTTGACAAAATTGGTCAAAATTTTATTAAATTTATTGTCATGTTTCTGCT 399
QY 78 Val-----Ala 79
Db 400 GTCTTTAAATTTCTTGACGCAAGTAAATTATGACACGCTGTTTACAGCGAAAGTTTATGAA 459
QY 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-----His 95
Db 460 TTACGTCAGAAATTAGACGCGAAATGAACAAAGTTCCAAATTCCTATTATGATATTCAT 519
QY 96 ValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSer 115
Db 520 AGTAATGGGACATTATGTCAC---CGGGCAATTACGACATGATAAATTGCGAGTACT 576
QY 116 LeuLys-----PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 577 TTACACCAAAACTTAACCCAAATTAATACAGTATCGTCACATTTGTGGGTGACTTTGG 636
QY 133 AsnGlyLeuThr-----LeuLeuIleLeuAlaLeu-----IleSer 144
Db 637 ATGATCTGACCAATTAGCTGGCGAGTTAACACTAAATTCCTTAGCAACAGTGCATTAAGT 696
QY 145 LeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr----- 162
Db 697 TTAATTGTTGTGATGTTGTGGCGCTCGCTCGCAA-----AAACATTTTGGCGCT 747
QY 163 -----LeuGlyLeuAlaAsnLysSerValLysAsp 172
Db 748 CAACAAAAAGCTTAGGATTTATTGAATAAACCAAGTCGAAGAA 789

RESULT 45
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-956-171E-322 (1-1302)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal---ValPheGlyAla 20
Db 68 ATAGTTATTATTGCTGCTGTTTAAAGAAACATTCGTACGACGCAATTCCTATTATATCGATT 127
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 128 CGGTTATCATCTCTTATGCGCTTATGCTCTGAAATTTGAGTGATGTTTCATTGATATA 187
QY 41 ---AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 59
Db 188 CTAACGTTAGTGCATTACACATGCGATTGGA---CGTGTATACACGATTCGATTGTA 244
QY 60 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79
Db 245 GTTGTGTTGAA-----AATATTATTCGACGCTTAAACAGATTCAGAAAGCAAA 289

; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 322:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1302 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 322:
US-09-956-171E-322

Alignment Scores:
Pred. No.: 0.0937 Length: 1302
Score: 86.00 Matches: 42
Percent Similarity: 41.80% Conservative: 37
Best Local Similarity: 22.22% Mismatches: 78
Query Match: 9.30% Indels: 32
DB: 4 Gaps: 7
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;; PRIOR APPLICATION NUMBER: US 60/024,428  
;; PRIOR FILING DATE: 1996-08-22  
;; NUMBER OF SEQ ID NOS: 3  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1 1664976  
;; LENGTH: 1664976  
;; TYPE: DNA  
;; ORGANISM: Methanococcus jannaschii  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (28222)..(28222)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (28257)..(28258)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (84773)..(84773)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (84808)..(84808)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (84812)..(84812)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98120)..(98120)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98159)..(98159)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98239)..(98239)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98266)..(98266)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98343)..(98343)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (103998)..(103998)  
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;; NAME/KEY: misc feature  
;; LOCATION: (148948)..(148948)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (163385)..(163385)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (191989)..(191989)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (191995)..(191995)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (231980)..(231980)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (234187)..(234187)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (234220)..(234220)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (234814)..(234814)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (309398)..(309398)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (309418)..(309418)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (312837)..(312837)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (312993)..(312993)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (319226)..(319226)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (559167)..(559167)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (559241)..(559241)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (600992)..(600992)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (622708)..(622708)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (657081)..(657081)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (657203)..(657203)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (674435)..(674435)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (682442)..(682442)  
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;; NAME/KEY: misc feature  
;; LOCATION: (713652)..(713652)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (741684)..(741684)  
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;; NAME/KEY: misc feature  
;; LOCATION: (779455)..(779455)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (779676)..(779676)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (855539)..(855539)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (871619)..(871619)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1084830)..(1084830)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1096846)..(1096846)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1119881)..(1119881)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1130881)..(1130881)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1310988)..(1310988)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1313224)..(1313224)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1349473)..(1349473)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1349491)..(1349491)

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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664855)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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## Alignment Scores:

Pred. No.:	1.32e+04	Length:	1664976
Score:	85.00	Matches:	46
Percent Similarity:	42.51%	Conservative:	25
Best Local Similarity:	27.54%	Mismatches:	56
Query Match:	9.19%	Indels:	40
DB:	4	Gaps:	8

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-916-421B-1 (1-1664976)

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QY 6 LeuTyrTrpArgAspIle-----LysLysThrGlyValValPhe 18
Db 771873 CTATATAAAGAACATAAAAGGAATATTATACCTCTTTAAAAAACTTCGTAAGGATTTT 771932
QY 19 GlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIle---ValSerValThr 37
Db 771933 GACGAAAAAAGTTTATATTATTTGTTAAATATAGTCGCGATACCTCTCTTAATATCA 771992
QY 38 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyVal 57
Db 771993 TATTATTACACTTAACCTTAAGAGTATGATTATTTGTAGTTATATACGTTGGAGCT 772052
QY 58 Ile-----GlnAlaIleGlnLysSerAspGluGlyHis 68
Db 772053 GCATTGTTCCATCTCTATTTTATATGAAAAATAAATAAGAACTCTTGAGATAACATT 772112
QY 69 ProPheArgAlaTyr-----LeuGluSerGluValAlaIleSerGluGlu 83
Db 772113 CCACAGCTCTTTATATTATGATTTAGCCCTCGAATCTGGAGGTCCTCAATACCGAAGCA 772172
QY 84 LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103
Db 772173 TTACTTGAAGTT-----GTTAAAGTAATATAAAGGAAGTT 772208
QY 104 -----ArgArgIlePheLeuValAspLeuValAspSerLeuLysPhe 118
Db 772209 AGCGATATATTTAGAAAAGTTTATACCTTAATCGGAAAC-----CAAAAATTAAGTTT 772262
QY 119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138
Db 772263 GAAGACTCTATG-----ACAATTGTATCAATTTATATGATTTCTAAAGTATTAAAG 772313
QY 139 IleLeuAlaLeuIleSerLeu 145
Db 772314 ATGTTAGCAAGAATTATGATT 772334
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## RESULT 50

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US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
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; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
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NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (309398)..(309398)
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (657203)..(657203)
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FEATURE:
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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LOCATION: (713652)..(713652)
FEATURE:
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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Alignment Scores:
Pred. No.: 1.32e+04 Length: 1664976
Score: 85.00 Matches: 46
Percent Similarity: 42.51% Conservative: 25
Best Local Similarity: 27.54% Mismatches: 56
Query Match: 9.19% Indels: 40
DB: Gaps: 8
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-692-570-1 (1-1664976)

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Qy 6 LeuTyrTrpArgAspIle-----LysLysThrGlyValValPhe 18
|||||
Db 771873 CTATATAAGACAACTAAAGGAATATATATCTTTAAAGAACTGGTAAGATT 771932

Qy 19 GlyAlaSerLeuPheLeuLeuLeuSerValThrValPheSerIle---ValSerValThr 37
|||||
Db 771933 GACGAAAAAAGTTTATATTATTCTTAATTATAGCTGGATACCTCTCTCTAATATCA 771992

Qy 38 AlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrGlyGlyVal 57
|||||
Db 771993 TATTATTACACTTAACCCCTAAAGATATGTTATTTTGTAGTTATATATCTGGAGCT 772052
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QY 58 Ile-----GlnAlaIleGlnLysSerAspGluGlyHis 68  
Db 772053 GCATTGTTCCATTCCTATTTTATATGAAATAAATAGAACTCTTCGAGAAATACATT 772112  
QY 69 ProPheArgAlaTyr-----LeuGluSerGluValAlaIleSerGluGlu 83  
Db 772113 CCACAGCTCTTTATATTATGATATTAGCCCTCGAATCTCGAAGGTCCATAACGAGCA 772172  
QY 84 LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103  
Db 772173 TTACTTTGAAGTT-----GTTAAAGTAATATAAAGGAAGTT 772208  
QY 104 -----ArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe 118  
Db 772209 AGCGATATATTTAGAAAGCTTTTATATCTTAATGGAAAC-----CAAAATTAAGTTT 772262  
QY 119 AlavalLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138  
Db 772263 GAAGAGTCTATG-----ACATTTGTATCCAATTTATATGATCTTAAGTATTAAAG 772313  
QY 139 IleLeuAlaLeuIleSerLeu 145  
Db 772314 ATGTTAGCAAGAATTATGATT 772334  
RESULT 51  
US-09-543-681A-2003  
; Sequence 2003, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 2003  
; LENGTH: 843  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-2003  
Alignment Scores:  
Pred. No.: 0.0755 Length: 843  
Score: 84.50 Matches: 38  
Percent Similarity: 39.25% Conservative: 35  
Best Local Similarity: 20.43% Mismatches: 67  
Query Match: 9.14% Indels: 46  
DB: 4 Gaps: 6  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-543-681A-2003 (1-843)  
QY 2 ValValAspLeuLeuTyr---TrpArgAspIleLysLysThr----- 14  
Db 58 GTGGTAGGATCATTTATGATGAG-----ATAAACGCTCTCTTACCCCTAAACAGGT 111  
QY 15 -----GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeu 28  
Db 112 ATCAATATATCTCGGGAGGAGTAATAGTAGGAATACTACTCTCTATTCTTTAGCTCT 171  
QY 29 ThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThr 48  
Db 172 AGCATTTATGGGTATTTAGTCTCTTTAGAGATATCTGGCAATCTCTGTTATGGTTATG 231  
QY 49 IleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln-----LysSerAspGluGly 67  
Db 232 ATGGAATCATTCCTCCCTCTATTAATTTGTTGATGCTGTCTATTTGATGATGAACAAAGGT 291  
QY 68 HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLys 87  
Db 292 AAATCACTAAAGCCAATATCGAAAC-----GAAATTGACACAAAAA 333

QY 88 TyrSerAsnSerAlaLeu----- 93  
Db 334 ACGCAACAAACAAAGTGTCTGGGGGATTTTACTGATCATCGCATTCGCCATTCGAGAGAA 393  
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 104  
Db 394 GCGCGGAGGTGGTTGTTTCTCAAGCCATATTATGGCTCTCACAGCACAAACCGCG 453  
QY 105 ArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
Db 454 TTGCTCTTCTTGATTGAAGTATTTCATTCGCCCTATTGATAGCGGACTAATCTCTATGTTA 513  
QY 125 PheThrTyrValGlyAlaLeu-PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSe 144  
Db 514 TTTTGTCAACATCAAAATGATTTCTTGGCGTAAATTTCTTTGTTATTATACCGGATTTT 573  
QY 144 rleuPheSerIlePro 149  
Db 574 CTGCTTTTCTCGCGC 589  
RESULT 52  
US-09-328-352-740  
; Sequence 740, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 740  
; LENGTH: 1782  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-740  
Alignment Scores:  
Pred. No.: 0.252 Length: 1782  
Score: 84.50 Matches: 35  
Percent Similarity: 44.06% Conservative: 28  
Best Local Similarity: 24.48% Mismatches: 48  
Query Match: 9.14% Indels: 33  
DB: 4 Gaps: 6  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-328-352-740 (1-1782)  
QY 8 TrpArgAspIleLysLysThr-----GlyValValPheGlyAlaSerLeuPheLeuLeu 25  
Db 772 TGGCGTGGTGTAAAGAAACITGGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831  
QY 26 LeuSerLeuThrValPheSerIleVal-----SerValThrAlaTyrIle 40  
Db 832 GCCCAGTATCTCACCTTAACCTTTATTGGCCCTGAGTACCAGACATTAACCGCAAT 891  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 892 GCT---TCATTGGTCAGCTGACGTGTTATTCCGTGTTTGGAAA----- 933  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 934 -----CCAAACATATTTCCGTTTTTGAACCTGAACGGGTGACAGCTTTG 978  
QY 81 SerGluGlu-----LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSer 98  
Db 979 GCTCAGCAACCTTCAACAGTTTCAACGTTATAGCATTTGGGAAATTTGCAAGGCGTCT 1038  
QY 99 -----ThrIleLysGluLeuArgLeu 106  
Db 1039 CCATTTGCTATTTTAAACGTAATGTCAGATTGCGGCTTAAGCCATTAAAGCATTTA 1098

Qy 107 PheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr 126  
Db 1099 TTTGCAAGATGGTCTTGAACACTGGATTTTAAACTTGAAGTGCC-GTATTTACA 1157  
Qy 127 TyrValGly 129  
Db 1158 CAATTTGGT 1166

## RESULT 53

US-09-602-787A-301  
; Sequence 301, Application US/09602787A  
; Patent No. 696561  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Mark  
; APPLICANT: Krüger, Burkhard  
; APPLICANT: Schöder, Hartwig  
; APPLICANT: Zeider, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; TITLE OF INVENTION: TRANSPORT  
; FILE REFERENCE: BGI-125CP  
; CURRENT APPLICATION NUMBER: US/09/602,787A  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: USN 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: DE 19931454.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931478.0  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931563.9  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932122.1  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932124.8  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932125.6  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932128.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932180.9  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932182.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932190.6  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932191.4  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932209.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932212.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932227.9  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932228.7  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932229.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932230.9  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932927.3  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933005.0  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933006.9  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19940764.9  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940765.7  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940766.5  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940830.0

; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940831.9  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940832.7  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940833.5  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19941378.9  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941395.9  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19942077.7  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: DE 19942078.5  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: DE 19942079.3  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: DE 19942088.2  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 678  
; SEQ ID NO 301  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1477)  
; OTHER INFORMATION: RXN00456  
US-09-602-787A-301

## Alignment Scores:

Pred. No.:	0.264	Length:	1500
Score:	83.50	Matches:	41
Percent Similarity:	40.38%	Conservative:	22
Best Local Similarity:	26.28%	Mismatches:	50
Query Match:	9.03%	Indels:	43
DB:	4	Gaps:	6

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-602-787A-301 (1-1500)

Qy	8	TrpArgAspIleLysLys-----ThrGlyVal-----ValPheGlyAla 20
Db	53	TGGCGTGTCTGTCGCAGACITTTGCTCATTCGCCCTAGGTGTACTTGGTGTCTGCAGGCA 112
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db	113	CTGCTGGCGATCATGTGTCTGTGAGCGTAGCCCATCTTGAGGGAAACCGAGCACTT 172
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db	173	GTTGGATTGCTGTGTGTACCACTTGGGTTTG-----GGGTTGGCGCAGTGG 220
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db	221	ATTCAAAA-----GTAGTG 235
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db	236	GCAGAAGATCTAGGCCAGCATTAT-----GTGCATGAGGTGCGT 274
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe----- 118
Db	275	CGTGAATTGGTGGTGTGCTGCTCGCTCGAATAACGGCCTCGTTGGGCGGTGACTGTC 334
Qy	119	-----AlaValLeuMetTrpValPheThrTyrValGlyAla 130
Db	335	ACCGAGCCAGCAATGATCTCACCGCGTGGCGCAATTGGGTGGCTTTGGGCATTGTTCCG 394
Qy	131	LeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPhe 146
Db	395	ATGCTCACCGGCTGCGGCTTGATTGCGATTGTGCTGGTGGCGGTGTTT 442

## RESULT 54

US-09-583-110-1302  
; Sequence 1302, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 1302  
; LENGTH: 1233  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-1302

Alignment Scores:  
Pred. No.: 0.266 Length: 1233  
Score: 82.50 Matches: 38  
Percent Similarity: 47.40% Conservative: 35  
Best Local Similarity: 24.68% Mismatches: 50  
Query Match: 8.92% Indels: 31  
DB: 4 Gaps: 7

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-583-110-1302 (1-1233)

QY 11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30  
Db 235 ATTGCCAAATCAAAATCTGCTACGCTATTTTGACAGTATTTCTGCTGTGCGCC 294  
QY 31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50  
Db 295 TTTTCATTAGTTTCAGTCATTATGATGTCATCACTCACTCTCTGACACCTTGAC 354  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
Db 355 TAC-----CTG 360  
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAen 90  
Db 361 TGTGCTACATGATGACCCCTCTACATCAGT-----GTAATTAGGACGACCTGCA 414  
QY 91 SerAlaLeuGlyHisValAenSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110  
Db 415 GATGCCATGGGTTTCAGGAGTCTCTGATGAGGGTTGTCGGT----- 456  
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr---TyrValGly 129  
Db 457 ---ATTGTGCCAAATCTGCTGCGCATTCCTTATCAATGTTATAGTATTCAAACTATT 513  
QY 130 AlaLeuPheAenGlyThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIle--- 148  
Db 514 TCCCTTATCAACTCTGACT---TTTGTCAITGCTCTTTTGGCTGTGATGTTATTCGA 570  
QY 149 ProValIleTyrGlu---ArgHisGlnValGlnIleAspHis 161  
Db 571 CATACCTTGTATGAGGTTGAAAAAGCAATTGAAATGTCACAT 612

## RESULT 55

US-09-107-433-2599  
; Sequence 2599, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN  
THERAPEUTICS

NUMBER OF SEQUENCES: 5206  
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354

COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 2599:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1275 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae  
FEATURE:

NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...1275

SEQUENCE DESCRIPTION: SEQ ID NO: 2599:  
US-09-107-433-2599

Alignment Scores:  
Pred. No.: 0.281 Length: 1275  
Score: 82.50 Matches: 38  
Percent Similarity: 47.40% Conservative: 35  
Best Local Similarity: 24.68% Mismatches: 50  
Query Match: 8.92% Indels: 31  
DB: 4 Gaps: 7

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-107-433-2599 (1-1275)

QY 11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30  
Db 277 ATTGCCAAATCAAAATCTGCTACGCTATTTTGACAGTATTTCTGCTGTGCGCC 336  
QY 31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50  
Db 337 TTTTCATTAGTTTCAGTCATTATGATGTCATCACTCACTCTCTGACACCTTGAC 396  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
Db 397 TAC-----CTG 402  
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAen 90  
Db 403 TCTGCTACATGATGACGCCCTCTACATCACT-----GTAATTAGGACGACCTGCA 456

```

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-961-527-146 (1-11887)

Qy 11 IlleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30
Db 9678 ATTGCCAAATCAAAATCTGCTTACGCTATTTTTCACAGTATTTCTCGTCTTTTCGCC 9737

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[illegible]

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Db      144846 GGGCGTGTTTTGACTGGATTCCACCCACTACTGACAGTGCCATTGTGTATTTTGGATTTTA 144900
Qy      139 IleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluAa-gHisGlnValGln 158
Db      144906 GCGCTTTTCGGCTTTATTGGTATTGTATTGGCCACGCCTTCAGCGTACCAGTCGGATACAG 144965
Qy      159 IleAspHisTyrLeuGluGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIle 177
Db      144966 GCGGAT---GCTCGTGTCTTTTGATGCACAGGTGCGAATTACCGATGCTTATGCTAAATATC 145019

RESULT 59
US-09-949-016-12900
; Sequence 12900, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 12900
; LENGTH: 462589
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12900

Alignment Scores:
Pred. No.:      4.42e+03      Length:      462589
Score:          82.00        Matches:      46
Percent Similarity: 38.71%    Conservative: 26
Best Local Similarity: 24.73%  Mismatches:  48
Query Match:      8.86%     Indels:      66
DB:               4         Gaps:         8

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-12900 (1-462589)

Qy      24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43
Db      110616 CTACTTTTGTCACTTAGTATCTAC-----ATTACCCGATTAACCTTAATCAGT 110663
Qy      44 LeuLeu-----SerValThrIleSerPheArgIleTyrIlySGly 56
Db      110664 GTCATGTGTCCTGCTCACTAACTGCATTAATTTGCTGTGATTTCATTCGCGCATCTACAAAATG 110723
Qy      57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db      110724 GTAATAACATA-----GGACATATTTTATAGGCGCTATATTGTAAT 110765
Qy      77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96
Db      110766 -----GTATTAAATGAGAAAATCCTTGAGTATTGCTTAGCACTGTGCTAGAACATGAA 110819
Qy      97 AsnSer-----ThrIleLysGluLeuArgAlaGluPheLeuValAsp 110
Db      110820 AACTCTTTAATAAAGCTTTGGCTATTAGTCTTGCTCTAAACGGTAAAGACTGTTTCTGCTTAT 110879
Qy      111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrp-----123
Db      110880 CCCTTGTTGTTATCCCCAGTCTTTTGGCAGACAACTTTGGCAGCAGATTAATCATAGAAA 110939
Qy      124 -----ValPheThr-----126
Db      110940 TTATTGAATAAATTAATGGTCCCACTTTTTCCTAGCTCCACTGTGGTGAAGTCTCAGAT 110999

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QY 127 -----TyrValGlyAlaLeuPheAsnGlyLeu----- 135  
Db 111000 TCCCAAGGATGGTGTGTGCAGATAGGTTCCATGTGCCAGGGCTCTTGTTCAGTTTA 111059  
QY 136 -----ThrLeuLeuLeuLeuAlaLeuLeuSerLeuPheSerIlePro 149  
Db 111060 GTGTATTATTCTGCCACACTTGTCTTAATCCAGATTGATTGCTTTTATATGAAGATA 111119  
QY 150 VallIleTyrGluArgHis 155  
Db 111120 GTAATATATGGAGGCAT 111137  
RESULT 60  
US-09-949-016-12412  
; Sequence 12412, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12412  
; LENGTH: 476044  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12412  
Alignment Scores:  
Pred. No.: 4,636+03 Length: 476044  
Score: 82.00 Matches: 46  
Percent Similarity: 38.71% Conservative: 26  
Best Local Similarity: 24.73% Mismatches: 48  
Query Match: 8.86% Indels: 66  
DB: 4 Gaps: 8  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-12412 (1-476044)  
QY 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43  
Db 124072 CTACTTTGTCTACCTAGTATCTAC-----ATTACACCGATTAACTTAATCAGT 124119  
QY 44 LeuLeu-----SerValThrIleSerPheArgIleTyrIlyGly 56  
Db 124120 GTCACTGGTCTGTCACTGATCAATTAATTTGTCTGATTATTCCTCCGATCTACAAAATG 124179  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
Db 124180 GTAATAACATA-----GGACATATTTTATAGGGCTATATATTGAAT 124221  
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96  
Db 124222 -----GTATTAAATGAGAAAATCCTTCAGTATTGCTTAGCAGTGTGCTAGAACATCAA 124275  
QY 97 AsnSer-----ThrIleLysGluLeuArgArgLeuPheLeuValAsp 110  
Db 124276 AACTCTTAATAAGCTTGGCTATTAGTCTTGTCAACCGTAAAGACTGTTTCTGTCTTAT 124335  
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrp----- 123  
Db 124336 CCCTTGTGTTATCCCACTTCTTTCACAGAACTTGTGGCAGGAGTAATCATAGAAA 124395  
QY 124 -----ValPheThr----- 126

Db 124396 TTATTGAATAAAATAATAGTCCACTTTTTCCTAGCTCCACTGTGTGGAAGTCTCAGAT 124455  
QY 127 -----TyrValGlyAlaLeuPheAsnGlyLeu----- 135  
Db 124456 TCCCAAGGATGGTGTGTGCAGATAGGTTCCATGTGCCAGGGCTCTTGTTCAGTTTA 124515  
QY 136 -----ThrLeuLeuLeuLeuAlaLeuLeuSerLeuPheSerIlePro 149  
Db 124516 GTGTATTATTCTGCCACACTTGTCTTAATCCAGATTGATTGCTTTTATATGAAGATA 124575  
QY 150 VallIleTyrGluArgHis 155  
Db 124576 GTAATATATGGAGGCAT 124593  
RESULT 61  
US-09-248-796A-730  
; Sequence 730, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 730  
; LENGTH: 1152  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-730  
Alignment Scores:  
Pred. No.: 0.329 Length: 1152  
Score: 81.50 Matches: 41  
Percent Similarity: 36.16% Conservative: 23  
Best Local Similarity: 23.16% Mismatches: 44  
Query Match: 8.81% Indels: 69  
DB: 4 Gaps: 7  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-248-796A-730 (1-1152)  
QY 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSer 32  
Db 91 AAAAATTCAATTGAATTCAATCAAAACACTC-----CTGACACTATTATT 135  
QY 33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArg 52  
Db 136 ATGATTTTCCTTAAGGGCAGTAAATCGCACTATTCTTTTACCACCTAAATTTATTATT 195  
QY 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72  
Db 196 TTAATCAA-----TATCCATTT----- 213  
QY 73 TyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAla 92  
Db 213 ----- 213  
QY 93 LeuGlyHisValAsnSerThrIleIysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 214 TTCGGGGGTGAACCCCTATATACAAG-----AATGATTG 249  
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValIleGlyAlaLeuPhe 132  
Db 250 GTCAATTCCTTGAATTAACCGTT-----TAT 276  
QY 133 AsnGlyLeuThrLeuLeuIleLeuAlaLeuLeuSerLeuPheSerIleProValIleTyr 152  
Db 277 CAAGCAATTAATCAATTTCCCACTTGCATGATGTTTATTTTCAATA----- 324











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QY 97 AsnSerThrIleLysGluLeuArgGluPhe-----LeuValAspAspLeuValAsp 114
Db 38153 CAATCTTATGTAACCAACACCGTTTCTTTAAGACACTGGCGTCATTGATCGGTCACTCG 38212
QY 115 SerLeuLysPheAlaValLeuMetTrp----- 123
Db 38213 ATGATCTCTTACAGCATTTTGTATGGGATGATGCGGTCCCAATGATAGTGTGGTGA 38272
QY 124 -----ValPheThrTyrValGlyValAlaLeuPheAsnGly 134
Db 38273 GAAATTCGCATATGATGATATTTTATGTTGGTTATGTC-----ATTTTCAAC 38326
QY 135 LeuThrLeuLeuLeuLeuLeuLeuSerLeuPheSerIleProValIleTyrGluArg 154
Db 38327 CTCATGCGCATTCGGCTCGGTGCG-----CCATTAAATCTCATTTGAATTTTAAATGAACG 38383
QY 155 HisGlnValGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysSerValLysAspAlaMe 174
Db 38384 CTAAACGCAACTAT---CGTTATCTTTTAATTCGCATTAAAGAAATATGCTGAAGCAT 38440
QY 174 talalysIleGlnAlaLys 180
Db 38441 GCTTTTATGCAGGCGAAA 38459

RESULT 69
US-09-583-110-2219
; Sequence 2219, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2219
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2219

Alignment Scores:
Pred. No.: 0.232 Length: 759
Score: 80.50 Matches: 49
Percent Similarity: 38.73% Conservative: 30
Best Local Similarity: 24.02% Mismatches: 62
Query Match: 8.70% Indels: 63
DB: 4 Gaps: 10

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-583-110-2219 (1-759)

QY 1 SerValValAspLeu---LeuTyrTrpArgAspIleLysLysThrGlyValValPheGly 19
Db 157 TCAATAGTATCACTACCTCTATATCTGTGAAAAATAAATAGTATCTATCTCTAGCC 216
QY 20 AlaSerLeuPheLeuLeuLeuSerLeuThrValPhe-----Ser 32
Db 217 ATAAATTCGATTCGTGTAATAGTGTTCCTCCATTTTAAATCAATAAGTTTTTCCAGAAAGT 276
QY 33 IleValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArg 52
Db 277 TTTTGACATTATACCGTATTAATAGTGTTTTATCTAGAGTTAGCAATCTTCAATTA 336
QY 53 Ile-----TyrLysGlyValIleGlnAlaIle 61
Db 337 ATTGGGAAGATTTTGTCTACTAAATGTACTAAGCAATATAAGAAATATTAGTCAGTTTGA 396
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 397 AGCAAGGTGTCCTCACTCT---CCTTGGATAAAATATTAGAG-----ATTCT 441
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-----HisVal--- 96
Db 442 AGTTTATATACTATATATTTCATCTATCTTTTATGGTACAGTTGATAATCATGTACTG 501
QY 97 -----AsnSerThrIleLysGluLeu----- 103
Db 502 ACTCTTATCTTTTTCATAAAATTTGTGCAGATACACAGATAAAATTTTATTCATCAGA 561
QY 104 -----ArgArgLeuPheLeuValAspLeuValAsp 114
Db 562 TTATTTGCACACAAGTACTTTAATGAAGAGGAGATATTTTCTT----- 606
QY 115 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyValAlaLeuPhe 132
Db 607 -----TTGCAATGGATGTATAGTTACTTATTTTATAGGATATCTTTTAGTGATT 657
QY 133 -----AsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerIleProVal 150
Db 658 CAAAAAGCAGGCTATTGTTTTCGGTTTACTTCTTTTCTAATTTTTCAGTCCATT 717
QY 151 IleTyrGluArg 154
Db 718 ATCAAAGAAAAG 729

RESULT 70
US-09-107-433-2215
; Sequence 2215, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
```

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;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...774
; SEQUENCE DESCRIPTION: SEQ ID NO: 2215:
US-09-107-433-2215

Alignment Scores:
Pred. No.: 0.24 Length: 774
Score: 80.50 Matches: 49
Percent Similarity: 38.73% Conservative: 30
Best Local Similarity: 24.02% Mismatches: 62
Query Match: 8.70% Indels: 63
DB: 4 Gaps: 10

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-107-433-2215 (1-774)
Qy 1 SerValValAspLeu---LeuTyrTrpArgAspIleLysLysThrGlyValValPheGly 19
Db 172 TCATAGTATCACTACCTCTATATCTGTGAAATAAATAAGTATCTCTGTCTAGCC 231
Qy 20 AlaSerLeuPheLeuLeuSerLeuThrValPhe-----Ser 32
Db 232 ATAAATTCGATTCTGTTAATGAGTTCCCATTTTAATCAATAAGTTTTCCAGAAAGT 291
Qy 33 lleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArg 52
Db 292 TTTTGGACTTATACCGTATTAATAAGTGTGTTTATCCTAGAGTTAGCAATCTTTCA 351
Qy 53 lle-----TyrLysGlyValIleGlnAlaIle 61
Db 352 ATGGGGAGAGATTTTGCTACTATAATGACTAAGCAATATAGAAATTAGTCAGTTAGA 411
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 412 AGCAAGGTGCTCAATCT---CCTTGGATAAAATATTAGAG-----ATTCT 456
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-----HisVal--- 96
Db 457 AGTTTATATTAACATATATTCCTATCTTCTTATGCTACAGTTGATAATCATGCTAG 516
Qy 97 -----AsnSerThrIleLysGluLeu----- 103
Db 517 ACTCTTATCTTTTGCATAAAATTTGTGCAGATACCCAGATAAATTTTATTCATCAGA 576
Qy 104 -----ArgArgLeuPheLeuValAspLeuValAsp 114
Db 577 TTATTTGACACAGTACTTTAATGAGAGGAGAGATATTTTCTT----- 621
Qy 115 SerLeuLysPheAlaValLeuMetTrpValPheThrValGlyAlaLeuPhe----- 132
Db 622 -----TTGCAATTCGATGTTATAGTTACTTATTTTATTTAGGATATCTTTTAGTGATT 672
Qy 133 -----AsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProVal 150
Db 673 CAAAGAGAGGCTATTGTTTTCGGTTTACTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTT 732
Qy 151 IleTyrGluArg 154
Db 733 ATCAAGAAAG 744

RESULT 71
US-08-853-659A-28
; Sequence 28, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Safer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella

;
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853.659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1797 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: the coding nucleotides of SEQ ID
; OTHER INFORMATION: NO:28 correspond to nucleotides 22630 through
; OTHER INFORMATION: 24426 of SEQ ID NO:2
US-08-853-659A-28

Alignment Scores:
Pred. No.: 0.932 Length: 1797
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-28 (1-1797)
Qy 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 487 TGGATGAGTTTCAGAAATTTAAACCCGTTTTTATTAACCTCGATCTTTCAACGTATAGCC 546
Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 547 GATATTCATATTTATATATATTTCTCATCTGTTATATATGTAATTTAGGTCGTGTTGTT 606
Qy 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 607 ATTGTACTATTTACCAGTTTATCGTCTCTATTTATTTCCCTCGTTAACCCATTAT 666
Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 667 ACTAATGAGTTAATGAACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
Qy 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 727 GAAGTTTCTTATCTATTAATAATGATCCATACCTTAATAATAATCAAGTTTACTTTTGTAT 786
Qy 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 105
Db 787 TGGGTTAATACATCAATCAATGACAGTCGTATCTTAACTGGAAGATAAGAGAAATTAATCTT 846
Qy 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 847 ATCTATCAATCTATATTGGGGAGTATGTCATCTATTACCCAAATAACTATTATTGTAATA 906
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Qy 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 907 GCCTTTTATGATCAAGGGTGATGTACTACTGGCGCAATTGTTTCATCTGTCATT 966
Qy 137 Leu-----LeuLeuAlaLeuLeuSerLeuPheSerIleProValIle 151
Db 967 GTCCTGGCGGATATTCGGGATCAATTCGAATTTTCTTACATTAAATC 1017

RESULT 72
US-08-853-659A-6
; Sequence 6, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:6 corresponds to
; OTHER INFORMATION: nucleotides 15735 through 24701 of SEQ ID NO:2
US-08-853-659A-6

Alignment Scores:
Pred. No.: 12.4 Length: 8967
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-6 (1-8967)
Qy 8 TrpArgAspIleIysIysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 7382 TCGAATGAGTTTCAGAAAAATTAACCCGTTTATTAAATCGATCTTTCAACGTATAGCC 7441
Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 7442 GATATTCGAATATTTATTAATTTCTTCATGTTATATATGTAATTTAGTCTGGTTGTT 7501
Qy 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
Db 7502 ATTGTACCTATTACCAGTTTATCGTCTCTATTATTATTTCCCTCGTTAACCACCATTTAT 7561
```

```
Qy 57 ValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 7562 ACTAATGAGTTTAATCAACAAACAAAGAGACAGACAGAAATATTTTATCTCA 7621
Qy 77 GluValAlaIleSerGluGluLeuValGlnIysTyrSerAsnSerAlaLeu----- 93
Db 7622 GAAGTTTCTTATCTATTAAATGATCATCATCACTTAAATATCAAGGTTTACTTTTGAT 7681
Qy 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 105
Db 7682 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAAGAAATTAATCTT 7741
Qy 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 7742 ATCTATCAATCTATATGGGAGTATGTCATCTATTACCCAAATAACTATTATGTAATA 7801
Qy 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 7802 GCCTTTTATGTTAATCAAGGTGATGTTACTACTGGGCNATGTTTCATCTGTCATT 7861
Qy 137 Leu-----LeuIleLeuAlaLeuSerLeuPheSerIleProValIle 151
Db 7862 GTCTCTGGCGGATTTCCGGGATCATTTTTCGAATTTTCTTCTACATTAAATC 7912

RESULT 73
US-08-853-659A-9/c
; Sequence 9, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-853-659A-9

Alignment Scores:
Pred. No.: 12.4 Length: 8967
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-9 (1-8967)
```



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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-853-659A-67

Alignment Scores:
Pred. No.: 12.4 Length: 8967
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-67 (1-8967)
QY 8 TpaArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 1586 TGAATGAGTTTCAGAAATTAACCCGTTTATTAACTCGATCTTCAACGTATAGCC 1527
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 1526 GATATTCCAATATTATTATTCTCTGTTTATATATGTAATTTAGGTTCTGGTTGTT 1467
QY 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 1466 ATGTGACCTATTACCATGTTTATGTCCTCTATTATTATTTCCTCGTTAACCCATTAT 1407
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 1406 ACTAATGAGTTAATGAACAAACAAAGAGGACAGAGAACAGGAATATTTTATCTCA 1347
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 1346 GAAGTTTCTTCTATTAAATGATCCATACCTTAAATCAAGGTTTACTTTTGTAT 1287
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105
Db 1286 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAAGGAATTAATCTT 1227
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 1226 ATCTATCAATCTATATTGGGAGTATGTCATCTATTACCAAAATCACTATTATGGTAATA 1167
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 1166 GCCTTTTGTGTAATCAAGGGTGATGTTACTACTCTGGCGCAATGTTTTCATCTGTCATT 1107
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151
Db 1106 GTCTCTGGCGGATTTCCGGGATCATTTCAATTTTCTTCTACATTAATC 1056

RESULT 76
US-08-853-659A-2
; Sequence 2, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24701 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
US-08-853-659A-2

Alignment Scores:
Pred. No.: 63.7 Length: 24701
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-2 (1-24701)
QY 8 TpaArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 23116 TGAATGAGTTTCAGAAATTAACCCGTTTATTAACTCGATCTTCAACGTATAGCC 23175
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 23176 GATATTCCAATATTATTATTCTCTGTTTATATATGTAATTTAGGTTCTGGTTGTT 23235
QY 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 23236 ATGTGACCTATTACCATGTTTATGTCCTCTATTATTATTTCCTCGTTAACCCATTAT 23295
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 23296 ACTAATGAGTTAATGAACAAACAAAGAGGACAGAGAACAGGAATATTTTATCTCA 23355
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 23356 GAAGTTTCTTCTATTAAATGATCCATACCTTAAATCAAGGTTTACTTTTGTAT 23415
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105
Db 23416 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAAGGAATTAATCTT 23475
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 23476 ATCTATCAATCTATATTGGGAGTATGTCATCTATTACCAAAATCACTATTATGGTAATA 23535
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 23536 GCCTTTTGTGTAATCAAGGGTGATGTTACTACTCTGGCGCAATGTTTTCATCTGTCATT 23595
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151

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Qy 94 -----GlyHisValaAnSerThrIleIysGluLeuA;Arg 105
Db 1286 TGGGTAAATACATCAAACTGAACAGTCTGTATCTTTAACTGAAGATTAAGGAAATTAATCTT 1227
Qy 106 LeuPhe-----LeuValAepAspLeuValAepSerLeuIysPheAlaValLeuMetTIp 123
Db 1226 ATCTATCAATCTATATTGGGGAGTATGTCATCTATTACCCAAATAACTATTATGGTAATA 1167
Qy 124 ValPheThrTyrVal-----GlyAlaLeuPheAenGlyLeuThr 136
Db 1166 GCCTTTTATGTAATCAAGGGTGATGTTACTACTGGCGCAATTGTTTCATCTGTCATT 1107
Qy 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151
Db 1106 GTCTCTGGCGTATTTCGGGATCAATTCGAATTTTCTCTACATAATC 1056

RESULT 78
US-08-853-659A-60
; Sequence 60, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K. K.; Saffer, J. D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; NUMBER OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:

```

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? APPLICATION NUMBER: US/06/853,659A
? FILING DATE: Unknown
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: none
? FILING DATE: n/a
? INFORMATION FOR SEQ ID NO: 60:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 24701 bases
? TYPE: nucleotide
? STRANDEDNESS: single stranded
? TOPOLOGY: linear
? US-08-853-659A-60

Alignment Scores:
Pred. ID.: 63.7 Length: 24701
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-60 (1-24701)

Qy 8 TrpArgAspIleuGlySerThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
||| : : : : : ||| : : : : :
Db 23116 UGGAUGAGUUCAGAAAUAUAAACCCGUUUUAUUAACUCGACUUCUCAAAGUAGCC 23175
||| : : : : : ||| : : : : :

Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
||| : : : : : ||| : : : : :

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QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56  
DB 23236 AUUGUACCUUAUACCAUGUUUAUUGUCUCUAUUUUUCCUGCUUAACCAUUAU 23295  
QY 57 ValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
DB 23296 ACUAUGAGUUUAUGAACCAACAAAGAAAGGACAGAAACAGGAAUUAUUUUUAUCUCA 23355  
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93  
DB 23356 GAAGUUUUAUCUAUUUAUAAUGAACCAUUAUACCUUAUAAAGGAAUUAUAAUUAU 23415  
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105  
DB 23416 UGGGUUAUAUCAUAAAGAACAGACUGCUUAUACCUUAUAAAGGAAUUAUAAUUAU 23475  
QY 106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTTP 123  
DB 23476 AUCUAUCAUUAUUAUUGGGAGUAUGUAUCAUUAUACCUUAUAAUAAUUAUUGGUAUA 23535  
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136  
DB 23536 GCCUUUUUAUGUAUAAUACGAGGUGAUGUAUCAUGGCGCAUUAUUAUUAUUAUUAU 23595  
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151  
DB 23596 GUCUCUGCGUAUUUCCGCGGAUCAUUUGAAUUUUUUUUUUUAUUAUUAUC 23646

## RESULT 79

US-08-853-659A-61/c  
; Sequence 61, Application US/08853659A  
; Patent No. 5925522  
; GENERAL INFORMATION:  
; APPLICANT: Wong, K.K.; Saffer, J.D.  
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection  
; TITLE OF INVENTION: Of A  
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Paul W. Zimmerman  
; ADDRESSEE: Intellectual Property Services  
; ADDRESSEE: Battelle Memorial Institute  
; ADDRESSEE: PNNL P.O. Box 999  
; STREET: Washington Way  
; CITY: Richland  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 99352  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage  
; COMPUTER: IBM PC/XT/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Processor (WordPerfect 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/853,659A  
; FILING DATE: Unknown  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: none  
; FILING DATE: n/a  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24701 bases  
; TYPE: nucleotide  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-853-659A-61  
Alignment Scores:  
Pred. No.: 63.7 Length: 24701  
Score: 80.50 Matches: 36  
Percent Similarity: 41.24% Conservative: 37

Best Local Similarity: 20.34% Mismatches: 71  
Query Match: 8.70% Indels: 33  
DB: 2 Gaps: 6  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-853-659A-61 (1-24701)  
QY 8 TrpArgAspIleLysIysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26  
DB 1586 TGGAAATGATTTTCAGAAAATTAAACCCGTTTTATTAAATCGATCTTTCAACGATATAGCC 1527  
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44  
DB 1526 GATATTCATATTTATTATATTTCTCTGTTATATATGTAATTAAGTTAGCTCTGTTGTT 1467  
QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56  
DB 1466 ATTTGACCTATTACCATTGTTTATCGTCTCTATTATTATTTCCCTCGTTAACCACTATTAT 1407  
QY 57 ValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
DB 1406 ACTAATGATTAATGAACAAACAAAGGACAGAAAGACAGAAATATTTTATCTCA 1347  
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93  
DB 1346 GAAGTTTCTTATCTATTAAATGATCCATACCTTAATTAATCAAGTTTACTTTTGTAT 1287  
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105  
DB 1286 TGGGTTAATACATCAATGAACAGTCGTATCTTAACCTGAAGATAAGGAAATTAATCTT 1227  
QY 106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTTP 123  
DB 1226 ATCTATCAATCTATATTTGGGAGTATGTCATCTATTACCAATAACTATTATGGTAATA 1167  
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136  
DB 1166 GCCTTTTATGTTATCAAGGGTGTACTACTCTGGCGCAATGTTTCTCATCTGTCATT 1107  
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151  
DB 1106 GTCTCTGCGCGTATTTCGCGGATCATTCGAATTTTCTTCTTACATTATATC 1056

## RESULT 80

US-09-247-373B-47/c  
; Sequence 47, Application US/09247373B  
; Patent No. 6168954  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1108-A  
; CURRENT APPLICATION NUMBER: US/09/247,373B  
; CURRENT FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 08/924,747  
; PRIOR FILING DATE: 1997-09-05  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 47  
; LENGTH: 859  
; TYPE: DNA  
; ORGANISM: SOYBEAN  
US-09-247-373B-47  
Alignment Scores:  
Pred. No.: 0.333 Length: 859  
Score: 80.00 Matches: 40  
Percent Similarity: 38.92% Conservative: 25  
Best Local Similarity: 23.95% Mismatches: 50  
Query Match: 8.65% Indels: 52  
DB: 3 Gaps: 9  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-247-373B-47 (1-859)



```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/008,180
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/848,932
: FILING DATE: 01-MAY-1997
: APPLICATION NUMBER: 9609125-1
: FILING DATE: 01-MAY-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Gimmi, Edward R
: REGISTRATION NUMBER: 38,891
: REFERENCE/DOCKET NUMBER: P31474
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-4478
: TELEFAX: 610-270-5090
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1666 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: mRNA

```

Alignment Scores:					
Pred. No.:	0.97	Length:	1566		
Score:	80.00	Matches:	45		
Percent Similarity:	43.89%	Conservative:	34		
Best Local Similarity:	25.00%	Mismatches:	63		
Query Match:	8.65%	Indels:	38		
DB:	2	Gaps:	10		
US-09-R30-972-2	COPY 975 1163 (1-189) x	US-09-008-180-1	(1-1666)		











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Db 952 ATCTATAACAACACCATGGCCAC---GTGCACAGCCACTTCGACGGAGAGGTGTTGGG 1008
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 79 AlalieserGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSer 98
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1009 GCTGTCCTCGCCAGGAGACGGAGTTTTCACACAGAACACGAGGTAACATCATGTCT 1068
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 99 ThrilleysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPhe 118
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1069 CGGGTAACAGAG---GACACGTCACCCCTGAGTGATTCCTGAGTGAGAACTG----- 1119
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 119 AlavalLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1120 AGCTTATTCTGTGTAC-----CTGGTCGAGGCGCTATGTCTCTTG 1161
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 139 -----lLeuAlaLeuLeuSerLeuPheSerIleProVal 150
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1162 GGGATCATGCTCGGGATCATGTCCTCACCATGGTCACCCCTGATCACCCTGCTCTG 1221
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 151 lletyrgluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerVal 170
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1222 CTTTTCCTCTGCCCAAG---AAGGTGGGAAATGGTACCAGTTGCTCGAAGTGCAGGTG 1278
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 171 LysAspAlaMetAlaLys 176
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1279 CGGGAATCTGTGCCAAG 1296
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 93
US-09-585-858-1
; Sequence 1, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigridur Hjordleifsdottir
; APPLICANT: Gudmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevartsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 129908
; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-09-585-858-1

Alignment Scores:
Pred. No.: 1.77e+03 Length: 129908
Score: 78.50 Matches: 41
Percent Similarity: 41.62% Conservative: 36
Best Local Similarity: 22.16% Mismatches: 61
Query Match: 8.49% Indels: 47
DB: Gaps: 8

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-585-858-1 (1-129908)

Qy 8 TrpArgAspIleLysLeuThrGlyValValPheGlyAlaSerLeu----- 22
Db 18117 TGGGAAGATCCAACTTCGGGACCACTTCGGGTGCCAATCTTATCAGCGTATCTTCC 18176
Qy 23 -----PheLeuLeuLeuSerLeuThrValPheSerIle 33
Db 18177 TTTGTTACTGGATACCCCGAAACAGTTTCTTGCTATAGCTTTCGTTTACTCT--- 18233
Qy 34 ValSerValThrAlaTyriLeAlaLeuAlaLeuSerValThrIleSerPheArgIle 53
Db 18234 GCTTCGCGCCACACCTAT-----CTTAACCTTAATGATGCTTACAGAATT 18278
```

```
Qy 54 TyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyr 73
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 18279 TACGTAGGAACAATTTTCGGCACCCCGCAATGGGAAGTGTGTTTACCGGTAGTTTCCAG 18338
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 74 LeuGluSerGluValAlaIleSerGluGlu-----LeuValGlnLysTyrSer 89
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 18339 GTTTCGTCTACGCCCTTCAATTTCTCACAAACGTTTCAGGATTTTACTTCTTCTTAAC 18398
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 90 AsnSerAlaLeuGlyHisValAsnSerThr----- 99
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 18399 GATAGTCACCTTAATATTACTATATTACTAGTTTCAGCGCACCGCAGCATTCGCCTCACAT 18458
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 100 lLelysGluLeuArgLeuPheLeuValAspLeu-----ValAspSer 115
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 18459 TTTCAGGTATACAGAAATATATAGAGTTGAGCCACTTTCTGCTTACACAGTACCGTCT 18518
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 116 LeuLysPheAlaValLeuMet-----TrpValPheThrTyrVal 128
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 18519 ATCGTGTGTTTCTACACGGTTTCAGCTACTAACAGCTTCGGGTGGAGCTATTCCAATATA 18578
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 129 -----GlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeuLysSerLeuPhe 146
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 18579 GAAATGGGGTCTCTTACAGAAATATCAACTATATGTCATTTCTAAGTTATCTTACCCCTAC 18638
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy 147 SerIleProValIle 151
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 18639 ACGGCACCGGCTATA 18653
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 94
US-10-270-878-1
; Sequence 1, Application US/10270878
; Patent No. 6818425
; GENERAL INFORMATION:
; APPLICANT: Sigridur Hjordleifsdottir
; APPLICANT: Gudmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevartsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,878
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 129908
; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-10-270-878-1

Alignment Scores:
Pred. No.: 1.77e+03 Length: 129908
Score: 78.50 Matches: 41
Percent Similarity: 41.62% Conservative: 36
Best Local Similarity: 22.16% Mismatches: 61
Query Match: 8.49% Indels: 47
DB: Gaps: 8

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-270-878-1 (1-129908)

Qy 8 TrpArgAspIleLysLeuThrGlyValValPheGlyAlaSerLeu----- 22
Db 18117 TGGGAAGATCCAACTTCGGGACCACTTCGGGTGCCAATCTTATCAGCGTATCTTCC 18176
Qy 23 -----PheLeuLeuLeuSerLeuThrValPheSerIle 33
Db 18177 TTTGTTACTGGATACCCCGAAACAGTTTCTTGCTATAGCTTTCGTTTACTCT--- 18233
Qy 34 ValSerValThrAlaTyriLeAlaLeuAlaLeuSerValThrIleSerPheArgIle 53
Db 18234 GCTTCGCGCCACACCTAT-----CTTAACCTTAATGATGCTTACAGAATT 18278
```

```
Db 18234 GCTTCGCCACACCTAT .....:|||||
QY 54 TyrLysGlyValIleGlnLysSerAspGluGlyHisProPheArgAlaTyr 73
Db 18279 TAGGTAGGGAACATTTTCGCCACCCGCAATGGGAAGTTGGTTTACCGGTAGTTTCACG 18338
QY 74 LeuGluSerGluValAlaIleSerGluGlu-----LeuValGlnLysTyrSer 89
Db 18339 GTTCTCTGCTACGCTTCAATTTCTCACAACCGTTTCAGGATTTTACTTCTTCTAACTTT 18398
QY 90 AsnSerAlaLeuGlyHisValAsnSerThr----- 99
Db 18399 GATAGTGCATTTAAATATATATATCTAGCTTCAGCGCACCGACGATTCGCTCACATTTCA 18458
QY 100 IleLysGluLeuArgArgLeuPheLeuValAspLeu-----ValAspSer 115
Db 18459 TTTACGTTATCAGGAATATATATGAAGTTGAGCCACTTTCGCTTACACAGTACCGTCT 18518
QY 116 LeuLysPheAlaValLeuMet-----TyrValPheThrTyrVal 128
Db 18519 ATCGTGTCTTTTACACGCTTTTACAGCTTACTAAGCTTCGCGTGGAGCTATTCCAATATA 18578
QY 129 -----GlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPhe 146
Db 18579 GAAATGGGTCTCTTTACAGAAATATCAACTATGTCCATCTTAAGTTATCTTACCCCTAC 18638
QY 147 SerIleProValIle 151
Db 18639 ACGGCACCGGCTATA 18653
```

## RESULT 95

```
US-09-134-001C-968
; Sequence 968, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 968
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-968
```

```
Alignment Scores:
Pred. No.: 1.18 Length: 1263
Score: 78.00 Matches: 46
Percent Similarity: 38.10% Conservative: 34
Best Local Similarity: 21.90% Mismatches: 70
Query Match: 8.43% Indels: 60
DB: Gaps: 10
```

```
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-134-001C-968 (1-1263)
```

```
QY 1 SerValValAspLeuLeuTyr-----TrpArgAsp 10
Db 457 TCTATAAGTACATTTGCTATATCCATATTTGGTATTACTCATCAATGGCAATGGGTAAA 516
QY 11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrVal 30
Db 517 TTAATAAATAAATGTGTTTCATTATATCAATATTTATATATACCTTTAGCAGTAACGCAT 576
QY 31 PheSerIleValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSer 50
```

```
Db 577 TACATGATTTTAAGATTTTCATAACTATTATTAGCTTTTAAATGAATGATATATATTT--- 633
QY 51 PheArgIleTyrLysGlyValIleGlnLysSerAspGluGlyHisProPhe 70
Db 634 -----GTAATTTTATTAGTCTCTAAAGACTTAAAGCAGCATCAC----- 669
QY 71 ArgAlaTyrLeu-----GluSerGluValAlaIleSerGluGluLeuValGlnLys 87
Db 670 -----TATTTACTTCCCTGGGAAAAAGTATTGCAATTGAA-----CAACAA 711
QY 88 TyrSerAsnSerAlaLeuGlyHisValAsn-----SerThrIleLysGluLeuArg--- 104
Db 712 CATCACACAATATATATAATTCGTTAATATGTTTACAGACGTTAAACACCTTAAGAGAA 771
QY 105 -----ArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 772 TCAGCAGTACGTCGTAGTTATCTTGATTTCTTACTACCGCTTCTCTAAAGGTGCCAAATTT 831
QY 122 -----MetTyrValPheThrTyrValGlyAlaLeuPheAsnGly----- 134
Db 832 AATGAGAAATCGGATGATTTATTTATTAAGAAGTTTGTTCAGAGGACGCGATGCT 891
QY 135 -----LeuThrLeuLeuIleLeuAlaLeuIle----- 143
Db 892 TTTTCTATTTTAAAGATTAGTATTATTCGTTATATTAATGTTATGTTATACACAA 951
QY 144 -----SerLeuPheSerIleProValIleTyrGluArgHis 155
Db 952 CCGGTTGTTTCATTAAATTCGTTAGTTGTTTATGATATATTATTTTATTAACAATGCT 1011
QY 156 GlnValGlnIleAspHisTyrLeuGlyLeu 165
Db 1012 CAATTTTATACGCAACAAGCATACGCTTTA 1041
```

## RESULT 96

```
US-09-543-681A-3338
; Sequence 3338, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3338
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3338
```

```
Alignment Scores:
Pred. No.: 1.2 Length: 1275
Score: 78.00 Matches: 42
Percent Similarity: 42.68% Conservative: 28
Best Local Similarity: 25.61% Mismatches: 60
Query Match: 8.43% Indels: 34
DB: Gaps: 7
```

```
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-543-681A-3338 (1-1275)
```

```
QY 9 ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu-----Phe 23
Db 157 CGTGATTTTCGCACTATTGTCAGATTTTAAAAATAATCTCGCTATCGCTGCTGTTTTT 216
QY 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu--- 42
Db 217 TTATTGCTCGCAATTTGGCTATTTCAGTGGTGAATTCGTTAGACGCCAGTACTGAGTCTAAAG 276
QY 43 -----AlaLeuLeuSerValThrIleSerPheArgIle--- 53
```

```
Db 277 GAGATGAATAAGCCGATTTTAAATGGCTTACTGCTCTTTCGCTATTGCGGTTTCCCATTCGTA 336
Qy 54 ---TyrLeuGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72
Db 337 TTGTATAAGAAACACCTACGCAATTCGCAAGATGGGTGATGGTTCATTCGCCATGGGT 396
Qy 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92
Db 397 TTATTG-----GTGATTATGCAAGAGATTGGTGCAGTATTAT----- 435
Qy 93 LeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspLeu 112
Db 436 TTGGAATATACGAAATATTTCCTTTTACAGAAAGATCAGTTCGGCGCAT----- 489
Qy 113 ValAspSerLeuLysPheAlaValLeu-----MetTrpVal 124
Db 490 ---AGAGAAATCTTATGCTCTGCTATTTCCTTTCCTATTATATGCGCTTATGGGCA 546
Qy 125 PheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeuIleSer 144
Db 547 TTGAAAAAATCATTCGATAATTAAATGGCTTTTATTAAAGTGTGTTAGCTATTATT 606
Qy 145 LeuPheSerIle 148
Db 607 TTATTGCAATC 618

RESULT 97
US-09-795-927-6
; Sequence 6, Application US/09795927
; Patent No. 6531309
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Kieke, James A.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Revelli, Jean-Pierre
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6531309el Human Transporter Proteins and Polynucleotides Enc
; FILE REFERENCE: Same
; CURRENT APPLICATION NUMBER: US/09/795,927
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,956
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2913
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-795-927-6

Alignment Scores:
Pred. No.: 4.56 Length: 2913
Score: 78.00 Matches: 48
Percent Similarity: 42.71% Conservative: 37
Best Local Similarity: 24.12% Mismatches: 68
Query Match: 8.43% Indels: 46
DB: 4 Gaps: 10

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-795-927-6 (1-2913)
Qy 21 SerLeuPheLeuLeuLeu-----SerLeuThrValPheSerIle 33
Db 1102 AGCTCCTTCTGCTCATATTTCTGGGCAAGAGATTGCGCAGTCTTCACAAATTACAGTGC 1161
Qy 34 ValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPhe----- 51
Db 1162 AATTCACACAGGATTAAATAGCCATCGCCTTCGCAATGTCGTCAGTTCAATTTTCAGA 1221
Qy 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
```

```
Db 1222 TCTTGTGTGTTTACTGGTGCTATTGCTAGGACTATTATCCAG-----GATAAAATCTGGA 1275
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Db 1276 GGAAGACAAACAGTTTGCATCTCTGTAGCGCAGGTGTGATGCTGCTC-----CTGATG 1329
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHis----- 95
Db 1330 GTGAAG-----ATGGGACACTTTTCTACACACTGCCAAATGCTGTGCTG 1374
Qy 96 -----ValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspAsp 111
Db 1375 GCTGTATTATTCTGAGCAAGCTCATTCCTTACCTTGAAACCATTTCTTAACCTACCACG 1434
Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
Db 1435 CTGTGGAGCGCAGGACCAATATGACTGTGCTCTTTGGATGATGACATTCTCATCTTCAATT 1494
Qy 132 PheAsnGlyLeuThrLeu---LeuIleLeuAlaLeuIleSerLeuPheSerIleProVal 150
Db 1495 TTCTGGGACTGGACATTGGACTAATTATCTCAGTAGTTTCTGCTTCTTCATCACCCT 1554
Qy 151 IleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsn----- 167
Db 1555 GTT---CGTTCACACAGAGCTAAGATTCTCTCTCGGGTCAAAATCCCTAACACCAACATT 1611
Qy 168 ---LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 1612 TATAGAAGCATCAATGATTATCGGAGATCATC-----ACCATTCCTGGGGTGAAA 1662

RESULT 98
US-09-328-352-932
; Sequence 932, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 932
; LENGTH: 3162
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-932

Alignment Scores:
Pred. No.: 5.2 Length: 3162
Score: 78.00 Matches: 34
Percent Similarity: 39.51% Conservative: 30
Best Local Similarity: 20.99% Mismatches: 54
Query Match: 8.43% Indels: 44
DB: 4 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-328-352-932 (1-3162)
Qy 5 LeuLeuTyrTrpArgAspIleLysLysThrGlyValValPhe----- 18
Db 2734 ATGATTCAGCTGAAGAGTTTCTCTCGGCAACAATTTGATTTTTGACTGCACCATTAGGC 2793
Qy 19 -----GlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal 36
Db 2794 TTAATTCGCGTGTGTTTATTTCTTACTTCTTGTGTTTAAATAAACCATTTGGTTTGTGCCAATG 2853
Qy 37 ThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 2854 CTAGAACCATTCGCTTATCCGCGCATGATTATGCGTAACCTCACTCATCTCTG----- 2904
Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
```

```
Db 2905 ATTGATCAGATTGAACAACAGACAGACAGGCGGCATCCA----- 2943
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96
Db 2944 -----ACGTGGGAAGCAATT-----ATT 2961
Qy 97 AnSerThrIleLysGluLeuArgLysGluPheLeuValAspLeuValAspSerLeu 116
Db 2962 GATGCAACAGTAGCGCGTTTCGTCGATCAATTC-----ACGGCA 3003
Qy 117 LysPheAlaValLeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThr 136
Db 3004 TTGGCAGCAGTACTCCCATGATCCTTCTTTCGGGAGATATTTATTCGTCATGGCT 3063
Qy 137 -----LeuLeuIleLeuAlaLeuLeuSerLeuPheSerIleProVal 150
Db 3064 GTTGGCATTTATGGCGGAGCTCATTTGTGTACCTTGCTGACATTTATTTTATACCTGCA 3123
Qy 151 IleTyr 152
Db 3124 TTGTAT 3129

RESULT 99
US-09-795-927-8
; Sequence 8, Application US/09795927
; Patent No. 6531309
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgowski, Nathaniel L.
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James A.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Revelli, Jean-Pierre
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6531309el Human Transporter Proteins and Polynucleotides Encod
; FILE OF INVENTION: Same
; FILE REFERENCE: LEX-0141-USA
; CURRENT APPLICATION NUMBER: US/09/795,927
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,956
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3749
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-795-927-8

Alignment Scores:
Pred. No.: 6.84 Length: 3749
Score: 78.00 Matches: 48
Percent Similarity: 42.71% Conservative: 37
Best Local Similarity: 24.12% Mismatches: 68
Query Match: 8.43% Indels: 46
DB: Gaps: 10

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-795-927-8 (1-3749)
Qy 21 SerLeuPheLeuLeuLeu-----SerLeuThrValPheSerIle 33
Db 1577 AGTCCTCTTCTGTCATATTTCTGGCAGAGAGATTGCGAGTTCACAAATACAGTGC 1636
Qy 34 ValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPhe----- 51
Db 1637 AATTCCAACAGGATTTAATAGCCATCGGCTTTGCAATGTCGTCAGTTCAATTTTTCAGA 1696
Qy 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 1697 TCTGTGTGTTTACTGGTGTATTTGCTAGGACTATTTATCCAG-----GATAAATCTGGA 1750
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
```

```
Db 1751 GGAACAGACAGTTTGCATCTCTGTAGGCGAGGTGTATGCTGCTC-----CTGATG 1804
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHis----- 95
Db 1805 GTGAAG-----ATGGGACACTTTTCTACACACTGCCAAATGCTGTGCTG 1849
Qy 96 -----ValAsnSerThrIleLysGluLeuArgLysGluPheLeuValAspAsp 111
Db 1850 GCTGGTATTATTTCTGAGCAACGTCATTCCTTACCTTGAACACCATTTTAAACATCCACG 1909
Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
Db 1910 CTGTGGAGCAGGACCAATATGACTGTGCTCTTTGGATGATGACATTTCTCATCTTCAAT 1969
Qy 132 PheAsnGlyLeuThrLeu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProVal 150
Db 1970 TTCTTGGGAGCTGGACATTTGGACTAATTTATCTCAGTAGTTTCTGCTTTCTTCATCACCAC 2029
Qy 151 IleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsn----- 167
Db 2030 GTT---CGTTACACAGAGCTAAGATTCTTCTCGGGTCAAAATCCCTAAACACCAACAT 2086
Qy 168 ---LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 2087 TATAGAGCATCAATGATTATCGGAGATCATC-----ACCATTTCTGGGTGAAA 2137

RESULT 100
US-09-453-702B-259
; Sequence 259, Application US/09453702B
; Patent No. 6165723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6165723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-Dec-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-453-702B-259
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 03:56:06 ; Search time 445.5 Seconds  
(without alignments)  
2633.504 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	925	100.0	4684	9	US-09-893-348-17	Sequence 17, Appl
2	925	100.0	4684	20	US-10-810-653-17	Sequence 17, Appl
3	922	99.7	2782	15	US-10-205-194-165	Sequence 165, App
4	908	98.2	600	21	US-10-956-157-9764	Sequence 9764, Ap
5	908	98.2	1400	21	US-10-956-157-9763	Sequence 9763, Ap
6	908	98.2	2883	21	US-10-956-157-4529	Sequence 4529, Ap
7	908	98.2	3478	21	US-10-956-157-4528	Sequence 4528, Ap
8	908	98.2	3579	9	US-09-789-386-1	Sequence 1, Appli
9	908	98.2	3579	9	US-09-893-348-22	Sequence 22, Appl
10	908	98.2	3579	18	US-10-267-502-212	Sequence 212, App
11	908	98.2	3579	19	US-10-327-213-8	Sequence 8, Appli
12	908	98.2	3579	19	US-10-466-258-8	Sequence 8, Appli
13	908	98.2	3579	20	US-10-810-653-22	Sequence 22, Appl
14	908	98.2	4053	9	US-09-758-140-5	Sequence 5, Appli
15	908	98.2	4053	9	US-09-972-599A-5	Sequence 5, Appli
16	908	98.2	4053	19	US-10-717-597-310	Sequence 310, App
17	908	98.2	4623	21	US-10-956-157-4532	Sequence 4532, Ap
18	908	98.2	4632	14	US-10-060-036-53	Sequence 53, Appl
19	906.5	98.0	3492	18	US-10-267-502-214	Sequence 214, App
20	904	97.7	799	18	US-10-660-946-2	Sequence 2, Appli
21	904	97.7	1122	9	US-09-789-386-5	Sequence 5, Appli
22	904	97.7	1160	14	US-10-175-523-156	Sequence 156, App
23	904	97.7	1609	21	US-10-956-157-4527	Sequence 4527, Ap
24	904	97.7	1610	9	US-09-765-205-5	Sequence 5, Appli
25	904	97.7	1610	21	US-10-347-669-5	Sequence 5, Appli
26	904	97.7	1785	17	US-10-439-388-62	Sequence 62, Appl
27	904	97.7	1785	21	US-10-956-157-1705	Sequence 1705, Ap
28	904	97.7	2052	21	US-10-956-157-4530	Sequence 4530, Ap
29	904	97.7	2052	19	US-10-466-258-3	Sequence 3, Appli
30	904	97.7	2226	21	US-10-956-157-4531	Sequence 4531, Ap
31	904	97.7	2235	14	US-10-060-036-54	Sequence 54, Appl
32	898	97.1	1980	17	US-10-220-891-22	Sequence 22, Appl
33	895	96.8	994	11	US-09-978-360A-110	Sequence 110, App
34	891	96.3	2610	18	US-10-641-643-382	Sequence 382, Appl
35	864	93.4	1798	19	US-10-466-258-10	Sequence 10, Appl
36	849	91.8	1400	21	US-10-956-157-9765	Sequence 9765, Ap
37	844	91.2	1514	9	US-09-823-245A-349	Sequence 349, App
38	782	84.5	1400	21	US-10-956-157-9762	Sequence 9762, Ap
39	782	84.5	1400	21	US-10-956-157-9767	Sequence 9767, Ap
40	695	75.1	1400	21	US-10-956-157-9766	Sequence 9766, Ap
41	679	73.4	1520	15	US-10-084-817-333	Sequence 333, App
42	679	73.4	2331	18	US-10-267-502-213	Sequence 213, App
43	679	73.4	3202	9	US-09-954-456-210	Sequence 210, App
44	679	73.4	3202	17	US-10-172-118-386	Sequence 386, App
45	679	73.4	3202	18	US-10-342-887-386	Sequence 386, App

ALIGNMENTS

RESULT 1  
US-09-893-348-17  
; Sequence 17, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michael  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONOGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161

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; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-09-893-348-17

Alignment Scores:
Pred. No.: 1.29e-101 Length: 4684
Score: 925.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Db 3175 TCAGTTGGTGGACCTCTCTACTGGAGACATTAAGAAGCTGGAGTGGTGTGGTCC 3234

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaVal 40
Db 3235 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGATTTGTCAGTGTAAAGCGCTACATT 3294

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3355 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA 3414

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3415 TCAGAGGAATGGTTCAGAAATACAGTAATTCCTGCTTGGTCATGTGAACGACACAATA 3474

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 3535 TTGATGTGGGTGTTACTTATGTTGGTGGCTTGTTCAAATGGTCTGACACTACTGATTATA 3594

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3595 GCTCTGATCTCACTTCTCAGTATTCCTGTTATTAATGACGGCATCAGGTGCAGATAGAT 3654

QY 161 HisTyrLeuGlyLeuAlaIleLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3655 CATTATCTAGGACTTGCAACAAGAGTGTAAAGGATGCCATGGCCAAAATCCAAGCAAAA 3714

QY 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741
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## RESULT 2

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US-10-810-653-17
; Sequence 17, Application US/10810653
; Publication No. US20040253218A1
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; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US-
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-10-810-653-17

Alignment Scores:
Pred. No.: 1.29e-101 Length: 4684
Score: 925.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-810-653-17 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaVal 40
Db 3235 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGATTTGTCAGTGTAAAGCGCTACATT 3294

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCT 3354

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3355 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA 3414

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3415 TCAGAGGAATGGTTCAGAAATACAGTAATTCCTGCTTGGTCATGTGAACGACACAATA 3474

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3475 AAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTTGCAAGT 3534

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 3535 TTGATGTGGGTGTTACTTATGTTGGTGGCTTGTTCAAATGGTCTGACACTACTGATTATA 3594

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3595 GCTCTGATCTCACTTCTCAGTATTCCTGTTATTAATGACGGCATCAGGTGCAGATAGAT 3654

QY 161 HisTyrLeuGlyLeuAlaIleLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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QY 181 IleProGlyLeuLysArgLysAlaAsp 189
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QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 511 CATTATCTAGGACTTCAAAATAAGATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA 570  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
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## RESULT 5

US-10-956-157-9763  
; Sequence 9763, Application US/10956157  
; Publication NO. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9763  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9763

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Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 21 Gaps: 0

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 548 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATT 607  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 608 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 667  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 668 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 727  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 728 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTTCGCTCTTGGTCATGTGAAGTCCAGGATA 787  
QY 101 LysGluLeuArgLysPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 788 AAGAACTCAGGCGCTCTCTTGTAGTGATGATTTAGTTGATTTCTCTGAAAGTTGAGTGG 847  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 848 TTGATGGGTATTTTACCTATGTTGGTCTGCTGTTTAAATGTTCTGACACTACTGATTTTG 907  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 908 GCTCTCATTTTCACTCTTCTAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 967  
QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 968 CATTATCTAGGACTTCAAAATAAGATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA 1027  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 1028 ATCCCTGGATTGAAGCGCAAGCTGAA 1054

## RESULT 6

US-10-956-157-4529  
; Sequence 4529, Application US/10956157  
; Publication NO. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4529  
; LENGTH: 2883  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4529

Alignment Scores:  
Pred. No.: 7,22e-100 Length: 2883  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-4529 (1-2883)

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Db 2314 TCAGTTGTTGACCTCTCTGTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGC 2373  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2374 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATT 2433  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 2434 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 2493  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 2494 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 2553  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 2554 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTTGGTCACTGTAAGTCCAGATA 2613  
QY 101 LysGluLeuArgLysPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 2614 AAGAACTCAGGCGCTCTCTTGTAGTGATGATTTAGTTGATTTCTCTGAAAGTTGAGTGG 2673  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 2674 TTGATGGGTATTTTACCTATGTTGGTCTGCTGTTTAAATGTTCTGACACTACTGATTTTG 2733  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 2734 GCTCTCATTTTCACTCTTCTAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 2793  
QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 2794 CATTATCTAGGACTTCAAAATAAGATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA 2853  
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RESULT 7
US-10-956-157-4528
; Sequence 4528, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent version 3.2
; SEQ ID NO 4528
; LENGTH: 3478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4528

Alignment Scores:
Pred. No.: 9.69e-100 Length: 3478
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4528 (1-3478)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValValPheGlyAla 20
Db 2566 TCAGTTGTGTGACCTCTGTACTGCGAGACATTAAGAAGACTGGAGTGGTGTGGTCC 2625
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 2626 AGCCTATTCTCTGCTGCTTTCATTGACAGTATTACAGATTGTGAGCGTAAAGCCTACATT 2685
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 2686 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCT 2745
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 2746 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATA 2805
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 2806 TCTGAGGAGTTGGTTTCAGAGTACAGTANNTCTGCTTGTGTCACTGTAAGTGCACGATA 2865
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 2866 AAGAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTG 2925
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140
Db 2926 TTGATGTGGGTATTTACCTATGTGGTGGCTTGTGTTAATGCTGCTGACACTACTGATTTTG 2985
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 2986 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3045
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3046 CATTATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTGCTGAAATCCAGCAAAA 3105
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3106 ATCCCTGGATTGAAGCGCAAGCTGAA 3132
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RESULT 8
US-09-789-386-1
; Sequence 1, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1

Alignment Scores:
Pred. No.: 1.01e-99 Length: 3579
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-789-386-1 (1-3579)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTGTGACCTCTGTACTGCGAGACATTAAGAAGACTGGAGTGGTGTGGTCC 3069
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCTCTGCTGCTTTCATTGACAGTATTACAGATTGTGAGCGTAAAGCCTACATT 3129
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCT 3189
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATA 3249
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3250 TCTGAGGAGTTGGTTTCAGAGTACAGTANNTCTGCTTGTGTCACTGTAAGTGCACGATA 3309
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTG 3369
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTGGTGGCTTGTGTTAATGCTGCTGACACTACTGATTTTG 3429
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3430 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3489
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTGCTGAAATCCAGCAAAA 3549
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
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Db      3550 ATCCCTGGATTGAGCGCAAGCTGAA 3576
RESULT 9
US-09-893-348-22
; Sequence 22, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22
Alignment Scores:
Pred. No.: 1.01e-99 Length: 3579
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 9 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-893-348-22 (1-3579)
QY      1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db      3010 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAGAGACATGGAGTGGTGTGGTGGC 3069
QY      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      3070 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTCAGCGTAAACAGCCTACATT 3129
QY      41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
Db      3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCT 3189
QY      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      3190 ATCCAGAAATCAGATGAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249
QY      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db      3250 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTTTGGTCATGTGAACATGCACGATA 3309
QY      101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db      3310 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGAGTG 3369
QY      121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db      3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTTG 3429
QY      141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db      3430 GCTCTCATTTTCACTCTTTCAGTGTCTCTGTTTATTTATTAACCGCATCAGCGCGAGATAGAT 3489
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QY 181 ileProGlyLeuLysArgLysAlaAsp 189  
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
RESULT 13  
US-10-810-653-22  
; Sequence 22, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3579)  
; OTHER INFORMATION:  
US-10-810-653-22  
Alignment Scores:  
Pred. No.: 1,01e-99 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 20 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-810-653-22 (1-3579)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3010 TCAGTTGTTGACCTCTCTGTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGCC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3070 AGCCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGACGCTAACAGCCTACATT 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3190 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTCGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3250 TCTGAGGAGTGGTTCAGAGTAGTACAGTAATTCCTGCTCTTGGTCTATGTAAGTCCACGATA 3309  
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

DB 3310 AAGGAACCTCAGCGCCTCTTCTTAGTTGATGATTTAGTTCTCTGAAGTTTCAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3370 TTGATGTGGTATTTTACCTATGTTGGTCTTGTAAATGTTGCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluAtrHisGlnValGlnIleAsp 160  
DB 3430 GCTCTCATTTCACTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGCGCGAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3490 CATTATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGCTAAATCCACAGCAA 3549  
QY 181 ileProGlyLeuLysArgLysAlaAsp 189  
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
RESULT 14  
US-09-758-140-5  
; Sequence 5, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.  
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(3710)  
; OTHER INFORMATION: Human mRNA for No. US20020012965A1o protein (K1AA0886, GenBank  
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)  
US-09-758-140-5  
Alignment Scores:  
Pred. No.: 1,23e-99 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-758-140-5 (1-4053)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3144 TCAGTTGTTGACCTCTCTGTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGC 3203  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3204 AGCCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATT 3263  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3323  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3324 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTCGAATCTCGAAGTTGCTATA 3383

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100  
Db 3384 TCTGAGGAGTGGCTTCTGAGAGTACAGTAATCTGCTCTGGTCTGTCGACGCGATA 3443  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAACATCAGCGCGCTCTCTCTAGTATGATGATTTAGTGTGATTTCTGAAGTTGCGAGTG 3503  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3504 TTGATGTGGTATTTACCTATGTTGGTGGCTTGTATGCTGTCGACACTACTGATTTTG 3563  
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3564 GCTCTCAATTCACCTCTCAGTGTCTCTGTTATTAAGATGCTATGGCTAAATCCAGCAAAA 3683  
QY 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlalys 180  
Db 3624 CATTATCTAGGACTTGCAGTGTCTCTGTTATTAAGATGCTATGGCTAAATCCAGCAAAA 3683  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710  
RESULT 15  
US-09-972-599A-5  
; Sequence 5, Application US/09972599A  
; Patent No. US20020077295A1  
; GENERAL INFORMATION:  
; APPLICANT: STRITTMATTER, STEPHEN M.  
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
; FILE REFERENCE: C077 CIP US  
; CURRENT APPLICATION NUMBER: US/09/972,599A  
; PRIOR FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: PCT/US01/01041  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(3710)  
; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein (K1AA0886, Ge  
; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)  
US-09-972-599A-5  
Alignment Scores:  
Pred. No.: 1,238-99 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-972-599A-5 (1-4053)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3144 TCAGTTGTTGACCTCTCTGCTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC 3203  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 3204 AGCCTATTCTCGCTGCTTTTCATTGACAGTATTGACAGTATTGACAGCTAACAGCCTACATT 3263  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3264 GCTTGGCCCTGCTCTCTGTCGACCATCAGCTTTTAGATATACAGGGTGTGATCCAGCT 3323  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGAAGTTGCTATA 3383  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100  
Db 3384 TCTCAGGAGTGTGGTTCAGAGTACAGTAATCTGCTCTTGGTCTATGTCGACGCGATA 3443  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAACATCAGCGCGCTCTCTCTAGTATGATGATTTAGTGTGATTTCTGGAAGTTGCGAGTG 3503  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3504 TTGATGTGGTATTTACCTATGTTGGTGGCTTGTATGCTGTCGACACTACTGATTTTG 3563  
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3564 GCTCTCAATTCACCTCTCAGTGTCTCTGTTATTAAGATGCTATGGCTAAATCCAGCAAAA 3623  
QY 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlalys 180  
Db 3624 CATTATCTAGGACTTGCAGTGTCTCTGTTATTAAGATGCTATGGCTAAATCCAGCAAAA 3683  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710  
RESULT 16  
US-10-717-597-310  
; Sequence 310, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 310  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-310  
Alignment Scores:  
Pred. No.: 1,238-99 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 19 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-717-597-310 (1-4053)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20



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Db 3144 TCAGTTGTTGACCTCTGCTGCTGAGAGACATTAAAGAACCTGGAGTGGTGGTGGTGGCC 3203
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3204 AGCCTATTCTGCTGCTCTTCATTGACAGTATTTCAGCATTTGAGCGTAAACAGCTACATT 3263
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3323
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3324 ATCCAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATA 3383
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3384 TCTGAGGACTTGGTTCAGAAATGACAGTAAATCTCTGCTCTTGGTCACTGTAAGTGCAGATA 3443
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3444 AAGGAACCTCAGCGCCCTCTCTCTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTG 3503
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3504 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTG 3563
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3564 GCTCTCATTTCACTCTTTCAGTGTCTCTGTTTATTAAGAACGCCATCAGGCACAGATAGAT 3623
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3624 CATTATCTAGGACTTGCATAAATGAAGTGTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 3683
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710

RESULT 17
US-10-956-157-4532
; Sequence 4532, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4532
; LENGTH: 4623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4532

Alignment Scores:
Pred. No.: 1 51e-99 Length: 4623
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4532 (1-4623)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAla 20
Db 3151 TCAGTTGTTGACCTCTGCTGCTGAGAGACATTAAAGAACCTGGAGTGGTGGTGGTGGCC 3210
```

```
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3211 AGCCTATTCTGCTGCTCTTCATTGACAGTATTTCAGCATTTGAGCGTAAACAGCTACATT 3270
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3330
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3331 ATCCAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATA 3390
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3391 TCTGAGGAGTTGGTTCAGAAATGACAGTAAATCTCTGCTCTTGGTCACTGTAAGTGCAGATA 3450
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3451 AAGGAACCTCAGCGCCCTCTCTCTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTG 3510
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3511 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTG 3570
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3571 GCTCTCATTTCACTCTTTCAGTGTCTCTGTTTATTAAGAACGCCATCAGGCACAGATAGAT 3630
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3631 CATTATCTAGGACTTGCATAAATGAAGTGTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 3690
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3691 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3717

RESULT 18
US-10-060-036-53
; Sequence 53, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53

Alignment Scores:
Pred. No.: 1 52e-99 Length: 4632
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-060-036-53 (1-4632)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAla 20
Db 3151 TCAGTTGTTGACCTCTGCTGCTGAGAGACATTAAAGAACCTGGAGTGGTGGTGGTGGCC 3210
```



QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3211 AGCTATTCTGCTGCTCTTCATTGACAGTAATTCAGCAATGTGAGGGTAACAGGCTACATT 3270  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3271 GCCTTGGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3330  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3331 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCAATATCTGGAATCTGAAGTTGCTATA 3390  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3391 TCTGAGGAGTTGTTTCAGAGTACAGTAATCTCTGCTCTTGGTCATGTAAGTGCACGATA 3450  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3451 AAGGAACCTCAGCGGCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCAAGTG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3511 TTGATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTTG 3570  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3571 GCTCTCATTTCTCTTCAGTGCTCTCTGTTATTTATGACGGCATCAGGCACAGTAGAT 3630  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3631 CATTATCTAGGACTTGCATAAAGAATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 3690  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3691 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3717

## RESULT 19

US-10-267-502-214  
; Sequence 214, Application US/10267502  
; Publication No. US20040071700A1

## GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 214  
; LENGTH: 3492  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-267-502-214

## Alignment Scores:

Pred. No.:	1,49e-99	Length:	3492
Score:	906.50	Matches:	187
Percent Similarity:	98.95%	Conservative:	1
Best Local Similarity:	98.42%	Mismatches:	1
Query Match:	98.00%	Indels:	1
DB:	18	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-267-502-214 (1-3492)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValVal---PheGly 19  
DB 2920 TCAGTTGTTGACCTCTCTACTGAGAGACATTAAAGAGCTGGAGTGTGTTTGTGT 2979  
QY 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
DB 2980 GCCAGCTTATTCCTGCTGCTGCTCTCTGACAGTGTTCAGCAATGTTCAGTGAACGCGCTAC 3039

QY 40 IleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 59  
DB 3040 ATTGCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAA 3099  
QY 60 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79  
DB 3100 GCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCAATATTTGGAATCTGAAGTTGCC 3159  
QY 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr 99  
DB 3160 ATATCAGAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTCTTGGTTCATGTAACACGACA 3219  
QY 100 IleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAla 119  
DB 3220 ATAAAGAAATGAGCGGCTCTCTCTTAGTTGATGATTTAGTTGCTCCCTGAAGTTTGCA 3279  
QY 120 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 139  
DB 3280 GTGTTGATGTGGGTATTTACTTTAGCTTGGTGGCTTGTTCATGTTTGCACACTACTGATT 3339  
QY 140 LeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIle 159  
DB 3340 TTAGCTCTGATCTCACCTTTCAGTATTTCTGTTATATATATGAACGCGCATCAGCGCGCAGATA 3399  
QY 160 AspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 179  
DB 3400 GATCATTTATCTAGACTTTCGAAACACAGAGCGTTTAAGGATGCGATGGCCAAATCCAGCA 3459  
QY 180 LysIleProGlyLeuLysArgLysAlaAsp 189  
DB 3460 AAAATCCCTGGATTGAAGCGCAAAAGCAGAA 3489

## RESULT 20

US-10-660-946-2  
; Sequence 2, Application US/10660946  
; Publication No. US20040063131A1

## GENERAL INFORMATION:

; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/660,946  
FILING DATE: 12-Sep-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/228,213A  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/700,607  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: Consensus  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-660-946-2

Alignment Scores:  
Pred. No.: 2,98e-100 Length: 799  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 18 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-660-946-2 (1-799)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 108 GTTGTGACCTCTCTGAGAGACATTAAAGACCTGGAGTGGTGTGGTGGCCAGC 167  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 168 CTATTCCTGCTGCTTTCATTGACAGTATTACAGCATTTGTGAGCGTAAACAGCTACATTGCC 227  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCTATC 287  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 288 CAGAAATCAGATGAAGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 347  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 348 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGATGAACTGCACGATAAAG 407  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 408 GAACCTCAGGCGCTCTCTTAGTGTAGTATTAGTTGATTTCTGAAAGTTTCAGAGTTTG 467  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 468 ATGTGGGTATTTACCTATGTTGGTCTGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 527  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 528 CTCATTTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 588 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 647  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 648 CCTGGATTGAAGCGCAAGCTGAA 671

## RESULT 21

US-09-789-386-5  
Sequence 5, Application US/09789386  
Patent No. US20020010324A1  
GENERAL INFORMATION:  
APPLICANT: MICHALOVICH, DAVID  
APPLICANT: PRINHA, RABINDER KUMAR  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30165-C1  
CURRENT APPLICATION NUMBER: US/09/789,386  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: U.K. 9916898.1

PRIOR FILING DATE: 1999-07-19  
PRIOR APPLICATION NUMBER: U.K. 9816024.5  
PRIOR FILING DATE: 1998-07-22  
PRIOR APPLICATION NUMBER: US 09/359,208  
PRIOR FILING DATE: 1999-07-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 1122  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
US-09-789-386-5

Alignment Scores:  
Pred. No.: 5.08e-100 Length: 1122  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-789-386-5 (1-1122)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 556 GTTGTGACCTCTCTGAGAGACATTAAAGACCTGGAGTGGTGTGGTGGCCAGC 615  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 616 CTATTCCTGCTGCTTTCATTGACAGTATTACAGCATTTGTGAGCGTAAACAGCTACATTGCC 675  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 736 CAGAAATCAGATGAAGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 795  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 796 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGATGAACTGCACGATAAAG 855  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 856 GAACCTCAGGCGCTCTCTTAGTGTAGTATTAGTTGATTTCTGAAAGTTTCAGAGTTTG 915  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 916 ATGTGGGTATTTACCTATGTTGGTCTGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 975  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 976 CTCATTTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1036 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1095  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 1096 CCTGGATTGAAGCGCAAGCTGAA 1119

## RESULT 22

US-10-175-523-156  
Sequence 156, Application US/10175523  
Publication No. US20030096264A1  
GENERAL INFORMATION:  
APPLICANT: Brockman, Jeffrey  
APPLICANT: Evans, David  
APPLICANT: Hook, Derek  
APPLICANT: Klimczak, Leszek  
APPLICANT: Laeng, Pascal

```
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/13795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-156

Alignment Scores:
Pred. No.: 5,35e-100 Length: 1160
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-175-523-156 (1-1160)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 228 GTTGTGACCTCCTCTGACCATCAGCTTAAAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCAGC 287
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 288 CTATTCTCGCTCTTTCATTGACATTTACAGATTTGAGCATTTGAGCGTTAACAGCCTACATTGCC 347
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 348 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 407
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 408 CAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAAGTTGCTATATCT 467
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 468 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTTTGGTCATGTGAAGTGCACGATAAAG 527
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 528 GAACTCAGCGCCCTCTTCTTAGTTGATTTAGTTGATTTCTGAAAGTTGACGTGTG 587
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 588 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGTTCTGACACTACTGATTTGGCT 647
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 648 CTCATTTCACTCTTCAGTGTCTCTTCTGATTTAGTTGATTTCTGAAAGTTGACGTGTG 707
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 708 TATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAATC 767
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
```

```
Db 768 CTTGGATTGAAGCGCAAGCTGAA 791

RESULT 23
US-10-956-157-4527
; Sequence 4527, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4527
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4527

Alignment Scores:
Pred. No.: 8,93e-100 Length: 1609
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4527 (1-1609)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 140 GTTGTGACCTCCTCTGACCATCAGCTTAAAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCAGC 199
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 200 CTATTCTCGCTCTTTCATTGACATTTACAGATTTGAGCATTTGAGCGTTAACAGCCTACATTGCC 259
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 260 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAGCTATC 319
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 320 CAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAAGTTGCTATATCT 379
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 380 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTTTGGTCATGTGAAGTGCACGATAAAG 439
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 440 GAACTCAGCGCCCTCTTCTTAGTTGATTTAGTTGATTTCTGAAAGTTGACGTGTG 499
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 500 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGTTCTGACACTACTGATTTGGCT 559
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 560 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGACCGCATCAGGCACAGATAGATCAT 619
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 620 TATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAATC 679
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 680 CTTGGATTGAAGCGCAAGCTGAA 703
```

```
RESULT 24
US-09-765-205-5
; Sequence 5, Application US/09765205
; Patent No. US2002003480A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-09-765-205-5

Alignment Scores:
Pred. No.:      8,94e-100      Length:      1610
Score:          904.00      Matches:      183
Percent Similarity: 98.94%      Conservative: 3
Best Local Similarity: 97.34%      Mismatches: 2
Query Match:      97.73%      Indels:      0
DB:              21          Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-765-205-5 (1-1610)

QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      687 GTTGTGACCTCTCTGACAGTATTAGAGACATTAAAGACATGGAGTGGTGTGGTCCACG 746
QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      747 CTATTCTCTGCTTTCATTGACAGTATTAGAGATATACAGGGTGTGATCCAGCTATC 806
QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      807 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 866
QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      867 CAGAAATCAGATGAAGCCACCCATTTCAGGCATATCTGGAATCTGGAATCTGATATCT 926
QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      927 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTTCACTGACGATAAG 986
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      987 GAACCTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTCAGTGTG 1046
QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      1047 ATGTGGGTATTTACCTATGTTGGTCCCTTGTGTTTAAATGGTCTGACACTACTGATTTGGCT 1106
QY      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      1107 CTCATTTCATCTTCTAGTGTCTCTGTTTATTATTAACGGCATCAGGCACAGATAGTATCAT 1166
QY      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1167 TATCTAGGACTTGCATAAATGAAGTAAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 1226
QY      182 ProGlyLeuLysArgLysAlaAsp 189
Db      1227 CCTGGATTGAAGCGCAAGCTGAA 1250

RESULT 26
US-10-439-388-62
; Sequence 62, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-765-205-5 (1-1610)

QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      687 GTTGTGACCTCTCTGACAGTATTAGAGACATTAAAGACATGGAGTGGTGTGGTCCACG 746
QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      747 CTATTCTCTGCTTTCATTGACAGTATTAGAGATATACAGGGTGTGATCCAGCTATC 806
QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      807 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 866
QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      867 CAGAAATCAGATGAAGCCACCCATTTCAGGCATATCTGGAATCTGGAATCTGATATCT 926
QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      927 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTTCACTGACGATAAG 986
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      987 GAACCTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTCAGTGTG 1046
QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      1047 ATGTGGGTATTTACCTATGTTGGTCCCTTGTGTTTAAATGGTCTGACACTACTGATTTGGCT 1106
QY      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      1107 CTCATTTCATCTTCTAGTGTCTCTGTTTATTATTAACGGCATCAGGCACAGATAGTATCAT 1166
QY      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1167 TATCTAGGACTTGCATAAATGAAGTAAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 1226
QY      182 ProGlyLeuLysArgLysAlaAsp 189
Db      1227 CCTGGATTGAAGCGCAAGCTGAA 1250

RESULT 25
US-10-347-669-5
; Sequence 5, Application US/10347669
```

APPLICANT: Olsen, Nancy J  
TITLE OF INVENTION: Method for Predicting Autoimmune Disease  
FILE REFERENCE: 1242/68  
CURRENT APPLICATION NUMBER: US/10/439,388  
CURRENT FILING DATE: 2003-05-16  
PRIOR APPLICATION NUMBER: US 60/381,055  
PRIOR FILING DATE: 2002-03-16  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 62  
LENGTH: 1785  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-439-388-62

Alignment Scores:  
Pred. No.: 1,05e-99 Length: 1785  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 17 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-439-388-62 (1-1785)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 247 GTTGTGGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 306
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 307 CTATTCTCGCTCTTTCATTCAGCATTTACAGATTGTGAGCGTAACAGCCCTACATTGCC 366
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGATCCAAGCTATC 426
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 427 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 486
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 487 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGGTTCATGTGAACTGCACGATAAAG 546
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 547 GAACCTCAGCGCGCTCTCTTAGTTGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 606
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 607 ATGTGGGTATTACCTATGTTGGTGCCTTGTAAATGCTGTGACACTACTGATTTGGCT 666
QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 667 CTCATTTCACTCTTCAGTGTTCTCTGTTTATTAAGCGGCATCAGGCACAGATAGATCAT 726
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 727 TATCTAGGACTTGCATAATAGAAATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAATC 786
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 787 CCTGGATTGAAGCGCAAGCTGAA 810
```

## RESULT 27

US-10-956-157-1705  
Sequence 1705, Application US/10956157  
Publication No. US20050118625A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
MOUNTS, William  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
FILE REFERENCE: 031896-043000 (AM 101081)  
CURRENT APPLICATION NUMBER: US/10/956,157  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 319805  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1705  
LENGTH: 1785  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-956-157-1705

Alignment Scores:  
Pred. No.: 1,05e-99 Length: 1785  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-1705 (1-1785)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 247 GTTGTGGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 306
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 307 CTATTCTCGCTCTTTCATTCAGCATTTACAGATTGTGAGCGTAACAGCCCTACATTGCC 366
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGATCCAAGCTATC 426
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 427 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 486
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 487 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGGTTCATGTGAACTGCACGATAAAG 546
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 547 GAACCTCAGCGCGCTCTCTTAGTTGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 606
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 607 ATGTGGGTATTACCTATGTTGGTGCCTTGTAAATGCTGTGACACTACTGATTTGGCT 666
QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 667 CTCATTTCACTCTTCAGTGTTCTCTGTTTATTAAGCGGCATCAGGCACAGATAGATCAT 726
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 727 TATCTAGGACTTGCATAATAGAAATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAATC 786
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 787 CCTGGATTGAAGCGCAAGCTGAA 810
```

## RESULT 28

US-10-956-157-4530  
Sequence 4530, Application US/10956157  
Publication No. US20050118625A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
MOUNTS, William  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
FILE REFERENCE: 031896-043000 (AM 101081)  
CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4530  
; LENGTH: 2050  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4530

Alignment Scores:  
Pred. No.: 1,31e-99 Length: 2050  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-4530 (1-2050)

```
QY 2 ValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 622 GTTGTGACCTCCTGACTCGAGACATTAAAGACACTCGAGTGGTGTGGTCCACG 681
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 682 CTATTCCTGCTGCTTTTCATTCAGCATTTGAGCGGTAAACAGCCTACATTCGCC 741
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 742 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 801
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 802 CAGAAATCAGATGAGAGCCACCCATTTCAGGCGCATATCTGGAATCTCGAAGTTGCTATATCT 861
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 862 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCACGATAAG 921
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 922 GAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGGTGTG 981
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 982 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGCACACTACTGATTTTGGCT 1041
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1042 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGATCAGGCACAGATAGATCAT 1101
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1102 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1161
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1162 CTGTGATTGAAGCGCAAGCTGAA 1185
```

RESULT 29  
US-10-466-258-3  
; Sequence 3, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 2052

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1188)  
US-10-466-258-3

Alignment Scores:  
Pred. No.: 1,31e-99 Length: 2052  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-466-258-3 (1-2052)

```
QY 2 ValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 622 GTTGTGACCTCCTGACTCGAGACATTAAAGACACTCGAGTGGTGTGGTCCACG 681
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 682 CTATTCCTGCTGCTTTTCATTCAGCATTTGAGCGGTAAACAGCCTACATTCGCC 741
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 742 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 801
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 802 CAGAAATCAGATGAGAGCCACCCATTTCAGGCGCATATCTGGAATCTCGAAGTTGCTATATCT 861
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 862 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCACGATAAG 921
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 922 GAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGGTGTG 981
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 982 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGCACACTACTGATTTTGGCT 1041
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1042 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGATCAGGCACAGATAGATCAT 1101
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1102 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1161
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1162 CTGTGATTGAAGCGCAAGCTGAA 1185
```

RESULT 30  
US-10-956-157-4531  
; Sequence 4531, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4531  
; LENGTH: 2226

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4531

Alignment Scores:
Pred. No.: 1.49e-99 Length: 2226
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4531 (1-2226)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 697 GTTGTGACCTCCCTGCTACTGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCCAGC 756
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 757 CTATTCTGCTGCTTTCATTGACAGTATTGACGATTGGAGCGTAACAGCCTACATTGCC 816
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 876
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 877 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAAGTTGCTATATCT 936
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 937 GAGGAGTTGGTTCAAGAGTACAGTAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 996
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 997 GAACTCAGCGCCCTCTCTTGTAGTGGTGTGATTTAGTGTGATCTCTGAAGTTTGCAGTGTG 1056
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 1057 ATGGGGGTATTACCTATGTTGGTGGCTGTTTAAATGTCGTGACACTACTGATTTGGCT 1116
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1117 CTCAATTCACCTTCAGTGTTCCCTGTTATTATGAACGCATCAGGCACAGATAGATCAT 1176
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1177 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 1236
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1237 CCTGGATTGAAGCGCAAAAGCTGAA 1260

RESULT 31
US-10-060-036-54
; Sequence 54, Application US/10060036
; Publication No. US200300731441
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060.036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
```

```
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-54

Alignment Scores:
Pred. No.: 1.5e-99 Length: 2235
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-060-036-54 (1-2235)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 697 GTTGTGACCTCCCTGCTACTGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCCAGC 756
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 757 CTATTCTGCTGCTTTCATTGACAGTATTGACGATTGGAGCGTAACAGCCTACATTGCC 816
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 876
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 877 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAAGTTGCTATATCT 936
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 937 GAGGAGTTGGTTCAAGAGTACAGTAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 996
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 997 GAACTCAGCGCCCTCTCTTGTAGTGGTGTGATTTAGTGTGATCTCTGAAGTTTGCAGTGTG 1056
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 1057 ATGGGGGTATTACCTATGTTGGTGGCTGTTTAAATGTCGTGACACTACTGATTTGGCT 1116
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1117 CTCAATTCACCTTCAGTGTTCCCTGTTATTATGAACGCATCAGGCACAGATAGATCAT 1176
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1177 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 1236
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1237 CCTGGATTGAAGCGCAAAAGCTGAA 1260

RESULT 32
US-10-220-891-22
; Sequence 22, Application US/10220891
; Publication No. US20030207286A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED
; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS
; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE
; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
; FILE REFERENCE: 7388-73435
; CURRENT APPLICATION NUMBER: US/10/220.891
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000/140387
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/159195
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
```



```
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-891-22

Alignment Scores:
Pred. No.: 6,7e-99 Length: 1980
Score: 898.00 Matches: 182
Percent Similarity: 98.41% Conservative: 4
Best Local Similarity: 96.30% Mismatches: 3
Query Match: 97.08% Indels: 0
DB: 17 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-220-891-22 (1-1980)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 1006 TCAGTTGTTGACCTCTCTGCTACTGGAGACATTAAAGAACCTGGAGTGGTGGTGGTGGCC 1065

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 1066 AGCCTATTCAGCTGCTTTTCATTGACAGTATTGAGCATTTGAGCGTAAACAGCTACATT 1125

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIlyGlyValIleGlnAla 60
Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 1185

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 1186 ATCCAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 1245

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 1246 TCTGAGGAGTTGTTTTCAGAAATACAGTAATCTGCTCTTGGTTCATGTGAATGCACGATA 1305

QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 1306 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGGAGTTTCAGTG 1365

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 1366 TTGATGTGGGTATTTACCTATGTTGGTGGCTGTTGTTTAAATGGTCTGACACTACTGATTTG 1425

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAep 160
Db 1426 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 1485

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaIlyIleGlnAlaLys 180
Db 1486 CATTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAAAGAAA 1545

QY 181 IleProGlyLeuLysArgLysAlaAep 189
Db 1546 ATCCCTGGATTGAAGCCCAAGCTGAA 1572

RESULT 33
US-09-978-360A-110
; Sequence 110, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.04.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 110
; LENGTH: 994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..631
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 35..160
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.6
; OTHER INFORMATION: seq ASLFLLLSLTVFS/IV
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 901...906
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 979..994
US-09-978-360A-110

Alignment Scores:
Pred. No.: 5,29e-99 Length: 994
Score: 895.00 Matches: 182
Percent Similarity: 98.40% Conservative: 3
Best Local Similarity: 96.81% Mismatches: 3
Query Match: 96.76% Indels: 0
DB: 11 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-978-360A-110 (1-994)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 68 GTTGTGGTACCTCTCTACTGGAGACATTAAAGAACCTGGAGTGGTGGTGGTGGCCAGC 127

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 128 CTATTCTGCTGCTTTTCATTGACAGTATTGACAGTATTGAGCGTAAACAGCTTACATTGCC 187

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 247

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 248 CAGAAATCAGATGAAGCCACCCATTAGGCGCATATCTGGAATCTGGAATCTGATATCT 307

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 308 GAGGAGTTGGTTTCAGAAAGTACAGTAAATCTGCTCTTGGTCAATGTGAACCTGCACGATAAG 367

QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
```



Db 368 GAACTCAGCGCCTCTCTTAGTTCATGATTAGTTCATCTCTCAAGTTTGCAGTGTG 427  
Qy 122 MetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141  
Db 428 ATGTGGGATTTACCTATGTTGGTGCCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 487  
Qy 142 LeuLeSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 488 CTCAATTCACCTCTCAGTGTCTCTCTTATTAAGCGGCATCAGGCACAGATAGATCAT 547  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 548 TATCTAGTACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAANAATCCAAGCAAAAATC 607  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 608 CCTGGATTGAAGCGCAAGCTGAA 631

## RESULT 34

US-10-641-643-382  
; Sequence 382, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 382:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2610 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGNOT14  
; CLONE: 1508778  
; SEQUENCE DESCRIPTION: SEQ ID NO: 382 :

US-10-641-643-382  
Alignment Scores:  
Pred. No.: 7,41e-98 Length: 2610  
Score: 891.00 Matches: 183  
Percent Similarity: 98.41% Conservative: 3  
Best Local Similarity: 96.83% Mismatches: 2

Query Match: 96.32% Indels: 1  
DB: 18 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-641-643-382 (1-2610)  
Qy 2 ValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 1311 GTTGTGACCTCCTGCTACTGAGAGACATTAAAGAACTGGAGTGGTGTGGTCCAGC 1370  
Qy 22 LeuPheIleLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41  
Db 1371 CTATTCTTCCTGCTCTTCAATGCAGCATATTCAGCAATTTGAGCGTAACAGCCCTACAATTC 1430  
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaI 61  
Db 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAGCTAT 1490  
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 1491 CCAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGCAATCTGAAGTTGCTATATC 1550  
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleIy 101  
Db 1551 TGAGGAGTTGGTTCAGAAGTACAGTAATTCCTCTTGGTTCATGTGAACCTGCACGATAA 1610  
Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValIle 121  
Db 1611 GGAATCTAGGCGCCTCTCTTAGTTAGTATGATTTAGTTCTCTGAAGTTTGCAGTGT 1670  
Qy 121 uMetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuIleAl 141  
Db 1671 GATGTGGGTATTTACCTATGTTGGTGCCTCTGTTAATGGTCTGACACTACTGATTTTGC 1730  
Qy 141 aLeuLeSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161  
Db 1731 TCTCATTTCACTTCTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1790  
Qy 161 sTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 1791 TTATCTAGGACTTCGCAATAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAAT 1850  
Qy 181 eProGlyLeuLysArgLysAlaAsp 189  
Db 1851 CCCTGGGTTGAAGCGCAAGCTGAA 1875  
RESULT 35  
US-10-466-258-10  
; Sequence 10, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 1798  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (215)..(814)  
US-10-466-258-10  
Alignment Scores:  
Pred. No.: 8,28e-95 Length: 1798  
Score: 864.00 Matches: 182  
Percent Similarity: 97.88% Conservative: 3  
Best Local Similarity: 96.30% Mismatches: 3  
Query Match: 93.41% Indels: 2  
DB: 19 Gaps: 0



```
Qy 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSer 32
Db 3 AAGACTGGAGTGTGTTGGTGCCAGCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 62
Qy 33 IleValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArg 52
Db 63 ATTGTGAGCGTAACAGCCCTACATTGCCCTTGGCCCTCTCTGTGACCATCAGCTTTAGG 122
Qy 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72
Db 123 ATATCAAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 182
Qy 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92
Db 183 TATCTGGAATCTGAAGTTGCTATATCTCGAGGATGGTTTCAGAGTACAGTAATCTGCT 242
Qy 93 LeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspLeu 112
Db 243 CTGTGCTATGTGAATCGCAGCATAAGAACTCAGCGCCTCTCTTAGTTGATGATTTA 302
Qy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 303 GTTGATCTCTGAAGTTGCAAGTTGATGGGTATTTACTATGTGGTGGCTTGTGT 362
Qy 133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSerIleProValIleTyr 152
Db 363 AATGCTCTGACACTACTGATTTGGCTCTCATTCACCTTCAGTGTTCTGTTATTTAT 422
Qy 153 GluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp 172
Db 423 GAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAATAAGAAATGTTAAAGAT 482
Qy 173 AlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
Db 483 GCTATGGCTAAATCCAGCAAAAATCCCTGGATTGAAGCGCAAGCTGAA 533

RESULT 38
US-10-956-157-9762
; Sequence 9762, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9762
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9762

Alignment Scores:
Pred. No.: 5,96e-85 Length: 1400
Score: 782.00 Matches: 159
Percent Similarity: 98.78% Conservative: 3
Best Local Similarity: 96.95% Mismatches: 2
Query Match: 84.54% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-9762 (1-1400)
Qy 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu 45
Db 3 CTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACAGCTACATTCGCTTGGCCCTGCTC 62
Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 63 TCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 123 GAAGCCACCCATTCAGGCGCATATCTGAAATCTGAAATGCTATATCTGAGGAGTTGGTT 182
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105
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Db 63 TCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 123 GAAGCCACCCATTCAGGCGCATATCTGAAATCTGAAATGCTATATCTGAGGAGTTGGTT 182
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105
Db 183 CAGAAGTACAGTAATCTGCTCTTGGTCACTGGAACGTCACAGATAAAGAACTCAGGCGC 242
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125
Db 243 CTCTCTTAGTTGATGATTTAGTTGATCTCTGAAATTTGCAAGTTTGCAGTGTTCATGTGGGTATTT 302
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeu 145
Db 303 ACCATGTTGGTGCTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTC 362
Qy 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165
Db 363 TTCAGTGTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTTACTAGACTT 422
Qy 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 423 GCAATAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAG 482
Qy 186 ArgLysAlaAsp 189
Db 483 CGCAAAAGCTGAA 494

RESULT 39
US-10-956-157-9767
; Sequence 9767, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9767
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9767

Alignment Scores:
Pred. No.: 5,96e-85 Length: 1400
Score: 782.00 Matches: 159
Percent Similarity: 98.78% Conservative: 3
Best Local Similarity: 96.95% Mismatches: 2
Query Match: 84.54% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-9767 (1-1400)
Qy 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu 45
Db 3 CTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACAGCTACATTCGCTTGGCCCTGCTC 62
Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 63 TCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 123 GAAGCCACCCATTCAGGCGCATATCTGAAATCTGAAATGCTATATCTGAGGAGTTGGTT 182
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105
```

Db 183 CAGAGTACAGTAATCTCTCTTGGTCAATGGAAGTCAAGTAAGGAACTCAGCC 242  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 243 CTCCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTGCGAGTTGTGATGGTATTT 302  
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeu 145  
Db 303 ACCTATGTTGGTGGCTTGTATTAATGGTCTGACACTACTGATTTGGCTCTCAATTCAC 362  
Qy 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165  
Db 363 TTCAGTGTCTCTGTTATTTATGACGGCATCAGGCATAGATAGATCAITATCTAGACTT 422  
Qy 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 423 GCAAAATAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAG 482  
Qy 186 ArgLysAlaAsp 189  
Db 483 CGCAAAGCTGAA 494

## RESULT 40

US-10-956-157-9766  
; Sequence 9766, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9766  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9766

Alignment Scores:  
Pred. No.: 2,596-74 Length: 1400  
Score: 695.00 Matches: 139  
Percent Similarity: 98.61% Conservative: 3  
Best Local Similarity: 96.53% Mismatches: 2  
Query Match: 75.14% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-9766 (1-1400)

Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 3 TCTGTGACCATCAGCTTTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGAT 62  
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85  
Db 63 GAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAATCTGATATCTCAGGAGTTGGTT 122  
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlnLeuArgArg 105  
Db 123 CAGAAGTACAGTAATTTCTGCTCTTGGTCAATGTAAGTGCACGACCAAGAACTCAGGCC 182  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 183 CTCCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTGCGAGTTGTGATGGTATTT 242  
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeu 145  
Db 243 ACCTATGTTGGTGGCTTGTATTAATGGTCTGACACTACTGATTTGGCTCTCAATTCAC 302

Qy 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165  
Db 303 TTCAGTGTCTCTGTTATTTATGACGGCATCAGGCATAGATAGATCAITATCTAGACTT 362  
Qy 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 363 GCAAAATAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAG 422  
Qy 186 ArgLysAlaAsp 189  
Db 423 CGCAAAGCTGAA 434

## RESULT 41

US-10-084-817-333  
; Sequence 333, Application US/10084817  
; Publication No. US20030119009A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan Stuart  
; APPLICANT: Jed G. Nuchtern  
; APPLICANT: Sharon E. Plon  
; APPLICANT: Jason M. Shohet  
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
; FILE REFERENCE: PA-0046 US  
; CURRENT APPLICATION NUMBER: US/10/084,817  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/270,784  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 365  
; SOFTWARE: PERL Program  
; SEQ ID NO 333  
; LENGTH: 1520  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030119009A1 092267CB1  
US-10-084-817-333

Alignment Scores:  
Pred. No.: 2,678-72 Length: 1520  
Score: 679.00 Matches: 127  
Percent Similarity: 84.49% Conservative: 31  
Best Local Similarity: 67.91% Mismatches: 29  
Query Match: 73.41% Indels: 0  
DB: 15 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-084-817-333 (1-1520)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 176 ATTGACCTGTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCTGTTTGGGAGTTCTCTG 235  
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 236 CTGCTGCTCTCTCTCCCTGACCAGTTTCAGCGGTGAGCGTCTGTCGCTACCTGGCCCTG 295  
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 296 GCGGCACCTCAGCCACCATCATGTTTCCGCATCTCAAGTCTGTTTACACAGCAGTGCAG 355  
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 356 AAACCCGACGAAGGCCACCCCTTTCAAGGCTACTTGGAGCTTGAGATCACTCTTCTCAG 415  
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
Db 416 GAGCAGATTTCAGAGTACACGACCTCCCTGCGCTCTACGTCAACAGCACACTTAAGGAA 475  
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 476 CTGAGGAGGCTCTTCTTGTGTCAGGACCTGGTGGATTCCTAAATTTTCAGTCTCTGATG 535  
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142

```
Db 536 TGGCTCCTGACCTACGTTGGGCGCTCTCTTCAATGGCGCTGACCGCTGCTCATGGCTGTG 595
Qy 143 lIeSerLeuPheSerIleProValIleTyArgHisGlnValGlnIleAspHisTyR 162
Db 596 GTTTCATGTTTACTCTACCTGTAGTGATGTTAAGCACCGACGACGATTAACCAATAT 655
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 656 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTCAGGCTAAATCCCA 715
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 716 GCGCGTAAGAGCGACGCTGAG 736

RESULT 42
US-10-267-502-213
; Sequence 213, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-267-502-213

Alignment Scores:
Pred. No.: 5,22e-72 Length: 2331
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 18 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-267-502-213 (1-2331)
Qy 3 ValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 1768 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCGTGTGGGAGTTCTCTG 1827
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAlaLeu 42
Db 1828 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGGTGAGCGTGGTGGCTACCTGGCCCTG 1887
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGln 62
Db 1888 GCGGACCTCTCAGCCACCATCAGTTTCGCGATCTACAAGTCTGTTTAAAGCAGTGCAG 1947
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyRileLeuGluSerGluValAlaIleSerGlu 82
Db 1948 AAAACCGAGAGGCGCCCTTTCAGGCGCTTTCAGGCGCTTTCAGGCTTTCAGTCCCTTCTCAG 2007
Qy 83 GluLeuValGlnLysTyRSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 2008 GAGCAGATTTCAGAGTACACGAGCTCCCTGCGAGTTCTACGTGAACAGCACACTTAAGGAA 2067
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2068 CTGAGGAGGCTCTCTCTTGTCCAGACCTCGTGGATTCCTTAAATTTGCAGTCTCTGATG 2127
Qy 123 TrpPheThrTyRValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
Db 2128 TGGCTCTCGACCTAGTTGGGCGCTCTCTTCAATGGCGCTGACCCCTGCTCTCATGGCTGTG 2187
Qy 143 lIeSerLeuPheSerIleProValIleTyArgHisGlnValGlnIleAspHisTyR 162
```

```
Db 2188 GTTTCATGTTTACTCTACCTGTAGTGATGTTAAGCACCGACGACGATTAACCAATAT 2247
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2248 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTCAGGCTAAATCCCA 2307
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 2308 GCGCGTAAGAGCGACGCTGAG 2328

RESULT 43
US-09-954-456-210
; Sequence 210, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-210

Alignment Scores:
Pred. No.: 8,58e-72 Length: 3202
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-954-456-210 (1-3202)
Qy 3 ValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 1890 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCGTGTGGGAGTTCTCTG 1949
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAlaLeu 42
Db 1950 CTGCTGCTCTCTCTCCCTGACCCAGTTTCAGCGTGGTGAGCGTGGTGGCCCTG 2009
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGln 62
Db 2010 GCGGACCTCTCAGCCACCATCAGTTTCGCGATCTACAAGTCTGTTTAAAGCAGTGCAG 2069
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyRileLeuGluSerGluValAlaIleSerGlu 82
```

```
Db 2070 AAAACGAGAGGCGCCCTTTCAAGGCTTACTTGAGCTTGAGATCAACCTTTCTCAG 2129
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 2130 GAGCAGATTGAGAGGTACAGGACTGCTGCGAGTTCAGTGCAGACACACATTAAGGAA 2189
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGCTGATTCCTTAAATTTGACGCTCTGATG 2249
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAlaLeu 142
Db 2250 TGCTCTGCTGACCTACCTGCGCTCTCTCAATGGCTGACCTGCTGCTGCTGCTGCTG 2309
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACCTGAGTGTATGTTAAGCACCAGGACAGATTCACCAATAT 2369
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2429
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 2430 GCGCTAAGAGGACGCTGAG 2450
```

## RESULT 44

```
US-10-172-118-386
; Sequence 386, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 386
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L10333
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-386
```

```
Alignment Scores:
Pred. No.: 8.58e-72 Length: 3202
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 17 Gaps: 0
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-172-118-386 (1-3202)

```
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 1890 ATTGACCTGTGTATTGGCGGACATCAAGCAGCGGATCGTGTGGGATTCCTCG 1949
Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaLeu 42
Db 1950 CTGCTGCTCTCTCTCCCTGACCCAGTTCAGCGTGGTGAGCGTCTGCTGCGCTTACCTGGCCCTG 2009
```

```
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
Db 2010 GCGCAGCTCTCAGCCACCACATCAGTTTCGCGATCTCAAGTCTGTGTTTACAGCAGTGCAG 2069
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 2070 AAAACGAGAGGCGCCCTTTCAAGGCTTACTTGAGCTTGAGATCAACCTTTCTCAG 2129
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 2130 GAGCAGATTGAGAGGTACAGGACTGCTGCGAGTTCAGTGCAGACACACATTAAGGAA 2189
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGCTGATTCCTTAAATTTGACGCTCTGATG 2249
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAlaLeu 142
Db 2250 TGCTCTGCTGACCTACCTGCGCTCTCTCAATGGCTGACCTGCTGCTGCTGCTGCTG 2309
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACCTGAGTGTATGTTAAGCACCAGGACAGATTCACCAATAT 2369
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2429
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 2430 GCGCTAAGAGGACGCTGAG 2450
```

## RESULT 45

```
US-10-342-887-386
; Sequence 386, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 386
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-386
```

```
Alignment Scores:
Pred. No.: 8.58e-72 Length: 3202
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 18 Gaps: 0
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-342-887-386 (1-3202)

Qy	3	ValAspLeuLeuTyrTrrArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu	22
Db	1890	ATTGACCTGTTGTAATTCGGCGGACATCAAGCAGCAGCGGCATCGTGTGTTGGAGATTTTCCTG	1949
Qy	23	PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu	42
Db	1950	CTGCTGCTTCTCCCTGACCCAGTTTCCAGCGTGTGAGCGTCGTGGCCTACCTTGGCCCTG	2009
Qy	43	AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln	62
Db	2010	GCGGCATCTCTCAGCCACCATCAGTTTCCGCATCTTACAAGTCGTGTTTACAAGCAGTGCAG	2069
Qy	63	LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu	82
Db	2070	AAACCCAGCAGGCCACCCCTTTCAAGCGCTACTTGGAGCTTGAGATCACCCTTTTCTCAG	2129
Qy	83	GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu	102
Db	2130	GAGCAGATTTCAGAAAGTACAGCATCGCTGCAGTTCTACGTGTAACACACACTTAAAGAA	2189
Qy	103	LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet	122
Db	2190	CTGAGGAGGCTTTCCTTGTCCAGGACCTGGTGGATTCCCTTAAATTTGCAGTCCCTGATG	2249
Qy	123	TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu	142
Db	2250	TGGCTCTGCACCTACGTTGGCGCTCTCTTCAATGGCGCTGACCCCTGCTGCTCATGGCTGTG	2309
Qy	143	IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr	162
Db	2310	GTITTCAAATGTTTACTCTACCTGTAGTGTATGTTTAAGCACCAGGCACAGATTGACCAATAT	2369
Qy	163	LeuGlyLeuAlaAsnLysSerValLysAlaMetAlaLysIleGlnAlaLysIlePro	182
Db	2370	CTGGCACTTGTGAGGACTTCATATAAATGCTGTGTCGCAAGATTACGGCTAAAATCCCA	2429
Qy	183	GlyLeuLysArgLysAlaAsp	189
Db	2430	GGCGCTAAGAGGCACGCTGAG	2450

RESULT 46

```

US-10-723-860-1480
; Sequence 1480, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1480
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1480

```

## RESULT 47

RESULT 47  
 US-10-843-641A-3237  
 ; Sequence 3237, Application US/10843641A  
 ; Publication No. US2005006454A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Avalon Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
 ; TITLE OF INVENTION: Signature Gene Sets  
 ; FILE REFERENCE: 689290-189  
 ; CURRENT APPLICATION NUMBER: US/10/843,641A  
 ; CURRENT FILING DATE: 2004-05-12  
 ; PRIOR APPLICATION NUMBER: US/09/873,367  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US/09/954,531  
 ; PRIOR FILING DATE: 2001-09-18  
 ; PRIOR APPLICATION NUMBER: US/09/954,456  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: US/09/962,436  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: US/09/962,832  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: US/09/964,824  
 ; PRIOR FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: US/09/967,768  
 ; PRIOR FILING DATE: 2001-09-28  
 ; PRIOR APPLICATION NUMBER: US/09/968,007  
 ; PRIOR FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: US/09/969,347  
 ; PRIOR FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: US/09/969,708  
 ; PRIOR FILING DATE: 2001-10-03  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 8447



; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3237  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-843-641A-3237

Alignment Scores:  
Pred. No.: 8,58e-72 Length: 3202  
Score: 679.00 Matches: 127  
Percent Similarity: 84.49% Conservative: 31  
Best Local Similarity: 67.91% Mismatches: 29  
Query Match: 73.41% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-843-641A-3237 (1-3202)

```
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1890 ATTGACCTGTTGATTGGCGGACATCAAGCAGCGGCATCGTGTTCGGAGTTCCCTG 1949

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1950 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCCCTACCTGGGCCCTG 2009

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2010 GCGGCACCTCTCAGCCACCATCATGTTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG 2069

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2070 AAACCGACGAGGCCACCCCTTCAAGGCTTCTTGAGCTTGAGATCACCCCTTCTCTAG 2129

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2130 GAGCAGATTCAAGATACAGGACTGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAA 2189

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2190 CTGAGAGAGCTCTTCCTCTGTCAGGACCTGGTGGATTCCTTAAAAVTTTCAGTCTCTGATG 2249

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2250 TGGCTCTGACCTACCTTGGCGCTCTCTCAATGGCTGACCTGCTGCTCTGCTGCTGCTG 2309

QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2310 GTTTCAAATGTTTACTCTACCTGATGTATGTTAAGCACAGGCACAGATTGACCAATAT 2369

QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaIleGlnAlaLysIlePro 182
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429

QY 183 GlyLeuLysArgLysAlaAsp 189
   ::::::::::::::::::::::
Db 2430 GCGGCTAAGAGGCACGCTGAG 2450
```

## RESULT 48

US-10-723-860-5926  
; Sequence 5926, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5926  
; LENGTH: 3305  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-5926

Alignment Scores:  
Pred. No.: 9,02e-72 Length: 3305  
Score: 679.00 Matches: 127  
Percent Similarity: 84.49% Conservative: 31  
Best Local Similarity: 67.91% Mismatches: 29  
Query Match: 73.41% Indels: 0  
DB: 20 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-723-860-5926 (1-3305)

```
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1890 ATTGACCTGTTGATTGGCGGACATCAAGCAGCGGCATCGTGTTCGGAGTTCCCTG 1949

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1950 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCCCTACCTGGGCCCTG 2009

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2010 GCGGCACCTCTCAGCCACCATCATGTTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG 2069

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2070 AAACCGACGAGGCCACCCCTTCAAGGCTTCTTGAGCTTGAGATCACCCCTTCTCTAG 2129

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2130 GAGCAGATTCAAGATACAGGACTGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAA 2189

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2190 CTGAGAGAGCTCTTCCTCTGTCAGGACCTGGTGGATTCCTTAAAAVTTTCAGTCTCTGATG 2249

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2250 TGGCTCTGACCTACCTTGGCGCTCTCTCAATGGCTGACCTGCTGCTCTGCTGCTGCTG 2309

QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2310 GTTTCAAATGTTTACTCTACCTGATGTATGTTAAGCACAGGCACAGATTGACCAATAT 2369

QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaIleGlnAlaLysIlePro 182
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429

QY 183 GlyLeuLysArgLysAlaAsp 189
   ::::::::::::::::::::::
Db 2430 GCGGCTAAGAGGCACGCTGAG 2450
```

## RESULT 49

US-10-205-219-94  
; Sequence 94, Application US/10205219  
; Publication No. US20030138803A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Pinnock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018200  
; CURRENT APPLICATION NUMBER: US/10/205,219  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27



; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.11  
; SEQ ID NO 94  
; LENGTH: 1502  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: rs-Rex-s  
US-10-205-219-94

Alignment Scores:  
Pred. No.: 3,478-72 Length: 1502  
Score: 678.00 Matches: 126  
Percent Similarity: 84.4% Conservative: 32  
Best Local Similarity: 87.3% Mismatches: 29  
Query Match: 73.3% Indels: 0  
DB: 15 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-205-219-94 (1-1502)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
Db 179 ATTGACCTTCTGTACTGGCGGACATCAAGCAGCGGATGTGTTTCGGAGCTTCCTG 238  
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 239 CTGCTGCTCTTCTCCCTGACCCAGTTTACGGTTGTGAGCGTGTGCTACCTGCTGCTG 298  
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 299 GCTGCCCTCTCTGCCACCATCATCAGCTTCGCGCATCTACAAGTCGGTTCTACAAGCTGTGCAG 358  
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 359 AAAACAGATGAGGGTACACCTTTCAAGGCTACCTGGAGCTGGAGTACCTGTCCTCCAG 418  
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
Db 419 GAGCAGATCCAGAGTACACAGACTCGCTGCAGCTATACGTGAACAGCAGCTCTGAAGGAG 478  
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 479 CTACGGAGGCTCTTCTGCTGCTCAGACCTCTGTTGATTCCTTAAATTTTGCAGTCTCATG 538  
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 539 TGCTCTGACCTACGTGGCGCACTCTTCAATGGCTGACCTGCTGCTTATGCTGTG 598  
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
Db 599 GTTTCGATGTTTACTTACTTACCTGCTGTATATGTTAAGCACCAGGACAGGTTGACCAATAT 658  
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 659 CTGGGACTTGTGAGGACTCACATAAACACCGTTGTGGCAAGATCCAGGCTAAATATCCCC 718  
Qy 183 GlyLeuLysArgLysAlaAsp 189  
Db 719 GCGCCCAAGAGGACGCTGAG 739

## RESULT 50

US-10-267-502-215  
; Sequence 215, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 215  
; LENGTH: 2343  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-267-502-215

Alignment Scores:  
Pred. No.: 6,978-72 Length: 2343  
Score: 678.00 Matches: 126  
Percent Similarity: 84.4% Conservative: 32  
Best Local Similarity: 87.3% Mismatches: 29  
Query Match: 73.3% Indels: 0  
DB: 18 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-267-502-215 (1-2343)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1780 ATTGACCTTCTGTACTGGCGGACATCAAGCAGCTGGGATGTGTTTCGGGAGCTTCCTG 1839  
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 1840 CTGCTGCTCTTCTCCCTGACCCAGTTTACGGTTGTGAGCGTGTGCTACCTGCTGCTG 1899  
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 1900 GCGGCCCTCTCTGCCACCATCATCAGCTTCGCGCATCTACAAGTCGGTTCTACAAGCTGTGCAG 1959  
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 1960 AAAACAGATGAGGGTACACCTTTCAAGGCTACCTGGAGCTGGAGTACCTGTCCTCCAG 2019  
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
Db 2020 GAGCAGATCCAGAGTACACAGACTCGCTGCAGCTGTATGTGAACAGCAGCTCTGAAGGAG 2079  
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2080 CTACGGAGGCTTTTCTGCTGCTCAGGACCTGCTGGATTCCTTAAATTTTGCAGTCTCATG 2139  
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 2140 TGGCTCTGACCTACGTGGCGCGCTCTTCAATGGCTGACCTGCTGCTTATGCTGTG 2199  
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
Db 2200 GTTTCGATGTTTACTTACTTACCTGTTGTGTACCTTGAACACAGGACCAAGTTGACCAATAT 2259  
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2260 CTGGGACTTGTGAGGACTCACATAAACACCGCTCGTGGCAAGATCCAGGCTAAATATCCCC 2319  
Qy 183 GlyLeuLysArgLysAlaAsp 189  
Db 2320 GCGCCCAAGAGGACGCTGAG 2340

## RESULT 51

US-09-960-352-8477  
; Sequence 8477, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 8477  
; LENGTH: 422

; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 36-LIB34-048-Q1-E1-A8  
US-09-960-352-8477

Alignment Scores:  
Pred. No.: 1,11e-72 Length: 422  
Score: 675.00 Matches: 136  
Percent Similarity: 98.57% Conservative: 2  
Best Local Similarity: 97.14% Mismatches: 2  
Query Match: 72.97% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-960-352-8477 (1-422)

QY 37 ThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 56  
DB 2 ACGGCCTACATTGCCCTTGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGCT 61  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
DB 62 GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGCGCATATTTGGAATCT 121  
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96  
DB 122 GAAGTTGCTATATCTCAGGAGTTGGTTCAAGAGTACGCAATTTCTGCTCTTGCTCATGTT 181  
QY 97 AsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 116  
DB 182 AACTGCACATAAAAGAACTCAGAGCCCTCTTCTTAGTTGATGATTTAGTTCTCTG 241  
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 136  
DB 242 AAGTTTGCAAGTGTGATGGGTATTTACCTATGTTGGTGCCTTGTTCATGCTCTGACA 301  
QY 137 LeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGln 156  
DB 302 CTACTAATTTTGCTCTGATTTTCACTTCTCAGTGTTCTTCTGTTATTTATGACGGCATCAG 361  
QY 157 ValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys 176  
DB 362 GCGCAATAGATCATTTCTGGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAA 421

## RESULT 52

US-10-205-194-128  
; Sequence 128, Application US/10205194  
; Publication No. US20030134301A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Pincock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018201  
; CURRENT APPLICATION NUMBER: US/10/205,194  
; CURRENT FILING DATE: 5200-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 128  
; LENGTH: 1473  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Cl-13 protein  
US-10-205-194-128

Alignment Scores:  
Pred. No.: 1.31e-70 Length: 1473  
Score: 665.00 Matches: 126  
Percent Similarity: 84.49% Conservative: 32

Best Local Similarity: 67.38% Mismatches: 29  
Query Match: 71.89% Indels: 1  
DB: 15 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-205-194-128 (1-1473)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
DB 146 ATTGACCTTCTGTACTGCGGACATCAAGCAGAGCGGATTTGTTCGGAGCTTCCTCG 205  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
DB 206 CTGCTGCTCTCTCTCCCTGACCCAGTTACGGTTGTGAGCGTCTCGCTACCTACCTGGCCCTG 265  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62  
DB 266 GCTGCCCTCTCTGCCACCATCAGCTTCGCGCATCTCAAGTCCGTTCTTACAAGCTGTGCAG 325  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
DB 326 AAAACAGATGAGGGTCACCCCTTCAAGGCTTACCTGGAGCTGAGAGTACCTGTCCCCAG 385  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
DB 386 GAGCAGATCCAGAGTACACAGACTGCCTGCAGCTATACGTGAACAGACACTCTGAAGGAG 445  
QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 446 CTACGAGGCTCTCTCTGTCACAGACCTAGTGGATTCCTTAAAAATTTGCAGTCTCATG 505  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuLeuLeuLeuAlaLeu 142  
DB 506 TGCTCTCTGACCTAGCTGGCGCACTTCAATGGCCTGACCTGCTGTATGGCTGTG 565  
QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
DB 566 GTTTCGATGTTTACTCTACTCTGTTATATGTTAAGCACCAGCAGAGTTGACCAATAT 625  
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 626 CTGGGACTTGTGAGGACTCACATAAACACCGTTGTGGCAAGATCCAGGCTAAATCCCC 685  
QY 183 GlyLeuLysArgLysAlaAsp 189  
DB 686 GGGCGC-AAGAGGCGATGCTGAG 705

## RESULT 53

US-09-960-352-11567  
; Sequence 11567, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 11567  
; LENGTH: 422  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 50-BOVMS1-005-Q1-E1-E6  
US-09-960-352-11567

Alignment Scores:  
Pred. No.: 1.76e-70 Length: 422  
Score: 657.00 Matches: 135  
Percent Similarity: 98.56% Conservative: 2  
Best Local Similarity: 97.12% Mismatches: 2

Query Match:	71.03%	Indels:	0
DB:	9	Gaps:	0
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-960-352-11567 (1-422)			
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIle	40
		:::	
Db	4	AACTTGTTCTGCTCTCGGTACAGATATTCAGCAATTGTGAGTGTAAACGGCGTCAATT	63
Qy	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	64	GCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGGCT	123
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	124	ATCCAGAAATCTGATGAAGGCCACCAATTCAGGGCATATTTGGAAATCTGAAGTTGCTATA	183
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	184	TCTGAGGAGTGTGGTTTCAGAAGTACAGCAAAATCTCTCTCTGTGTCATGTAACTCCACAATA	243
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	244	AAAGAACTCAGACGGCTCTTCTTAGTGTGATGATTTAGTTGATTCCTGAAGTTTGCAAGT	303
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	304	TTGATGTGGTATTTACCTATGTTGGTGCCTTGTTCATAGTCTGCACACTACTAAATTTTG	363
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIle	159
Db	364	GCTCTGAATTTCACTCTTCAGTGTCTCTCTGTTATTTATGAACGGCATCAGGCGCAATA	420

```

RESULT 54
US-10-408-967-1
; Sequence 1, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-408-967-1

```

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Alignment Scores:
Pred. No.:          6,59e-66          Length:          711
Score:             622.50           Matches:         113
Percent Similarity: 81.05%          Conservative:    41
Best Local Similarity: 59.47%       Mismatches:     35
Query Match:       67.30%          Indels:         1
DB:                18              Gaps:           1

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-408-967-1 (1-711)

QY      1  SerValValAspLeuLeuTyTTPArgAspIleLySlyThrGlyValValPheGlyAla  20
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      139  GCGGTGCAGCATCTGATTTCTCGAGAGATGTGAAGAAGACTCGGTTTGTCTTGGCACC  198
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle  40
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      199  AGCTGTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCACTAGTGGGTTCTTACACCT  258
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrllysGlyValIleGlnAla  60

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259	Db	ATCCTGGCTCTTCTCTCTGTCACCATCATGCTTCAAGATCTACAACTCCGTCATCAAGCT	318
61	Qy	IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
319	Db	GTACAGAAGTCAGAAGAAGGCCATTCATTCAAGACCTACCTGGACGTAGACATTA	378
81	Qy	SerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
379	Db	TCCTCAGAGCTTTCCTAATAATCATGTAATGCTGCCATGGTGCAATCAACAGGGCCCTG	438
101	Qy	LysGluLeuArgGlyLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
439	Db	AAACTCATTATTCGGCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAGCTGGCTGTC	498
121	Qy	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
499	Db	TTCATGTGGCTGATCACCTATGTGGTGCTGTTTAAACGGAATCACCTCTCTAATCTT	558
141	Qy	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
559	Db	GCTGAACGTGCTCAATTTTCAGTGTCCCGATTCTCTATGAGAAGTACAAGACCCAGATTGAT	618
161	Qy	HisTyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlaLysIleGlnAlaLys	180
619	Db	CACATATGTTGGCATCGGCCGAGATCAGACCAAGTCAATTGTTGAAAGAATCAACAGCAAA	678
181	Qy	IleProGlyLeu---LysArgLysAlaAsp	189
679	Db	CTTCCTCGGAATCGCCAAAGAAAAAGGCAGAA	708

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RESULT 55
US-10-106-698-1945
; Sequence 1945, Application US/101066598
; Publication No. US20030105690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and P
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1945
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-1945

```

```
Alignment Scores:
Pred. No.:      1,76e-65                Length:          1330
Score:         622.50                  Matches:        113
Percent Similarity:   81.05%           Conservative:    41
Best Local Similarity: 59.47%           Mismatches:     35
Query Match:       67.30%             Indels:         1
DB:               15                   Gaps:            1


US -09-830-372-2_COPY_975_1163 (1-189) x US-10-106-698-1945 (1-1330)

Qy      1 SerValValAspLeuLeuYrTrrPAGspIlelyslvThrGIvAlvalPhcGlyAla 20
      :|||:::||||:::::::::::|||:::|||||
Db      297 GCGETGCACCATCTGAATTTTCGTGGAGAGTGTAAGAAGACTGGSTTTGCTTTGGCACC 356

Qy      21 SerLeuPheLeuLeuSerLeuThrvAlpheserlleVaservalThralatyrile 40
      :|||:::||||:::::::::::|||:::|||||
Db      357 ACGCTGATCATGCTGCTTTTTCCCTGCCAGCTTTTCAGTGTCACTAGTGGTTTCTTTACCTC 416

Qy      41 AlaleuAlalaLeuSerValThrlleSerpheArqilleTvryvsGlVallleglnAla 60
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Db      417 ATCTGGCTCTTCTCTCTGTACCATCAGCTTCCAGGATCTAAGGTCCTCATCCAAAGCT 476
Qy      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      477 GTACAGAGTCAGAGAGGCCATCCATTCAAGGCTACTCGACGTAGACATTACTCTG 536
Qy      81  SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGluGlyHisValAsnSerThrile 100
Db      537 TCTCAGAAAGCTTCCATAATTACATGAATGCTGCGCATGCTGACATCAACAGAGGCCCTG 596
Qy      101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db      597 AAACATCAATTATTCGTCCTCTTCTGGTGAAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 656
Qy      121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db      657 TTCATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCCCTTCTAATTCCT 716
Qy      141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db      717 GCTGAACCTGCTCATTTTCAGTGTCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 776
Qy      161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db      777 CACTATGTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAGATCAAGCAAAA 836
Qy      181 IleProGlyLeu---LysArgLysAlaAsp 189
Db      837 CTCCTTGGAAATCGCCCAAAAAAAGGCAGAA 866

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## RESULT 56

```

US-09-729-674-19
; Sequence 19, Application US/09729674
; Patent No. US2001003935A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-729-674-19

Alignment Scores:
Pred. No.:      2 48e-65      Length:      1656
Score:          622.50      Matches:      113
Percent Similarity: 81.05%      Conservative: 41
Best Local Similarity: 59.47%      Mismatches: 35
Query Match:      67.30%      Indels:      1
DB:              9          Gaps:      1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-729-674-19 (1-1656)

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Qy      1  SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db      165 GCGGTGTCAGCATCTCATTTTCTGGAGAGATGTGAAGAAGACTGGGTGTTGTTCTTTGGCACC 224
Qy      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      225 AGCGTGATCATGCTGCTTCTCCCTGGCAGCTTTCAGTGTGTCATCAGTGTGGTGTCTTACCTC 284
Qy      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db      285 ATCTGGCTCTTCTCTCTGTCCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 344
Qy      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      345 GTACAGAAAGTCAGAGAAGGCCATCCATTCAAGGCTTACCTGAGCATGACATTACTCTG 404
Qy      81  SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100
Db      405 TCTCAGAAAGCTTTCATTAATTACATGAATGCTGCGATGTCATCAACAGAGGCCCTG 464
Qy      101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db      465 AAACATCAATTATTCGTCCTCTTCTGGTGAAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 524
Qy      121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db      525 TTCATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCCCTTCTAATTCCT 584
Qy      141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db      585 GCTGAACCTGCTCATTTTCAGTGTCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 644
Qy      161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db      645 CACTATGTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAGATCAAGCAAAA 704
Qy      181 IleProGlyLeu---LysArgLysAlaAsp 189
Db      705 CTCCTTGGAAATCGCCCAAAAAAAGGCAGAA 734

RESULT 57
US-10-913-553-19
; Sequence 19, Application US/10913553
; Publication NO. US20050003491A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/10/913,553
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US/09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-913-553-19

```

Alignment Scores:  
Pred. No.: 2,48e-65 Length: 1656  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservatives: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 21 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-913-553-19 (1-1656)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 165 GCGGTGCGACGATCTGATTTCTGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC 224  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 225 AGCTGTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTGATCAGTGTGGTTCTTACCTC 284  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 285 ATCTGGCTCTTCTCTGTCAACATCAGCTTCAGAGATCTACAAGTCCGTATCAAGCT 344  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 345 GTACAGAAGTCAGAAAGAGGCCCATCCATTCAAAGCTACCTGGACCTAGACATTACTCTG 404  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 405 TCCTCAGAAAGCTTCCATAATACATGATGCTGCGCATGCTGATCAACAGGCCCCCTG 464  
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 465 AAATCATATTATTCGTCCTCTTCTGGTAGAGATCTGGTTGACTCTTGAAGCTGGCTGTC 524  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140  
Db 525 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCAACCTTCTTAATCTT 584  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 585 GCTGAACGTGCTCATTTTCAGTGTCCCGATGTTCTATGAGAAGTACAGACCCAGATTGAT 644  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 645 CACTATGTGGATCGCCCAAAAAAAGGCAGAA 734

Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
Db 705 CTCCTCGAATCGCCCAAAAAAAGGCAGAA 734

RESULT 58  
US-09-763-205-25  
; Sequence 25, Application US/09765205  
; Patent No. US20020034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 1668  
; TYPE: DNA  
; ORGANISM: human  
US-09-763-205-25

Alignment Scores:  
Pred. No.: 2,51e-65 Length: 1668  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservatives: 41  
Best Local Similarity: 59.47% Mismatches: 35

Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservatives: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 9 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-765-205-25 (1-1668)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 237 GCGGTGCGACGATCTGATTTCTGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC 296  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 297 AGCTGTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTGATCAGTGTGGTTCTTACCTC 356  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 357 ATCTGGCTCTTCTCTGTCAACATCAGCTTCAGGATCTACAAGTCCGTATCAAGCT 416  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 417 GTACAGAAGTCAGAAAGAGGCCCATCCATTCAAAGCTACCTGGACCTAGACATTACTCTG 476  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 477 TCCTCAGAAAGCTTCCATAATACATGATGCTGCGCATGCTGATCAACAGGCCCCCTG 536  
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 537 AAATCATATTATTCGTCCTCTTCTGGTAGAGATCTGGTTGACTCTTGAAGCTGGCTGTC 596  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140  
Db 597 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCAACCTTCTTAATCTT 656  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 657 GCTGAACGTGCTCATTTTCAGTGTCCCGATGTTCTATGAGAAGTACAGACCCAGATTGAT 716  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 717 CACTATGTGGATCGCCCAAAAAAAGGCAGAA 776

Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
Db 777 CTCCTCGAATCGCCCAAAAAAAGGCAGAA 806

RESULT 59  
US-10-347-669-25  
; Sequence 25, Application US/10347669  
; Publication No. US20050084850A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/10/347,669  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 1668  
; TYPE: DNA  
; ORGANISM: human  
US-10-347-669-25

Alignment Scores:  
Pred. No.: 2,51e-65 Length: 1668  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservatives: 41  
Best Local Similarity: 59.47% Mismatches: 35

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Query Match: 67.30% Indels: 1
DB: 21 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-347-669-25 (1-1668)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 346

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB AGCGTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTGTCATCAGTGTGGTTTCTTACCTC 406

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB ATCTCTGGCTCTTCTCTGTCCATCAGCTTCAGGATCTACCAAGTCGTCATCCAAGCT 466

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB GTACAGAAGTCAGAAAGAGCCATCCATTTCAAAGCTTACCTGGACGTAGACATTACTCTG 526

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB TCTCTCAGAAAGCTTTCATTAATACATGATGCTGCATGCTGTCACATCAACAGGCGCTG 586

QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB TCTCTCAGAAAGCTTTCATTAATACATGATGCTGCATGCTGTCACATCAACAGGCGCTG 646

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB TTCTATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAATCACCTTCTAATTCCT 706

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB GCTGAACCTGCTCATTTTCAGTGTCCGATGTCTATGAGAAGTACAGACCCAGATTGAT 766

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB CACTATGTGGTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 826

QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
DB CTCCCTGGAATCGCCAAAAAAGGCGAGAA 856

RESULT 61
US-09-882-171-254
; Sequence 254, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23

US-09-809-391-254
; Sequence 254, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 254
; LENGTH: 1766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-254

Alignment Scores:
Pred. No.: 2,746-65 Length: 1766
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-809-391-254 (1-1766)
```

1	PRIOR FILING DATE: 1997-08-22	
2	PRIOR APPLICATION NUMBER: 60/056,893	
3	PRIOR FILING DATE: 1997-08-22	
4	PRIOR APPLICATION NUMBER: 60/056,630	
5	PRIOR FILING DATE: 1997-08-22	
6	PRIOR APPLICATION NUMBER: 60/056,878	
7	PRIOR FILING DATE: 1997-08-22	
8	PRIOR APPLICATION NUMBER: 60/056,662	
9	PRIOR FILING DATE: 1997-08-22	
10	PRIOR APPLICATION NUMBER: 60/056,872	
11	PRIOR FILING DATE: 1997-08-22	
12	PRIOR APPLICATION NUMBER: 60/056,882	
13	PRIOR FILING DATE: 1997-08-22	
14	PRIOR APPLICATION NUMBER: 60/056,637	
15	PRIOR FILING DATE: 1997-08-22	
16	PRIOR APPLICATION NUMBER: 60/056,903	
17	PRIOR FILING DATE: 1997-08-22	
18	PRIOR APPLICATION NUMBER: 60/056,888	
19	PRIOR FILING DATE: 1997-08-22	
20	PRIOR APPLICATION NUMBER: 60/056,879	
21	PRIOR FILING DATE: 1997-08-22	
22	PRIOR APPLICATION NUMBER: 60/056,880	
23	PRIOR FILING DATE: 1997-08-22	
24	PRIOR APPLICATION NUMBER: 60/056,894	
25	PRIOR FILING DATE: 1997-08-22	
26	PRIOR APPLICATION NUMBER: 60/056,911	
27	PRIOR FILING DATE: 1997-08-22	
28	PRIOR APPLICATION NUMBER: 60/056,636	
29	PRIOR FILING DATE: 1997-08-22	
30	PRIOR APPLICATION NUMBER: 60/056,874	
31	PRIOR FILING DATE: 1997-08-22	
32	PRIOR APPLICATION NUMBER: 60/056,910	
33	PRIOR FILING DATE: 1997-08-22	
34	PRIOR APPLICATION NUMBER: 60/056,864	
35	PRIOR FILING DATE: 1997-08-22	
36	PRIOR APPLICATION NUMBER: 60/056,631	
37	PRIOR FILING DATE: 1997-08-22	
38	PRIOR APPLICATION NUMBER: 60/056,845	
39	PRIOR FILING DATE: 1997-08-22	
40	PRIOR APPLICATION NUMBER: 60/056,892	
41	PRIOR FILING DATE: 1997-08-22	
42	PRIOR APPLICATION NUMBER: 60/057,761	
43	PRIOR FILING DATE: 1997-08-22	
44	PRIOR APPLICATION NUMBER: 60/047,595	
45	PRIOR FILING DATE: 1997-05-23	
46	PRIOR APPLICATION NUMBER: 60/047,599	
47	PRIOR FILING DATE: 1997-05-23	
48	PRIOR APPLICATION NUMBER: 60/047,588	
49	PRIOR FILING DATE: 1997-05-23	
50	PRIOR APPLICATION NUMBER: 60/047,585	
51	PRIOR FILING DATE: 1997-05-23	
52	PRIOR APPLICATION NUMBER: 60/047,586	
53	PRIOR FILING DATE: 1997-05-23	
54	PRIOR APPLICATION NUMBER: 60/047,590	
55	PRIOR FILING DATE: 1997-05-23	
56	PRIOR APPLICATION NUMBER: 60/047,594	
57	PRIOR FILING DATE: 1997-05-23	
58	PRIOR APPLICATION NUMBER: 60/047,589	
59	PRIOR FILING DATE: 1997-05-23	
60	PRIOR APPLICATION NUMBER: 60/047,593	
61	PRIOR FILING DATE: 1997-05-23	
62	PRIOR APPLICATION NUMBER: 60/047,614	
63	PRIOR FILING DATE: 1997-05-23	
64	PRIOR APPLICATION NUMBER: 60/043,578	
65	PRIOR FILING DATE: 1997-04-11	
66	PRIOR APPLICATION NUMBER: 60/043,576	
67	PRIOR FILING DATE: 1997-04-11	
68	PRIOR APPLICATION NUMBER: 60/047,501	
69	PRIOR FILING DATE: 1997-05-23	
70	PRIOR APPLICATION NUMBER: 60/043,670	
71	PRIOR FILING DATE: 1997-04-11	
72	PRIOR APPLICATION NUMBER: 60/056,632	
73	PRIOR FILING DATE: 1997-08-22	





## RESULT 63

US-10-276-774-980  
; Sequence 980, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 980  
; LENGTH: 1915  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-980

## Alignment Scores:

Pred. No.: 3,11e-65 Length: 1915  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservative: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 18 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-276-774-980 (1-1915)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspLeuLeuTyrLysThrGlyValValPheGlyAla	20
Db	287	CGGGTGCAGATCTGATTTCTTCTGGAGAGATGTGAAGAAGCTGGGTTGTCTTTGGCACC	346
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	347	ACGCTGATCATGCTCTTCCCTGGCAGCTTTCAGTGTCATCAGTGTTCTTACCTC	406
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	407	ATCTGGCTCTTCTCTGTCCACATCAGCTTCAGATCTCAAGTCCGTCATCCAGCT	466
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	467	GTACAGAAGTCAGAGAAGGCGCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG	526
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	527	TCCTCAGAAGCTTTCATAATATACATGATGTCGTCATGTCATCAACAGGGCCCTG	586
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	587	AAACTATTATTCGTCCTCTTCTGGTAGAGATCTGGTTGACTCTTGAAGCTGCTCTC	646
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	647	TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTCTTAATCTT	706
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
Db	707	GCTGAACCTGCTCATTTTCAGTGTCGCGGATGTCTATGAGAAGTACAAACCCAGATTGAT	766
Qy	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	767	CACATATGTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAGAAGATCCAGCAGAA	826
Qy	181	IleProGlyLeu---LysArgLysAlaAsp	189
Db	827	CTCCCTGGAATCGCCAGAAAGGAGGAGAA	856

## RESULT 64

US-09-809-391-255  
; Sequence 255, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 255  
; LENGTH: 2664  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2623)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2640)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2652)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2662)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-809-391-255

## Alignment Scores:

Pred. No.: 5,22e-65 Length: 2664  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservative: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 10 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-809-391-255 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspLeuLeuTyrLysThrGlyValValPheGlyAla	20
Db	262	CGGGTGCAGATCTGATTTCTTGGAGAGATGTGAAGAAGCTGGGTTGTCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCATCAGTGTTCTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCTGGCTCTTCTCTGTCCACATCAGCTTCAGGATCTCAAGTCCGTCATCCAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAAGTCAGAGAAGGCGCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	502	TCCTCAGAAGCTTTCATAATATACATGATGTCGTCATGTCATCAACAGGGCCCTG	561
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	562	AAACTATTATTCGTCCTCTTCTGGTAGAGATCTGGTTGACTCTCTTGAAGCTGCTCTC	621
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	622	TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTCTTAATCTT	681
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160

Db	682	GCTGAAGTCTCAATTTTCAGTGTCCGATGTCTATGAGAGATCAAGACCCAGATTGAT	741
Qy	161	HiertyxleudlyLeuAlaAhenLysSerVallyLysAspAlaMetAlaLysAlaLys	180
Db	742	CACATATGTTGGCATCCGCCGAGATCAGACCAAGTCAATTTGTTGAAAGATCCAAGCAAAA	801
Qy	181	IleProGlyLeu---LysArglyLysAlaLeu	189
Db	802	CTCCCTGGGAATGCCCAAAAAAAGGCAGAA	831
Db	65	US-09-882-171-255	
Qy	Sequence 255	Application US/09882171	
Db	Publication No.	US2003017588A1	
Qy	GENERAL INFORMATION:		
Db	APPLICANT:	Ruben et al.	
Qy	TITLE OF INVENTION:	186 Human Secreted proteins	
Db	FILE REFERENCE:	PZ002P2	
Qy	CURRENT APPLICATION NUMBER:	US/09/882,171	
Db	CURRENT FILING DATE:	2001-06-18	
Qy	PRIOR APPLICATION NUMBER:	09/809,391	
Db	PRIOR FILING DATE:	2001-03-16	
Qy	PRIOR APPLICATION NUMBER:	09/149,476	
Db	PRIOR FILING DATE:	1998-09-08	
Qy	PRIOR APPLICATION NUMBER:	PCT/US98/04493	
Db	PRIOR FILING DATE:	1998-03-06	
Qy	PRIOR APPLICATION NUMBER:	60/040,162	
Db	PRIOR FILING DATE:	1997-03-07	
Qy	PRIOR APPLICATION NUMBER:	60/040,333	
Db	PRIOR FILING DATE:	1997-03-07	
Qy	PRIOR APPLICATION NUMBER:	60/038,621	
Db	PRIOR FILING DATE:	1997-03-07	
Qy	PRIOR APPLICATION NUMBER:	60/040,626	
Db	PRIOR FILING DATE:	1997-03-07	
Qy	PRIOR APPLICATION NUMBER:	60/040,334	
Db	PRIOR FILING DATE:	1997-03-07	
Qy	PRIOR APPLICATION NUMBER:	60/040,336	
Db	PRIOR FILING DATE:	1997-03-07	
Qy	PRIOR APPLICATION NUMBER:	60/040,163	
Db	PRIOR FILING DATE:	1997-03-07	
Qy	PRIOR APPLICATION NUMBER:	60/047,600	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,615	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,597	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,502	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,633	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,583	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,617	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,618	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,503	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,592	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,581	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,584	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,500	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,587	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,492	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,598	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,613	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,585	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,586	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,596	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,612	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,632	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/047,601	
Db	PRIOR FILING DATE:	1997-05-23	
Qy	PRIOR APPLICATION NUMBER:	60/043,580	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,568	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,314	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,569	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,311	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,671	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,674	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,669	
Db	PRIOR FILING DATE:	1997-04-11	
Qy	PRIOR APPLICATION NUMBER:	60/043,312	
Db	PRIOR FILING DATE:	1997-04-11	
Qy			

; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Alignment Scores:
Pred. No.: 5 22e-65 Length: 2664
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1

DB: 10 Gaps: 1
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-882-171-255 (1-2664)
QY 1 SerValValAspLeuLeuTyrTrpArgAspLeuLysLysThrGlyValValPheGlyAla 20
Db 262 CGGTCGACGATCTGATTTCTCGAGAGATGTGAAGAGACTGGGTTGCTTTGGCACC 321
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 ACGTCGATCATGCTGCTTTCCCTGCACGCTTTCACTGTGTCAGTGTGGTCTTCACTACCTC 381
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 382 ATCTGGGCTCTCTCTGTCCATCATCAGTTCAGGATCTACAACTCCGTCATCCAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 442 GTACAGAAGTCAGAAGAGGCGCATCCATTCAAAGCTTACCTGACGTAGACATTACTCTG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 502 TCCTCAGAAGCTTCCATAATTACATGAATGCTGCCATGTCGACATCAACAGGCGCCCTG 561
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 562 AAACCTATTATTCGTCCTCTTCTGTGAGAAGATCTGGTTGACTCTCTTGAGCTGGCTGTC 621
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 622 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCTTCTAATTCTT 681
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 682 GCTGAACGTGCTCACTTTTCAGTGTCCGATGTCATGAGAAGTACAGACCCAGATTGAT 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 742 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 802 CTCCTCGAATCGCAAAAAGGCGAGAA 831
RESULT 66
US-10-184-861-255
; Sequence 255, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 255
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2623)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2640)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:

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; NAME/KEY: SITE
; LOCATION: (2652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2662)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-255

Alignment Scores:
Pred. No.: 5,22e-65 Length: 2664
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 17 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-164-861-255 (1-2664)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysGlyThrGlyValValPheGlyAla 20
Db 262 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAGAGAGACTGGGTTTCTTTGGCACC 321
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 ACCTCATGATCTGCTCTCCCTGGCAGCTTTCCAGTGTCTATCAGTGTGTTCTTACCTC 381
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 382 ATCTCGCTCTCTCTCTCCATCAGCTTCCAGGATCTACAGTCCGTCATCCAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuLeuGluSerGluValAlaIle 80
Db 442 GTACAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 502 TCTCAGAGAGCTTCCATTAATACATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuVal 120
Db 562 AAATCATATTCTGCTCTCTCTGTTAGAGAGATCTGTTGACTCTCTTGAAGCTGGCTGC 621
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeu 140
Db 622 TTCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 682 GCTGAAGCTGCTCATTTTCTAGTGTCCCGATGCTATGAGAGAGATGAGAGAGAGAGAG 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 742 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAGAGATCCAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 802 CTCCTCGGAATCGCCAAAAAAGGAGAGAA 831

RESULT 67
US-10-723-860-6867
; Sequence 6867, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739

; NAME/KEY: SITE
; LOCATION: (2652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2743) (2747)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6867

Alignment Scores:
Pred. No.: 5,54e-65 Length: 2768
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 20 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-723-860-6867 (1-2768)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysGlyThrGlyValValPheGlyAla 20
Db 320 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAGAGAGACTGGGTTTCTTTGGCACC 379
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 380 ACCTCATGATCTGCTCTCCCTGGCAGCTTTCCAGTGTCTATCAGTGTGTTCTTACCTC 439
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 440 ATCTCGCTCTCTCTCTCTCCATCAGCTTCCAGGATCTACAGTCCGTCATCCAGCT 499
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 500 GTACAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 559
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 560 TCTCAGAGAGCTTCCATTAATACATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 619
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuVal 120
Db 620 AAATCATATTCTGCTCTCTCTGTTAGAGAGATCTGTTGACTCTCTTGAAGCTGGCTGC 679
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeu 140
Db 680 TTCTATGCTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 739
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 740 GCTGAAGCTGCTCATTTTCTAGTGTCCCGATGCTATGAGAGAGATGAGAGAGAGAGAG 799
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 800 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAGAGATCCAGCAAAA 859
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 860 CTCCTCGGAATCGCCAAAAAAGGAGAGAA 889

RESULT 68
US-10-108-260A-449
; Sequence 449, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
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; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 449  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-449

Alignment Scores:  
Pred. No.: 3 47e-64 Length: 3637  
Score: 617.50 Matches: 113  
Percent Similarity: 80.53% Conservative: 40  
Best Local Similarity: 59.47% Mismatches: 36  
Query Match: 66.76% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-108-260A-449 (1-3637)

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Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 1379 TCAGTGCAGCATCTGATTTCTGGAGAGATGGAAGAGACTGGGTTGTCTTTGGCACC 1438
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 1439 ACGCTGATCATCTGCTTTCCCTGCGCAGCTTTTCAGTGTCTCATCAGTGTGTTCTTACCTC 1498
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 1499 ATCTGGCTCTTCTCTGTCAACCATCAGCTTCAGGATCTACAGTCCGTCTATCAAGCT 1558
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 1559 GTACAGAAGTCAGAGAAGGCCATTCATTCAAAGCTTACCTGGAGCTAGACATTACTCTG 1618
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 1619 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCATGTCATCAACAGAGGCCCTG 1678
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 1679 AAATCATATTTCGTCTCTTCTGTAGAAGATCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 1739 TTCAATGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCCTCTTAATCTT 1798
Qy 141 AlaLeuLysLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTTGCTATGAGAAGTACAAGACCAGATTGAT 1858
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysValIleGlnAlaLys 180
Db 1859 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCAAGCAAAA 1918
Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 1919 CTCCTGGATCGCCCAAAAAAGGACAGAA 1948
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## RESULT 69

US-10-159-563-443  
; Sequence 443, Application US/10159563  
; Publication No. US20040009154A1

## GENERAL INFORMATION:

; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159,563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133,937

; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 443  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-443

Alignment Scores:  
Pred. No.: 3 47e-64 Length: 3637  
Score: 617.50 Matches: 113  
Percent Similarity: 80.53% Conservative: 40  
Best Local Similarity: 59.47% Mismatches: 36  
Query Match: 66.76% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-159-563-443 (1-3637)

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Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 1379 TCAGTGCAGCATCTGATTTCTGGAGAGATGGAAGAGACTGGGTTGTCTTTGGCACC 1438
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 1439 ACGCTGATCATCTGCTTTCCCTGCGCAGCTTTTCAGTGTCTCATCAGTGTGTTCTTACCTC 1498
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 1499 ATCTGGCTCTTCTCTGTCAACCATCAGCTTCAGGATCTACAGTCCGTCTATCAAGCT 1558
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 1559 GTACAGAAGTCAGAGAAGGCCATTCATTCAAAGCTTACCTGGAGCTAGACATTACTCTG 1618
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 1619 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCATGTCATCAACAGAGGCCCTG 1678
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 1679 AAATCATATTTCGTCTCTTCTGTAGAAGATCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 1739 TTCAATGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCCTCTTAATCTT 1798
Qy 141 AlaLeuLysLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTTGCTATGAGAAGTACAAGACCAGATTGAT 1858
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysValIleGlnAlaLys 180
Db 1859 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCAAGCAAAA 1918
Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 1919 CTCCTGGATCGCCCAAAAAAGGACAGAA 1948
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## RESULT 70

US-09-823-245A-510  
; Sequence 510, Application US/09823245A  
; Publication No. US20020039760A1

## GENERAL INFORMATION:

; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakari  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.

```
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 510
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-510

Alignment Scores:
Pred. No.: 4,87e-62 Length: 1636
Score: 595.50 Matches: 112
Percent Similarity: 80.53% Conservative: 41
Best Local Similarity: 58.95% Mismatches: 36
Query Match: 64.38% Indels: 2
DB: Gaps: 9

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-823-245A-510 (1-1636)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 248 GCGGTGCAGATCTGATTTCTGGAGAGATGGAAGAGACTGGGTGCTTTGGCACC 307
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 308 ACGTGCATCATGCTGCTTC-CTGGCAGCTTTCAGTGCATCATGCTGGTTCCTTACCTC 366
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
Db 367 ATCTTGGCTCTTCTCTGTCACCATCAGCTTCAGGATCTCAAGTCCGTCATCCAAAGCT 426
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 427 GTACAGAGTCAGAGAGAGGCCATCCATTCAAAGCCTTACTGGACGTAGACATTACTCTG 486
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 487 TCTCAGAGCTTCTCCATAATATACATGAATGCTGCCATGTGCACATCAACAGGGCCCTG 546
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaVal 120
Db 547 AAACATCATATTCTGCTCTCTCTGTGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGC 606
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 607 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAAGGATACCCCTTCTAATCTT 666
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 667 GCTGAACCTGCTCATTTTCACTGTCGCCGATGCTATGAGAAGTACAAAGCCAGATTGAT 726
QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 727 CACTATGTTGGCATCCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAAGCAAAA 786
QY 181 IleProGluLeu--LysArgLysAlaAsp 189
Db 787 CTCCTTGGATCCGCAAAAAGGCGAGAA 816

RESULT 71
US-09-960-352-5154
; Sequence 5154, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9092
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 2.84e-57 Length: 423
Score: 549.00 Matches: 110
Percent Similarity: 98.28% Conservative: 4
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5154
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-043-Q1-E1-F5
US-09-960-352-5154

Alignment Scores:
Pred. No.: 4.83e-59 Length: 389
Score: 563.00 Matches: 116
Percent Similarity: 99.15% Conservative: 1
Best Local Similarity: 98.31% Mismatches: 1
Query Match: 60.86% Indels: 0
DB: Gaps: 9

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-960-352-5154 (1-389)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 34 GTTGTGTACCTCTCTACTGGAGACACATTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 93
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 94 TTGTTCTCTGCTCTCTGCTGACATTAATCAGCATTTGAGTGTAAACGGCCTACATTCGC 153
QY 42 IleAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 154 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 213
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 214 CAGAAATCTGATGAAGGCCACCCATTCAGGCATATTTGGAATCTGAAGTTCGTATCT 273
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 274 GAGGAGTTGGTTTCAGAAAGTACAGCAATTCCTCTCTTGGTCACTGTTAACTGCACAATAAAA 333
QY 102 GluLeuArgGlnLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAla 119
Db 334 GAACCTCAGACGCTCTCTTCTAGTATGATTTAGTGTATCTCTGAAGTTTGCA 387

RESULT 72
US-09-960-352-9092
; Sequence 9092, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9092
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 2.84e-57 Length: 423
Score: 549.00 Matches: 110
Percent Similarity: 98.28% Conservative: 4
```

Best Local Similarity: 94.83%  
 Query Match: 59.35%  
 DB: 9

Mismatches: 2  
 Indels: 0  
 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-960-352-9092 (1-423)

Qy 74 LeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu 93  
 Db 3 TTGGAATCTGAAGTTGCTATATCTGATGAGTTGGTTTCAAGAGTACAGCAATTCGTCTT 62  
 Qy 94 GlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspLeuVal 113  
 Db 63 GGTGATGTTAACTGCACAAATAAAGAACTCAGACGCCCTTCTTGTAGTTGATGATTTAGTT 122  
 Qy 114 AspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeuPheAsn 133  
 Db 123 GATTCCTGAAGTTTGCAGTTGTGATGTTGGTATTACTATGTTGGTCTTGTTCAT 182  
 Qy 134 GlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSerIleProValIleTyrGlu 153  
 Db 183 GGTCTGACACTACTAAATTTGGCTGCTGATTTCACTCTTCAGTGTTCCTGTTATTATGAA 242  
 Qy 154 ArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173  
 Db 243 CGGCATCAGGCGCAATAATAGATCATTTATCTGGGACTTGCANAATAAGAAATGTTAAAGATGCT 302  
 Qy 174 MetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189  
 Db 303 ATGCTAATAATCCAAAGCAAAATCCCTGATGTAAGCGTTAAAGCTGAA 350

## RESULT 73

US-10-302-172-111  
 ; Sequence 111, Application US/10302172  
 ; Publication No. US20040053250A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Xue, Aidong J.  
 ; APPLICANT: Drmanac, Radolje T.  
 ; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and  
 ; FILE REFERENCE: 803.1NCP  
 ; CURRENT APPLICATION NUMBER: US/10/302,172  
 ; CURRENT FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 10/225,251  
 ; PRIOR FILING DATE: 2002-08-20  
 ; PRIOR APPLICATION NUMBER: PCT US02/05095  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US 09/799,451  
 ; PRIOR FILING DATE: 2001-03-05  
 ; NUMBER OF SEQ ID NOS: 950  
 ; SOFTWARE: pt FL\_genes Version 2.0  
 ; SEQ ID NO 111  
 ; LENGTH: 3517  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (196)..(654)  
 US-10-302-172-111

Alignment Scores:  
 Pred. No.: 7,46e-55 Length: 3517  
 Score: 541.00 Matches: 102  
 Percent Similarity: 58.97% Conservative: 38  
 Best Local Similarity: 50.25% Mismatches: 35  
 Query Match: 58.49% Indels: 28  
 DB: 18 Gaps: 2

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-302-172-111 (1-3517)

Qy 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 2906 GTGCACGATCTGATTTCTGAGAGATGTGAAGAGATGGGTTGTCTTTGGCACCACG 2965

Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 2966 CTGATCATGCTGCTTTCCTGGCAGCTTTCAGTGCATCAGTGTGGTTCTTCTTCTTCTTCTC 3025  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 3026 CTGGCTCTTCTCTCTGTCACCATCAGCTTCAAGATCTCAAGATCGTTCATCCAGCTGTA 3085  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 3086 CAGAAGTCAGAGAAGGCCATCCATTCAAGGCCCTACCTGGAGCTAGACATTACTCTGTCC 3145  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 3146 TCAGAGCTTTCATATATACATGATGCTGCCATGCTGCATCATCAAGGCCCTGAAA 3205  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 3206 CTCAATTATTCCTCTCTTCTGTTAGAGATCTGGTTGACTCCTTGAAGCTGGCTGTCTTC 3265  
 Qy 122 MetTyrValPheThrTyrValGlyAlaLeuPheArgGlyLeuThrLeuIleLeuAla 141  
 Db 3266 ATGTGGCTGATGACTATGTTGGTGTCTTTTAAACCGAATCACCCCTTCTAATCTTGTCT 3325  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGln----- 156  
 Db 3326 GAATGCTCATTTTCAGTGTCCGATGCTATGATGAGAGTACAGGATGCACGTGTGCTA 3385  
 Qy 157 -----ValGlnIle----- 159  
 Db 3386 GCGCTGAGCAGGCAAGAGTCCACACTGAAGTATCAGAGAAGCTCCAGGGCAAAAGCAA 3445  
 Qy 160 -----AspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173  
 Db 3446 GAGCACCAGCACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3505  
 Qy 174 MetAlaLys 176  
 Db 3506 GTTCAAAAG 3514

RESULT 74  
 US-10-660-946-4  
 ; Sequence 4, Application US/10660946  
 ; Publication No. US2004006313A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; Au-Young, Janice  
 ; Goli, Surya K.  
 ; Hillman, Jennifer L.  
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/660,946  
 ; FILING DATE: 12-Sep-2003  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/228,213A  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: 08/700,607  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:

```
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: TBPINOBO1
; CLONE: 31870
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-660-946-4
Alignment Scores:
Pred. No.: 1.25e-53 Length: 1095
Score: 524.50 Matches: 102
Percent Similarity: 72.7% Conservative: 37
Best Local Similarity: 53.4% Mismatches: 30
Query Match: 56.7% Indels: 22
DB: 18 Gaps: 2
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-660-946-4 (1-1095)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 329 GCGGTGACGATCTGATTTTGGAGAGATGGAAGAGACTGGGTGTCTTTGGCACC 388
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 389 AGCGTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTGATCATGTTGGTTCCTACCTC 448
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 449 ATCTGGCTGCTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCGCTCATCCAAGCT 508
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 509 GTACAGAACTGAGAGAGCGCCATTCATCAAGCTCTACCTGGAGTAGACATTACTCTG 568
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 569 TCTCAGAGCTTTCATTAATACATGATGTCGTCATGTCACATCAACAGGCGCTG 628
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 629 AAACATCATTTTCGTCCTCTGTTGAGAGATCTGTTGACTCTCTTGAAGCTGGCTGC 688
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 689 TTTCATGTGCTGATGACCTATGTTGCTGTGTTTACGGAATCACCCCTCTAATTCCT 748
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 749 GCTGAACTGCTCATTTTNAAGTCTCCGATGTTGTTATNAGAAAGTAC----- 793
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 794 -----AAGGTTCCAAAGCAA 808
QY 180 stleProGlyLeu---LysArgLysAlaAsp 189
DB 809 ACTCCCTGGAATCGCCCAAAAAAAGGCAGAA 839
RESULT 75
US-10-267-502-211
; Sequence 211, Application US/10267502
; Publication No. US20040071700A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 211
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-267-502-211
Alignment Scores:
Pred. No.: 2.05e-53 Length: 669
Score: 520.00 Matches: 94
Percent Similarity: 74.5% Conservative: 41
Best Local Similarity: 51.9% Mismatches: 46
Query Match: 56.2% Indels: 0
DB: 18 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-267-502-211 (1-669)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 76 GTGGAATCCCTTATCTACTGCGCGCATGTGAAGAAATCCGGCATTTGCTTCGGCGCTGC 135
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 136 CTGATCACACTGGCGCGCATCTCCAGCTTCTCGGTGATCAGCGTGTTCGCCTTACTTGTG 195
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 196 CTCCTAACCTCTTTCGGCACCGCTCGCTTCAGAACTTCAAAATCTGTGACACAGCCGCTG 255
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 256 CAAAGACAAAGAGAGGCTCACCCCTTTAAGGATTACCTGGAGCTGGATCTGACGCTGTG 315
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 316 CACGAAAGGTACAGAACATTCGCCGCGTGGCTGTGGACATATCATGGCTTCACTCC 375
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 376 GAGCTGAGCGCTCTGTTCTTGTGAGGATATCATCGATTGATCAAGTTCCGCTCAT 435
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 436 CTGTGGTCTTCCACTAGCTGGTGGCTGGTTCAATGGCATGACTCTGTGTCATCTTGGCC 495
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 496 TTTGCTCGCTGTTTACCTTGCCCAAGGTCTACAGAGAACACACGAATCGATCGACACT 555
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 556 CACTTGGATCTGGTGGCAGCAAAATTGACAGAAATCACCGACAAGATCCGAGTGGCCATC 615
QY 182 Pro 182
DB 616 CCC 618
RESULT 76
US-09-809-391-102
; Sequence 102, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
```



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; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-102

Alignment Scores:
Pred. No.: 5,15e-52 Length: 794
Score: 509.50 Matches: 101
Percent Similarity: 76.3% Conservative: 38
Best Local Similarity: 55.4% Mismatches: 41
Query Match: 55.0% Indels: 3
DB: 10 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-809-391-102 (1-794)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyVala 20
Db 254 GCGGTGCACGATCTATTTCCTGGAGAGATGGAAGAGACTGGGTTGTCTTTGGAC-- 311
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIl 40
Db 312 ACGTGATCATGCTGCTTCCCTGCGACGCTTCAGTGTTCATGCTGGGTTCTTAMCT 371
Qy 40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60
Db 372 CATCTGGCTCTTCTCTCTGTCCACCATCATCTTCAGGATCTACAAGTCCGTCATCCAAGC 431
Qy 60 alLeGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuCluSerGluValAlaI 80
Db 432 TGTWAGAAATCAGAAAGGCCATCCCAATCCAAAGCCTACCTGGACGATGACATTATCTC 491
Qy 80 LeSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI 100
Db 492 TGTCTCTCAGAGCTTCCATAATTACATGATGCTGCCATGTCACATCAACAGGGCCC 551
Qy 100 LeLysGluLeuArgLeuPheLeuValAlaAspLeuValAspSerLeuLysPheAlav 120
Db 552 TGAAGACTCATTTATTCCTCTCTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTG 611
Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL 140
Db 612 TCTTCATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAATCACCCCTTCTAATTC 671
Qy 140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160
Db 672 TTGCTGAAGTCTCATTTTCAGTGTCCCGATGCTGTATGAGAGTACAGACCCAGATTG 731
Qy 160 pHisTyrLeuGlyLeuAlaLeuAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180
Db 732 ATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTTGAAGATGCCAAGCA 791
Qy 180 ys 180
Db 792 AA 793

RESULT 77
US-09-882-171-102
; Sequence 102, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
```

Qy	1	SerValValAspLeuLeu	YrrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	254	CGCGTGCAGATCTGATTTCTTGGAGAGATGTGAAGAACACTGGGTTCCTCTTTGGAC--	311	
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle	40	
Db	312	ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTTCATCATCTGGGGTTCTCTTAMCT	371	
Qy	40	eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl	60	
Db	372	CATCTGGCTCTTCTCTGTGCACCATCACTTCAGATCTCAAGTCGCTCATCCAGC	431	
Qy	60	alleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrIleuGluSerGluValAlaI	80	
Db	432	TGTTWCAGAAARTCAGAAAGAAGCCATCCAAWTCCAAAGCCCTACTCGGACGTAGACATTACTC	491	
Qy	80	leSerGluGluLeuValGlnLysTyrIserArgAsnSerAlaLeuGlyHisValAsnSerThrI	100	

Db 492 TGTCCTCAGAGCTTCCATGAATATACATGAATGCTGCCATGCTGCACATCAACAGGGCCC 551  
Qy 100 leYsGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaV 120  
Db 552 TGAACACTATATTCGCTCTCTTCTGGTAGAGATCTGGTGACTCCTTGAAGCTGGCTG 611  
Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeL 140  
Db 612 TCTTCATGTGGCTGATGACCTATGTGGTGTCTTTTAAACGGAATCACCCCTTCTAAATTC 671  
Qy 140 euAlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160  
Db 672 TTGCTGAACCTGCTCATTTTTCAGTGTCCGATTTCTATGAGAAGTACAAAGACCCAGATTG 731  
Qy 160 spHisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180  
Db 732 ATCACTATGTGGCATCGCCCGAGATCAGACCAGTCAATTGTTGAAAAGATCCCAAGCA 791  
Qy 180 Ys 180  
Db 792 AA 793  
RESULT 78  
US-10-164-861-102  
; Sequence 102, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002PI  
; CURRENT APPLICATION NUMBER: US/10/164,861  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 794  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-164-861-102

Alignment Scores:  
Pred. No.: 5,15e-52 Length: 794  
Score: 509.50 Matches: 101  
Percent Similarity: 76.37% Conservative: 38  
Best Local Similarity: 55.49% Mismatches: 41  
Query Match: 55.08% Indels: 3  
DB: 17 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-164-861-102 (1-794)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 254 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTGTCTTGGAC-- 311  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrI 40  
Db 312 ACGCTGATCATCTGCTTTCCCTGGCAGCTTTCAGTGTTCATCATGTGGGTTCCTTAMCT 371  
Qy 40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
Db 372 CATCTGGCTCTTCTCTGTGCACCATCARCTTCAGGATCTACAAAGTCCGTCATCCCAAGC 431  
Qy 60 alLeuGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80  
Db 432 TGTWCAGAAATCAGAAAGGCCATCCATTCAAAGCCTACTCGACCTAGACATTACTC 491  
Qy 80 leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI 100  
Db 492 TGTCTCAGAGCTTTCATGAATATACATGAATGCTGCCATGCTGCACATCAACAGGGCCC 551

Qy 100 leYsGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaV 120  
Db 552 TGAACACTATATTCGCTCTCTTCTGGTAGAGATCTGGTGACTCCTTGAAGCTGGCTG 611  
Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeL 140  
Db 612 TCTTCATGTGGCTGATGACCTATGTGGTGTCTTTTAAACGGAATCACCCCTTCTAAATTC 671  
Qy 140 euAlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160  
Db 672 TTGCTGAACCTGCTCATTTTTCAGTGTCCGATTTCTATGAGAAGTACAAAGACCCAGATTG 731  
Qy 160 spHisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180  
Db 732 ATCACTATGTGGCATCGCCCGAGATCAGACCAGTCAATTGTTGAAAAGATCCCAAGCA 791  
Qy 180 Ys 180  
Db 792 AA 793  
RESULT 79  
US-10-424-599-57998  
; Sequence 57998, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 57998  
; LENGTH: 878  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_23384C.1  
US-10-424-599-57998

Alignment Scores:  
Pred. No.: 1.06e-51 Length: 878  
Score: 507.50 Matches: 95  
Percent Similarity: 75.00% Conservative: 46  
Best Local Similarity: 50.53% Mismatches: 46  
Query Match: 54.86% Indels: 1  
DB: 18 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-424-599-57998 (1-878)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 152 GTGGAGAGCCTGATCTACTGCGCGGATTCCAAGAAATCCGCTCCAGTGTTCGGAGGACTA 211  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 212 CTCGTGCTTCTACTCGCTTACATATTTCTCTAATCAGTGTGTAGCTTACGTTTCA 271  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 272 CTCATACCCCTGGCATAACTTTTAGCGTTTGAAGATTTACAAAGTATTTGTACAAAGCAGTT 331  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 332 CAAAAGACTGGGATGGACATCCATTCAGAAATATCTGGAACTCGATGTCTCTACCC 391  
Qy 82 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 392 CAAGAAAAGTTAAACAAATCACAGAAAGTGGCGCTTGCACACATCAATGCCGCTATTGTG 451



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US-09-830-972-2_COPY_975_1163 (1-189) x US-10-264-237-163 (1-668)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db GTTGTGGACCTCTCTGCTACTGAGACATTAAGAGACTGGAGTGTGTGGTGCCAGC 307
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db CTTATCTCTGCTCTTTCATTGACAGTATTGACAGTATTGAGCGTAACAGCCTACATTGCC 367
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db TTGGCCCTGCTCTCTGTCACCATCATCTTATAGGATATACAAAGGGTGTGATCCAGCTATC 427
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db CAGAAATCAGATGAGAGCCACCATTCAGGCGATATCTGGAATCTGGAATGCTATATCT 487
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db GAGGAGTGTGTTTCAGAACTACAGTAATCTGCTCTTGTGTCATGTGACCTGCACGATTAAG 547
Qy 102 -GluLeuArgArgLeuPheLeu 108
Db GAAACTCAGGCGCCTCTTNCCT 569
RESULT 82
US-10-491-213-80
; Sequence 80, Application US/10491213
; Publication No. US20050048490A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; BECHA, Shaoya D.;
; APPLICANT: BOROWSKY, Mark L.; CHAWLA, Nainder K.;
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.;
; APPLICANT: GANDHI, Ameena R.; GRIFFIN, Kimberly J.;
; APPLICANT: GORVAD, Ann E.; GRIFFIN, Jennifer A.;
; APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
; APPLICANT: KABLE, Amy E.; KALAFUS, Daniel P.;
; APPLICANT: LEHR-MASON, Patricia M.; LU, Dying Aina M.;
; APPLICANT: MARQUIS, Joseph P.; NGUYEN, Damiel B.;
; APPLICANT: RAMKUMAR, Jayalaxmi; RICHARDSON, Thomas W.;
; APPLICANT: KAREHT, Stephanie K.; SWARNAKAR, Anita;
; APPLICANT: TANG, Y. Tom; TRAN, Uyen K.;
; APPLICANT: WARREN, Bridget A.; XU, Yuming;
; APPLICANT: YAO, Monique G.; YUE, Huibin;
; APPLICANT: YUE, Henry
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: PF-1213 USN
; CURRENT APPLICATION NUMBER: US/10/491,213
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: PCT/US02/31095
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,389
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/327,380
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/328,186
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/329,690
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/345,384
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/348,165
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/350,219
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/344,518
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/345,143
; PRIOR FILING DATE: 2001-11-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
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; SOFTWARE: PERL Program
; SEQ ID NO 80
; LENGTH: 2017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7503970CB1
US-10-491-213-80
Alignment Scores:
Pred. No.: 3,68e-47 Length: 2017
Score: 475.00 Matches: 92
Percent Similarity: 70.33% Conservative: 36
Best Local Similarity: 50.55% Mismatches: 54
Query Match: 51.35% Indels: 0
Dbs: 21 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-491-213-80 (1-2017)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db GTGGCGGACCTCTGCTACTGGAAGGACAGCAGGAGCGTCAAGAGTGTCTTCACAGGCGCTG 1013
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db ATGGTCTCTCTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1073
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db CTGTTGTGCTCTCTGCGGACCATCTCTCTCAGGGTTTACCGCAAGTGTCTGCGGCGCTG 1133
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db CACCGGGGGATGAGCAACCCCTTTCAGGCGCTACCTGGATGAGGACCTCACCTGACT 1193
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db CGGGAGCAGACGGAACCTTGTCTCCACCATCATCTCCCGCTGGTCTCGGCGGCCAGC 1253
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuValPheAlaVal 121
Db CAGCTGCGGCACTTCTTCTGTTAGTAAAGACCTCTGTTGATTCCTCAAGTGTGCGCTCTC 1313
Qy 122 MetTrpValPheThrTyrValGlyValAlaLeuPheArgGlyLeuThrLeuLeuAla 141
Db TTCTACATCTGACCTTCGTGGTGGCCATCTTCATATGTTGACTCTTCTCATTTCTGGGA 1373
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db GTGATTGCTTATTACCATCTCCCTGCTGTACCGGAGCAGCAGGCTCAGATCGACCAA 1433
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db TATGTGGGTGTTGTGACCAATCAGTTGAGCCACATCAAGCTAAGTCCGAGCTAAATC 1493
Qy 182 ProGly 183
Db 1494 CCAGGG 1499
RESULT 83
US-10-723-860-3043
; Sequence 3043, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
```

; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3043  
; LENGTH: 2190  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-3043

Alignment Scores:  
Pred. No.: 4 18e-47 Length: 2190  
Score: 475.00 Matches: 92  
Percent Similarity: 70.33% Conservative: 36  
Best Local Similarity: 50.55% Mismatches: 54  
Query Match: 51.35% Indels: 0  
DB: 20 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-723-860-3043 (1-2190)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 1162 GTGGCGGACCTGCTGCTACTGGAAGACACGAGGACGTCAGGAGTGGTCTTACAGGCGCTG 1221  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 1222 ATGGTCTCCCTCCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 1282 CTGTGCT 1341  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 1342 CACCGGGGGGATGGAGCCAAACCTTTCCAGGCTACCTGGATGTGGACCTCACCTCTGACT 1401  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1402 CGGGAGCAGACGGAACGTTTGTCCACACAGATCACCTCCCGCTGGTCTCGGGCGGCACG 1461  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1462 CAGCTGCGGCACCTTCTCTGTTAGAGACCTCTGTTGATTCCTCAAGTGGCCCTCTCT 1521  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 1522 TTCTACATCTTGACCTTCGTTGGTGGCATCTTCAATGTTTGAATCTTCTCAATCTCTGGA 1581  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 1582 GTGATTGGTCTATTACCATCCCTGCTGTTACCGGACGACGACGAGCTCAGATCGACCAA 1641  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1642 TATGTGGGGTGGTGACCAATCAGTTGAGCCACATCAAGCTAAGATCCGAGCTAAATC 1701  
QY 182 ProGly 183  
DB 1702 CCAGGG 1707

## RESULT 84

US-10-723-860-7073  
; Sequence 7073, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Gineburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7073  
; LENGTH: 3044  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-7073

Alignment Scores:  
Pred. No.: 7e-47 Length: 3044  
Score: 475.00 Matches: 92  
Percent Similarity: 70.33% Conservative: 36  
Best Local Similarity: 50.55% Mismatches: 54  
Query Match: 51.35% Indels: 0  
DB: 20 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-723-860-7073 (1-3044)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 872 GTGGCGGACCTGCTGCTACTGGAAGACACGAGGACGTCAGGAGTGGTCTTACAGGCGCTG 931  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 932 ATGGTCTCCCTCCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 992 CTGTGCT 1051  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 1052 CACCGGGGGGATGGAGCCAAACCTTTCCAGGCTACCTGGATGTGGACCTCACCTCTGACT 1111  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1112 CGGGAGCAGACGGAACGTTTGTCCACACAGATCACCTCCCGCTGGTCTCGGGCGGCACG 1171  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1172 CAGCTGCGGCACCTTCTCTGTTAGAGACCTCTGTTGATTCCTCAAGTGGCCCTCTCT 1231  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 1232 TTCTACATCTTGACCTTCGTTGGTGGCATCTTCAATGTTTGAATCTTCTCAATCTCTGGA 1291  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 1292 GTGATTGGTCTATTACCATCCCTGCTGTTACCGGACGACGACGAGCTCAGATCGACCAA 1351  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1352 TATGTGGGGTGGTGACCAATCAGTTGAGCCACATCAAGCTAAGATCCGAGCTAAATC 1411  
QY 182 ProGly 183  
DB 1412 CCAGGG 1417

## RESULT 85

US-10-424-599-51318  
; Sequence 51318, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599

;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 285684  
;; SEQ ID NO 51318  
;; LENGTH: 613  
;; TYPE: DNA  
;; ORGANISM: Glycine max  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_17354C.1  
US-10-424-599-51318

Alignment Scores:  
Pred. No.: 1.75e-47 Length: 613  
Score: 471.00 Matches: 83  
Percent Similarity: 73.65% Conservative: 40  
Best Local Similarity: 49.70% Mismatches: 44  
Query Match: 50.92% Indels: 0  
DB: 18 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-424-599-51318 (1-613)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 110 AACGCTGCTGAGCTGCTACTGCGTGACGTAAGAACTCGGCGATGTCTTTGGCAGT 169  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLyrile 40  
Db 170 GGCCTGGTCACTCTCTCACTCTCCATCTTCTCGGTCACTCTCTGTGGTGCATACA 229  
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleLysGlyValIleGlnla 60  
Db 230 CTTCTCTTTACCTCTTGGGACACTTCTTCCGCAATTTACAAGAAATGTCATGAAGCC 289  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaLysLeuGluSerGluValAlaIle 80  
Db 290 GTTCATAGACGATGACGATCATTCATCAAGAGTACCTTGAATCGAATTCCTCCA 349  
Qy 81 SerGluGluLeuValGlnLysTyrSerAenSeraLaLeuGlyHisValAasnSerThrile 100  
Db 350 CCACAGGAACGAATTCATGAATAGTCGATTTCAGTTGTTGTCACGGTACCTGCTTCATT 409  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 410 AACCGAATGCGAAGTGTCTTCTGCTGAGGACATTTGCGATTCTCACTGAAGTACCTTCTT 469  
Qy 121 LeuMetTrpValPheThrTrpValGlyValAlaLeuPheAenGlyLeuThrLeuLeuLeu 140  
Db 470 ATCTTCTGGCTCTCACCTACATTCAGGCTGTTCAATGGCATGACCTTAATCTTTTG 529  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 530 GCCTACCTTGGTGCACTTCTCGCTTCCCAAGGTTTACGAGCTAAACAAGGTTTCAGATTGAC 589  
Qy 161 HisTyrLeuGlyLeuAlaAasn 167  
Db 590 CAGTACCTGGATCTGGCAAC 610

RESULT 86

US-10-242-535A-17576  
; Sequence 17576, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12

;; PRIOR APPLICATION NUMBER: US 60/271,955  
;; NUMBER OF SEQ ID NOS: 58994  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 17576  
;; LENGTH: 566  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-242-535A-17576

Alignment Scores:  
Pred. No.: 6.33e-47 Length: 566  
Score: 466.00 Matches: 97  
Percent Similarity: 97.12% Conservative: 4  
Best Local Similarity: 93.27% Mismatches: 3  
Query Match: 50.38% Indels: 1  
DB: 17 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-242-535A-17576 (1-566)

Qy 86 GlnLysTyrSerAenSerAlaLeuGlyHisValAasnSerThrIleLysGluLeuArgArg 105  
Db 1 CAGAAGCACATTAATCTGCTCTTGG-CATGTGAACCTCACGATTAAGAACTCAGGCGC 59  
Qy 106 LeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 60 CTCCTCTTAGTTGATGATTGATTCTCTGAAGTTTGCAGTATTGATGTGGGTATTT 119  
Qy 126 ThrTyrValGlyAlaLeuPheAasnGlyLeuThrLeuLeuLeuLeuLeuLeuLeu 145  
Db 120 ACCTATGTGTGCTGCTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTTCACTC 179  
Qy 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165  
Db 180 TTCAGTGTCTCTGTTTATTAAGCGCATCAGGCACAGATAGATCATTTTCTAGACTT 239  
Qy 166 AlaAasnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 240 GCAATAAGATGTTTAAAGATGCTATGCTTAAATCCAAGCAAAATCCCTGGATTGAAG 299  
Qy 186 ArgLysAlaAsp 189  
Db 300 CGCAAGCTGAA 311

RESULT 87

US-10-085-783A-17576  
; Sequence 17576, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17576  
; LENGTH: 566  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-17576  
Alignment Scores:  
Pred. No.: 6.33e-47 Length: 566  
Score: 466.00 Matches: 97  
Percent Similarity: 97.12% Conservative: 4

Best Local Similarity: 93.27% Mismatches: 3  
Query Match: 50.38% Indels: 1  
DB: 18 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-085-783A-17576 (1-566)

QY 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArg 105  
DB 1 CAGAAGCACAGTAATCTCTCTTGG-CATGTGAACCTGCACGATAAAGGAACCTCAGGCGC 59  
QY 106 LeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
DB 60 CTCCTCTTAGTGAATGATTAGTTGATCTCTGAAGTTTGCAGATTGATGTTGGTATTT 119  
QY 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeu 145  
DB 120 ACTATGTTGGTGGCTTGTATTAATGCTGACACTACTGATTTGGCTCTCAATTCACATC 179  
QY 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165  
DB 180 TTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACATAGATCATTTATCAGGACTT 239  
QY 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
DB 240 GCANATGAAGTGTAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAG 299  
QY 186 ArgLysAlaAsp 189  
DB 300 CGCAAGCTGAA 311

## RESULT 88

US-09-960-352-2205  
; Sequence 2205, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21 (10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 2205  
; LENGTH: 431  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (309)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 10-LIB3058-011-Q1-K1-C5  
US-09-960-352-2205

Alignment Scores:  
Pred. No.: 1.83e-42 Length: 431  
Score: 428.00 Matches: 89  
Percent Similarity: 98.89% Conservative: 0  
Best Local Similarity: 98.89% Mismatches: 1  
Query Match: 46.27% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-960-352-2205 (1-431)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrClyValValPheGlyAlaSer 21  
DB 161 GTTGTTGACCTCTCTACTGGAGAGACATTAAAGAACCTGGAGTGTGTGGTGGCAGC 220  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaVal 41  
DB 221 TTGTTCTGCTCTCGCTGACAGTATTTCAGCATTTGAGTGTAAAGCGCTACATTGCC 280

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 281 TTGGCCCTGCTCTCTGTGACTATCAGCTNTAGGATATATAAGGGTGTGTATCCAGGCTATC 340  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 341 CAGAAATCTGATGAAGGCCACCCATTCAAGGCATATTTGGAATCTGAAGTGTCTATATCT 400  
QY 82 GluGluLeuValGlnLysTyrSerAsnSer 91  
DB 401 GAGGAGTTGGTTCAGAGTACAGCAATCT 430

## RESULT 89

US-10-052-283-137  
; Sequence 137, Application US/10052283  
; Publication No. US20030064379A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND METHOD OF USE THEREOF  
; FILE REFERENCE: P2751R1C1  
; CURRENT APPLICATION NUMBER: US/10/052,283  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: PCT/US00/20006  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US 60/145,701  
; PRIOR FILING DATE: 1999-07-26  
; NUMBER OF SEQ ID NOS: 564  
; SEQ ID NO 137  
; LENGTH: 598  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-052-283-137

Alignment Scores:  
Pred. No.: 1.43e-38 Length: 598  
Score: 398.00 Matches: 74  
Percent Similarity: 80.83% Conservative: 23  
Best Local Similarity: 61.67% Mismatches: 23  
Query Match: 43.03% Indels: 0  
DB: 14 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-052-283-137 (1-598)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 234 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGACAGCTGGTTCCTTTGGCACC 293  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 294 AGCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTCTCATCAGTGTGTTCTTACCTC 353  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 354 ATCTGGGCTCTCTCTGTCCATCAGCTTCAGATCTACAGCTCAGTCCGTCATCCAGCT 413  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 414 GTACAGAGCTCAGAAAGAGGCCATCCATTTCAAAGCCTACCTGGACGTAGACATTACTCTG 473  
QY 81 SerGluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 474 TCCTCAGAGCTTTCATAAATACATGATGTGCTGATGTGTCATGTCACATCAACAGGGCCCTG 533  
QY 101 LysGluLeuArgArgLeuLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 534 AAATCAATTATTCGTCCTCTTCTGTGAGAAGATCTGGTTGACTCTCTTGAAGCTGCTGTC 593

## RESULT 90

US-10-764-420-1065  
; Sequence 1065, Application US/10764420



Publication No. US20050084872A1

GENERAL INFORMATION:  
APPLICANT: Lum, Pek Yee  
APPLICANT: Tan, Yajun  
APPLICANT: Dai, Hongyue  
TITLE OF INVENTION: Methods For Determining Whether An Agent Possesses A Defined Biological Activity  
FILE REFERENCE: ROSA122057  
CURRENT APPLICATION NUMBER: US/10/764,420  
PRIORITY FILING DATE: 2004-01-23  
PRIORITY APPLICATION NUMBER: US 60/442,797  
PRIORITY FILING DATE: 2003-01-24  
PRIORITY APPLICATION NUMBER: US 60/474,413  
PRIORITY FILING DATE: 2003-05-30  
NUMBER OF SEQ ID NOS: 3683  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1065  
LENGTH: 682  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 267, 544, 623  
OTHER INFORMATION: n = A,T,C or G  
US-10-764-420-1065

Alignment Scores:  
Pred. No.: 6,81e-37 Length: 682  
Score: 385.00 Matches: 74  
Percent Similarity: 78.86% Conservative: 23  
Best Local Similarity: 60.16% Mismatches: 25  
Query Match: 41.62% Indels: 1  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-764-420-1065 (1-682)

Qy 1 SerValValAspLeuLeuTyrTrp-ArgAspIleLysLysThrGlyValValPheGlyVal 20  
Db 316 GCGGTGCATGATCTGATTTCTTGGCGGAGATGTGAAGAAGCTGGTGTGCTTGGCAC 375  
Qy 20 aSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIl 40  
Db 376 CACGCTGATCATGCTGCTCTCTGCGCAGCTTTTCAGTGTATTCAGTGTGCTCTTACCT 435  
Qy 40 eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
Db 436 CATCTGGCTCTACTCTCTGTCACCATCAGCTTCAGAGTCTACAGTCTGTCATCCCAAGC 495  
Qy 60 aileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaI 80  
Db 496 TGTGCAAGTCAAGAGAGGACATCCATTCAAGCCCTACCTGGATGNGACATTACACT 555  
Qy 80 eSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIl 100  
Db 556 GGCCTCAGAAGCTTCCACAGCTACATGATGTCATGTCATGTCATGTCATGTCATGTCAT 615  
Qy 100 eLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 616 CAATCTNTTATTCGTCTCTTCTGTTAGAGAGCTTGGTTCACCTCTTGAAGCTGGCTGT 675  
Qy 120 lLeuMet 122  
Db 676 CTTCAATG 682

RESULT 91

US-10-425-115-152719/c  
Sequence 152719, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 152719  
LENGTH: 745  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MFT4577\_70862C.1  
US-10-425-115-152719

Alignment Scores:  
Pred. No.: 1,31e-35 Length: 745  
Score: 375.00 Matches: 68  
Percent Similarity: 67.72% Conservative: 39  
Best Local Similarity: 43.04% Mismatches: 51  
Query Match: 40.54% Indels: 0  
DB: 20 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-425-115-152719 (1-745)

Qy 25 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44  
Db 705 TTGTTGTCGTCGCATATATGTCAGTATGAGCTAGTGTCTTCTCGCTATGTTCTATA 646  
Qy 45 LeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSer 64  
Db 645 CAATCTGGATGCAATCTTTTACGCTGTATATAAACTGCTCTACAGACAGTAAATAAACT 586  
Qy 65 AspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeu 84  
Db 585 AATGAAGTCAACCAATATCTTCAAGTGGACATCAGCTACGCTACCAAGGAAAAA 526  
Qy 85 ValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 104  
Db 525 GCTGAAGACCTGACCAAAATTAGCTGTTGTGCACATCAATGCGTATGTTGTAACCTTGT 466  
Qy 105 ArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
Db 465 CGCTTGTACTTGTGTAAGACTTGTGTTGACTCTGCCAAATCTTTTGGTATTCTCTGGGTG 406  
Qy 125 PheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAlaLeuLysSer 144  
Db 405 TTGACATATGTTGGCGCTTTGTTCAAGCGCTTACACTCATAATTTATTTGGATTATTGCT 346  
Qy 145 LeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGly 164  
Db 345 CTGTTCACTACCAAGTTTATGAGAACAACTAAGACTCAATTTGATCAAAATATTGAA 286  
Qy 165 LeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 285 GTAGTTAGAACAGATTGCTGAATTGCTAATTAAGTAAACAAAGTTCGAGCAGCTATTCCA 232

RESULT 92

US-10-050-704-93  
Sequence 93, Application US/10050704  
Publication No. US20030050442A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 62 Human Secreted Proteins  
FILE REFERENCE: P2039P1  
CURRENT APPLICATION NUMBER: US/10/050,704  
CURRENT FILING DATE: 2002-01-18  
PRIORITY APPLICATION NUMBER: 09/684,524  
PRIORITY FILING DATE: 2000-10-10  
PRIORITY APPLICATION NUMBER: PCT/US00/08979  
PRIORITY FILING DATE: 2000-04-06  
PRIORITY APPLICATION NUMBER: 60/128,693  
PRIORITY FILING DATE: 1999-04-09  
PRIORITY APPLICATION NUMBER: 60/130,991



Query Match: 37.62% Indels: 8  
DB: 9 Gaps: 2

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-880-107-3484 (1-639)

QY 2 ValValAspLeuLeuTyTTPArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 233 GTTGTGACCTCTCTGTACTGGAGACATTAGAAGACTGGAGTGGTGTGGTCCAGC 292

QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyRileAla 41  
DB 233 CTATTCTCTGCTCTCTGTGACCATTCAGCATTTGAGGTGAGGTAAACAGCTACATTGCC 352

QY 42 LeuAlaLeuLeuSerValThrPheSerPheArgLileTyLysGlyValLileGlnAlaIle 61  
DB 353 TTGGNCCTGCTCTCTGTGACCATTCAGCATTTAGGATATACAAAGGTGTGATCCAGCTATC 412

QY 62 GlnLysSer-AspGluGlyHisProPheArgAlaTyRileuGluSerGluValAlaIle-- 80  
DB 413 CAGAAATCAAGATGAAGGCCACCCATTCAGGCATATCTGGNATCTGAAGTGNTATTCT 472

QY 81 ---SerGluGluLeuValGlnLysTy-SerAsnSerAlaLeuGlyHisValAsnSerTh 99  
DB 473 TAGGAGTGGTCCANAGTCAGAAATCTGTCT-----GGGCANGTGAAGTGC-AC 519

QY 99 rileLysGlu 102  
DB 520 GATAAAGGAC 529

RESULT 95  
US-10-633-423-9  
; Sequence 9, Application US/10633423  
; Publication No. US20040191240A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; APPLICANT: Yamashita, Toshihide  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023.US900  
; CURRENT APPLICATION NUMBER: US/10/633,423  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: US 10/427,741  
; PRIOR FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-633-423-9

Alignment Scores:  
Pred. No.: 1.85e-28 Length: 60615  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.86% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-633-423-9 (1-60615)

QY 2 ValValAspLeuLeuTyTTPArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 45956 GTTGTGACCTCTCTGTACTGGAGACATTAGAAGACTGGAGTGGTGTGGTCCAGC 46015

QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyRileAla 41  
DB 46016 TTATTCTCTGCTCTCTGTGACCATTCAGCATTTGAGGTGAGGTAAACAGCTACATTGCC 46075

QY 42 LeuAlaLeuLeuSerValThrPheSerPheArgLileTyLysGlyValLileGlnAlaIle 61  
DB 46076 TTGGCCCTGCTCTCTGTGACCATTCAGCATTTAGGATATATAAGGGTGTGATCCAGCTATC 46135

QY 62 GlnLysSerAspGluGlyHisProPheArg 71  
DB 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165

RESULT 97  
US-09-918-995-5532  
; Sequence 5532, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5532  
; LENGTH: 497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature

QY 62 GlnLysSerAspGluGlyHisProPheArg 71  
DB 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165

RESULT 96  
US-10-427-741-9  
; Sequence 9, Application US/10427741  
; Publication No. US20040191291A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; APPLICANT: Yamashita, Toshihide  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023  
; CURRENT APPLICATION NUMBER: US/10/427,741  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 60615  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-427-741-9

Alignment Scores:  
Pred. No.: 1.85e-28 Length: 60615  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.86% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-427-741-9 (1-60615)

QY 2 ValValAspLeuLeuTyTTPArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 45956 GTTGTGACCTCTCTGTACTGGAGACATTAGAAGACTGGAGTGGTGTGGTCCAGC 46015

QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyRileAla 41  
DB 46016 TTATTCTCTGCTCTCTGTGACCATTCAGCATTTGAGGTGAGGTAAACAGCTACATTGCC 46075

QY 42 LeuAlaLeuLeuSerValThrPheSerPheArgLileTyLysGlyValLileGlnAlaIle 61  
DB 46076 TTGGCCCTGCTCTCTGTGACCATTCAGCATTTAGGATATATAAGGGTGTGATCCAGCTATC 46135

QY 62 GlnLysSerAspGluGlyHisProPheArg 71  
DB 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165

```
; LOCATION: (1)...(497)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5532

Alignment Scores:
Pred. No.: 3 36e-30 Length: 497
Score: 328.50 Matches: 59
Percent Similarity: 81.55% Conservatives: 25
Best Local Similarity: 57.28% Mismatches: 18
Query Match: 35.51% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-918-995-5532 (1-497)

QY 88 TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPhe 107
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 57 TACATGAATGCTGCCATGCGCACATCAACAGGTCCTGAAACTCATTATTCTCTCTT 116

QY 108 LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyr 127
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 117 CTGGTAGAAGATCTGGTTCACCTCTTGAAGCTGGCTGTCTTCATGTGGCTGATGACCTAT 176

QY 128 ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLysLeuAlaLeuLysSerLeuPhe 147
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 177 GTTGGTCTGTTTAAACGAATCACCTCTTAATCTTCTGTAACCTGCTCAITTTCACT 236

QY 148 IleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAla 167
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 237 GTCCCGATTGCTCTATGAGAAGTACAAAGACCAGATTGATCACTATGTGGCATGCCCGA 296

QY 168 LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---Lys 186
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 297 GATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAACTCCCTGGAATGCCAAAAA 356

QY 187 LysAlaAsp 189
   ::::::::::::::
Db 357 AAGGCAGAA 365

RESULT 98
US-10-101-510-401
; Sequence 401, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-401

Alignment Scores:
Pred. No.: 4 84e-30 Length: 573
Score: 328.00 Matches: 59
Percent Similarity: 79.21% Conservatives: 21
Best Local Similarity: 58.42% Mismatches: 21
Query Match: 35.46% Indels: 0
DB: 15 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-101-510-401 (1-573)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 263 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAAGACTGGTGTGTTCTTTGGCACC 322

; LOCATION: (1)...(561)
; OTHER INFORMATION: n = A,T,C or G
US-10-052-283-128

Alignment Scores:
Pred. No.: 2 54e-29 Length: 561
Score: 322.00 Matches: 64
Percent Similarity: 71.19% Conservatives: 20
Best Local Similarity: 54.24% Mismatches: 33
Query Match: 34.81% Indels: 1
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-052-283-128 (1-561)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 205 GCGGTGCAGCATNTGATTTTNTGGAGAGATGTGAAGAAGACTGGGTTGTTTGGCACC 264

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 265 AGCTGATCATGTGCTTTCCCTGGCAGCTTTTCAGTGTNATCAGTGTGGTTCTTACCTC 324

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 325 ATCTCGNTTTTCTCTCTGTCCATCAGNTTCAGATTACAGTCCGATNATCCAGCT 384

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluVal-Ala 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 385 GTACAGAAGTCAAGAAGGCCCATTCATTCAAAGCCTACCTGGANGTAGACATTAAATT 444
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QY 80 eSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI1 100  
Db 445 GTCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGTCANATCAACAGGGCCCT 504  
QY 100 eLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLys 117  
Db 505 GAAATCATATTGTTGTTNTTNTGTTAGAAGATTTGGTTGANTCCTTGAAG 556

RESULT 100  
US-09-758-140-19  
; Sequence 19, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.  
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(198)  
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene  
US-09-758-140-19

Alignment Scores:  
Pred. No.: 6.57e-30 Length: 198  
Score: 321.00 Matches: 65  
Percent Similarity: 98.48% Conservative: 0  
Best Local Similarity: 98.48% Mismatches: 1  
Query Match: 34.70% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-758-140-19 (1-198)  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
Db 1 TTTAGGATATACAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 60  
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90  
Db 61 AGGGCATATCTGGAATCTGAAGTTCATATCTGAGGAGTTGGTTTCAGAAATGACAGTAAT 120  
QY 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110  
Db 121 TCTGCTCTTGGTCATGTGAACGTGCACGATAGAGAACTCAGGCGCTCTTCTTAGTTGAT 180  
QY 111 AspLeuValAspSerLeu 116  
Db 181 GATTAGTTGATTCCTG 198

Search completed: June 19, 2005, 07:08:18  
Job time : 511.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 06:25:42 ; Search time 2558 Seconds  
(without alignments)  
2812.411 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKPKAD 189

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 190322134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q/cgn2\_1/USPTO\_spool\_p/US09830972/runat\_16062005\_153945\_19031/app\_query.fasta\_1.654  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972@cgn 1\_1\_6228 @runat\_16062005\_153945\_19031 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	779	7	CO401465
2	921	99.6	695	7	CV077130 AGENCOURT
3	921	99.6	791	7	CF977898 F26A06.04
4	913	98.7	600	9	AY404972 Mus muscu
5	913	98.7	679	4	B1149602 602848410
6	913	98.7	708	4	B1157842
7	907	98.1	794	1	AU080127
8	907	98.1	799	1	AU080133
9	904	97.7	598	7	CF118424 f8543.z1

10	904	97.7	600	9	AY404970
11	904	97.7	650	6	CB215381 NISC np05
12	904	97.7	667	7	CN429712 17006000
13	904	97.7	672	7	CK977984 4109431 B
14	904	97.7	682	6	CB162885 K-EST0223
15	904	97.7	712	7	CK971318 4087182 B
16	904	97.7	743	6	CD102817 AGENCOURT
17	904	97.7	758	4	BG697436 602660623
18	904	97.7	788	1	AL533461 602590632
19	904	97.7	843	4	BG570231 602590632
20	904	97.7	849	7	CR765672 DRFP469C
21	904	97.7	875	1	AL573494 AL573494
22	904	97.7	1540	3	CR611869 full-length
23	904	97.7	1785	3	AF077050 Homo sapi
24	903	97.6	781	4	BI079496 602876306
25	901	97.4	730	1	AU297347 AU297347
26	898	97.1	634	6	CB067821 iq38a06.y
27	898	97.1	670	7	CV030029 9024 Full
28	898	97.1	960	7	CN646472 ILLUMIGEN
29	898	97.1	983	7	CN803408 ILLUMIGEN
30	898	97.1	1031	7	CN647521 ILLUMIGEN
31	898	97.1	3533	3	AK034902 Mus muscu
32	895	96.8	990	4	BI691132 603314519
33	894	96.6	751	7	CK357937 AGENCOURT
34	893	96.5	718	1	AA986233 uc73g12.y
35	892	96.4	592	7	CN482802 hw24h12.y
36	892	96.4	805	7	CO735185 SLR04c10
37	892	96.4	958	4	BM801698 AGENCOURT
38	891	96.3	749	4	BG296048 602393712
39	891	96.3	757	4	BG715173 602675631
40	890	96.2	924	5	B0845601 AGENCOURT
41	890	96.2	1042	7	CN805577 ILLUMIGEN
42	889	96.1	871	6	CD110203 AGENCOURT
43	887	95.9	921	5	BU503291 AGENCOURT
44	885	95.7	1013	7	CO048918 ILLUMIGEN
45	885	95.7	1018	7	CN801888 ILLUMIGEN

#### ALIGNMENTS

RESULT 1  
CO401465  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CO401465 779 bp mRNA linear EST 01-JUL-2004  
AGENCOURT 26749547 NIH MGC 255 Rattus norvegicus cDNA clone  
IMAGE:7317070 5', mRNA sequence.  
CO401465  
CO401465.1 GI:495833381  
EST.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 779)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [csapbe@mail.nih.gov](mailto:csapbe@mail.nih.gov)  
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical  
College of Wisconsin  
cDNA Library Preparation: Express Genomics  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM15373 row: 0 column: 20  
High quality sequence start: 23  
High quality sequence stop: 690.

FEATURES  
source

Location/Qualifiers  
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/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:7317070"  
/sex="both"  
/tissue\_type="Brain - Pooled from several tissues from one or more individuals"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH MGC 255"  
/note="Organ: brain/CNS; Vector: pExpress-1; Site: 1: EcorV; Site: 2: NotI; RNA obtained from brain tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer: 5'-pCAGTAGTTCTAGATCGGAGCGGCC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.7 kb. This primary library is a normalized (primary library is NIH MGC 254) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH\_MGC library"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.09e-103 Length: 779  
Score: 925.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x C0401465 (1-779)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 114 TCAGTTTGTGACCTCTCTCTGAGAGACATTAGAGACTGGAGTGGTGGTGGTGC 173  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 174 AGCTATTCTCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATT 233  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 234 GCCTTTGGCCCTCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGGTGATCCAGGCT 293  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 294 ATCCAGAAATCAGATGAGGCCACCCATTCAGGGCATATTAGATCTGAAGTTGCTATA 353  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 354 TCAGAGGAATTGGTTGAGAAATACAGTAATCTCTCTTGGTCATGTGAACAGCAATA 413  
QY 101 LysGluLeuArgArgLeuPheIleValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 414 AAGAACTCTGAGCGGCTTTCTTAGTGTATGATTTAGTTGATTCCTGAAAGTTTCAGTG 473  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 474 TTGATGTGGGTGTTTACTATGTTGGTGGCTTGTTCATGGTCTGACACTACTGATTTTA 533  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 534 GCTCTGATCTCACTCTTCAGTATCTCTGTTATTTATGAACGCATCAGGTGCAGATAGAT 593  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 594 CATTATCTAGGACTTGCAAAACAGAGTGTAAAGATGCCATGGCCAAATCAAGCAAAA 653  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 654 ATCCCTGGATTGAGCGCAAGCAGAT 680

## RESULT 2

CV077130

LOCUS

DEFINITION

AGENCOURT 31475102 NIH MGC 251 Rattus norvegicus cDNA clone

ACCESSION

CV077130

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus

Rattus norvegicus

Rattus norvegicus

Rattus norvegicus

Rattus norvegicus

Rattus norvegicus

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Rattus norvegicus

Rattus norvegicus



Db 246 TTGGCCCTGCTCGCTGACTATCATGCTTTAGGATATATAAGGGCGTGCATCCAGGCTATC 305  
 Qy 62 GlnlySerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 306 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAAATCTGAAGTTGCTATATCA 365  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 366 GAGGAATTTGGTTTCAGAAATACAGTAATTTCTGCTTGTGTCATGTGAACAGCACATAAAA 425  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 426 GAACGTAGCGCGCTTTCTTCTAGTTAGTATGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 485  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAlaGlyLeuThrLeuLeuIleAla 141  
 Db 486 ATGTGGGTGTTTACTATGTTGGTCCCTGTGTTCAATGGTCTGACACTACTGATTTAGCT 545  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 546 CTGATCTCACCTCTTCAGTATTCCTGTTTATGAACGCATCAGGTGCAGATAGATCAT 605  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 606 TATCTAGGACTTGCAAAACAGAGTGTAAAGATGCGATGCGCAAAATCCAAAGCAAAATC 665  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 666 CCTGGATTGAAGCGCAAGCAGAT 689

RESULT 3  
 CF977898 791 bp mRNA linear EST 24-JUN-2004  
 LOCUS F26A06\_048.abl.R Rat retinal ganglion cell Rattus norvegicus cDNA,  
 DEFINITION mRNA sequence.

ACCESSION CF977898

VERSION CF977898.1 GI:49173356

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 791)

AUTHORS Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.  
 TITLE Gene Expression Profiling of Highly Purified Rat Retinal Ganglion  
 Cells

JOURNAL Unpublished (2003)

COMMENT

Contact: Farkas RH  
 Department of Ophthalmology  
 Johns Hopkins University School of Medicine  
 600 North Wolfe Street, Baltimore, MD 21287, USA  
 Tel: 410 502 5230  
 Fax: 410 502 5382  
 Email: rfarkas@jhmi.edu.

FEATURES

source

1..791

/organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
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 /lab\_host="DH10B"

/clone\_lib="Rat retinal ganglion cell"  
 /note="Organ: Eye; Vector: pDNR-LIB; Site 1: Sfil; Site 2:  
 Sfil; The library was constructed from purified rat  
 retinal ganglion cells. The Creator SMART cDNA Library  
 method (Clontech) was used. EST analysis was performed on  
 the unamplified, non-normalized, non-subtracted library."

ORIGIN

Alignment Scores:

Pred. NO.: 3.48e-103 Length: 791  
 Score: 921.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: ~ 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CF977898 (1-791)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 167 GTTGTGACCTCCCTCTACTGAGAGACATTAAGAAGACTGGAGTGTGTTTGGTCCAGC 226  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 227 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATTC 286  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 287 TTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAAGGGCGTGCATCCAGGCTATC 346  
 Qy 62 GlnlySerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 347 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAAATCTGAAGTTGCTATATCA 406  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 407 GAGGAATTTGGTTTCAGAAATACAGTAATTTCTGCTTGTGTCATGTGAACAGCACATAAAA 466  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 467 GAACGTAGCGCGCTTTCTTCTAGTTAGTATGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 526  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAlaGlyLeuThrLeuLeuIleAla 141  
 Db 527 ATGTGGGTGTTTACTATGTTGGTCCCTGTGTTCAATGGTCTGACACTACTGATTTAGCT 586  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 587 CTGATCTCACCTCTTCAGTATTCCTGTTTATGAACGCATCAGGTGCAGATAGATCAT 646  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 647 TATCTAGGACTTGCAAAACAGAGTGTAAAGATGCGATGCGCAAAATCCAAAGCAAAATC 706  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 707 CCTGGATTGAAGCGCAAGCAGAT 730

RESULT 4

AY404972

LOCUS

DEFINITION

Mus musculus RTM4 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY404972

VERSION AY404972.1 GI:39760946

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 600)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

TITLE

Infering nonneutral evolution from human-chimp-mouse orthologous

gene trios

JOURNAL

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

2 (bases 1 to 600)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 /locus\_tag="HMC2068"  
 ORIGIN  
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 Score: 913.00 Matches: 186  
 Percent Similarity: 99.47% Conservative: 1  
 Best Local Similarity: 98.94% Mismatches: 1  
 Query Match: 98.70% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY404972 (1-600)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 34 GTTGTGACCTCTCTGTTGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 93  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 94 TTATTCCTGCTGCTCTGACAGTGTTCAGCAATTTGTCAGTGAACGGCTACATTGCC 153  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 154 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 213  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 214 CAGAAATCAGATGAGGCCCAACCAATTCAGGCAATATTTGGAATCTGAAGTTGCCATATCA 273  
 QY 82 GluGluLeuValGlnLysTyrSerIleValSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 274 GAGGAATTTGGTTTTCAGAAATATATAGTAATCTGCTTTGGTCAATGTAACAGCAATAAAA 333  
 QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 334 GAATTTGAGCGGCTCTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTCAGTGTG 393  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 DB 394 ATGTGGTATTTACTTACGTTGGTGGCTTTGTTCAATGGTTTGACACTACTGATTTAGCC 453  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 DB 454 CTGATCTCACTCTTCAGTATTCCTGTTATATATGAACGGCATCAGCGGCAGATAGATCAT 513  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaValIle 181  
 DB 514 TATCTAGGACTTGCACAAACAGAGCGTTAAGGATGCCATGGCCAAATCCAGCAAAATC 573  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 DB 574 CTGTGATTGAGCGCAACAGCA 597  
 RESULT 5  
 BI149602  
 LOCUS 60284841.0F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:5011899 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI149602

VERSION BI149602.1 GI:14609603  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Mammalia; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 679)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-re@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM11062 row: c column: 04  
 High quality sequence stop: 679.  
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 /strain="CZECH II"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5011899"  
 /tissue\_type="spontaneous tumor, metastatic to mammary."  
 Stem cell origin.  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Lu29"  
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 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.74e-102 Length: 679  
 Score: 913.00 Matches: 186  
 Percent Similarity: 99.47% Conservative: 1  
 Best Local Similarity: 98.94% Mismatches: 1  
 Query Match: 98.70% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x BI149602 (1-679)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 37 GTTGTGACCTCTCTGTTGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 96  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 97 TTATTCCTGCTGCTCTGACAGTGTTCAGCAATTTGTCAGTGAACGGCTACATTGCC 156  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 157 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 216  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 217 CAGAAATCAGATGAGGCCCAACCAATTCAGGCAATATTTGGAATCTGAAGTTGCCATATCA 276  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 277 GAGGAATTTGGTTTTCAGAAATATAGTAATCTGCTTTGGTCAATGTAACAGCAATAAAA 336  
 QY 102 GluLeuArgGluLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 337 GAATTTGAGCGGCTCTCTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTCAGTGTG 396  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141

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Db      397 ATGTGGGTATTACTTACCTGGTGGTCCCTTGTTCATGCTTTGACACTACTGATTTAGCC 456
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Db      457 CTGATCTCACCTCTTCAGTATTCTCTGTTATATATGAACGGCATCAAGCGCAGATAGATCAT 516
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      517 TATCTAGGACTTGCAACACAGAGTGTAAAGATGCCATGCCAAATCCAGCAAAATC 576
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      577 CCTGGATTGAAGCGCAAAAGCAGAA 600

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RESULT 6
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DEFINITION 602923001F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5062944 5',
mRNA sequence.
VERSION  B1157842
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 708)
TITLE    NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL  National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-roman@nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1170 row: b column: 01
High quality sequence stop: 708.
Location/Qualifiers
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/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5062944"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam3"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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## FEATURES

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/organism="Mus musculus"
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/clone_lib="NCI_CGAP Mam3"
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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## ORIGIN

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Alignment Scores:
Pred. No.: 2 91e-102 Length: 708
Score: 913.00 Matches: 186
Percent Similarity: 99.47% Conservative: 1
Best Local Similarity: 98.94% Mismatches: 1
Query Match: 98.70% Indels: 0
DB: 4 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x B1157842 (1-708)

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Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

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Db      59 GTTCTTGACCTCTCTACTGCGAGACACATTAAAGACTGGAGTGGTGTCTTTGGTCCAGC 118
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      119 TTATTCCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTCACTGTAACGGCCTACATTCGCC 178
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      179 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 238
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      239 CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATTGGAATCTGAAGTTGCCATATCA 298
Qy      82 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      299 GAGGAATGGTTCAGAAATATAGTAATTCCTCTTGGTCAATGTAACAGCACAAATAA 358
Qy      102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121
Db      359 GAATTGAGGGCTCTCTCTTAGTTAGTATTTAGTTCCCTGAGTTTGCAGTGTG 418
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db      419 ATGTGGGTATTACTTACCTGCTGCTTGTTCATGATGTTGACACTACTGATTTAGCT 478
Qy      142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      479 CTGATCTCACCTCTTCAGTATTCTCTGTTATATGAACGGCATCAGCGCAGATAGATCAT 538
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      539 TATCTAGGACTTGCAACACAGAGGTTAAGATGCCATGCCAAATCCAGCAAAATC 598
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      599 CCTGGATTGAAGCGCAAAAGCAGAA 622
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DEFINITION AU080127 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-5261
5', mRNA sequence.
ACCESSION AU080127.1 GI:6084881
VERSION AU080127
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 794)
TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
JOURNAL library made by oligo-capping method
COMMENT Unpublished (1999)
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
FEATURES
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
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## ORIGIN

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Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY404970 (1-600)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 94 CTATTCTCTGCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTGCC 153  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61  
DB 154 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGTATC 213  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 214 CAGAAATCAGATGAAGCCACCATTTCAGGCATATCTGGATCTGGAATCTGATATCT 273  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 274 GAGGAGTTGTTTTCAGAAAGTACAGTAATCTCTGCTTTGGTTCATGTGAACCTGCAGATAAG 333  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 334 GAACCTCAGCGCGCTCTCTTAGTGTATGATTTAGTTGATTTCTGGAAGTTTCAGTGTG 393  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 394 ATGTGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTGGCT 453  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 454 CTCATTTTCACTCTCTCAGTCTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 513  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 514 TATCTAGGACTTGCATAAATGAAGTGTAAAGATGCTATGGCTAAATCCAAAGAAATC 573  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 574 CTTGGATTGAAGCGCAAGCTGAA 597

RESULT 11  
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LOCUS NISC np05d12.y1 NICHD\_HS\_Ut1 Homo sapiens cDNA clone IMAGE:5937070  
DEFINITION 5', mRNA sequence.  
ACCESSION CB215381  
VERSION CB215381.1 GI:28263573  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 650)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index

JOURNAL  
COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
CDNA Library Preparation:  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
info@image.llnl.gov  
Plate: LLAM13163 row: G column: 23  
Seq primer: M13RPI reverse primer (ABI).  
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phase, cycle day 13"  
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Cloned unidirectionally from microquantity amounts of mRNA  
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cycle day 13). Average insert size 1.9 kb. Library  
constructed by ResGen (Invitrogen Corporation)."

FEATURES  
source

## ORIGIN

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Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB215381 (1-650)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 19 GTTGTTGACCTCTGTTACTGGAGACATTAAAGACTGGAGTGGTGTGGTGGCCAC 78  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 79 CTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTGCC 138  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61  
DB 139 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGTATC 198  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 199 CAGAAATCAGATGAAGCCACCATTTCAGGCATATCTGGAATCTGGAATCTGATATCT 258  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 259 GAGGAGTTGTTTTCAGAAAGTACAGTAATCTCTGCTTTGGTTCATGTGAACCTGCAGATAAG 318  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 319 GAACCTCAGCGCGCTCTCTTAGTGTATGATTTAGTTGATTTCTGGAAGTTTCAGTGTG 378  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 379 ATGTGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTGGCT 438  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
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Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 559 CCTGGATTGAAGCGCAAGCTGAA 582

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LOCUS 1700060059220 GRN_PRENU Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN429712
VERSION CN429712.1 GI:47417306
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 667)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 667 Std Error: 0.00.
Location/Qualifiers
1..667
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/notes="Oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

ORIGIN
Alignment Scores:
Pred. No.: 3,47e-101 Length: 667
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CN429712 (1-667)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 143 CTATTCTCGCTGCTTTCATTGACAGTATTGACAGTATTGAGCGTAACAGCCTACATTGCC 202

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 203 TTGGCCCTGCTCTGTGCACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 262

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Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 383 GAACTCAGGGCCCTCTTCTTAGTTGATGATTTAGTTCATTCTCTGAAGTTGCAGTGTG 442

Qy 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 443 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 502

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Db 503 CTCAATTCACCTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGTATCAT 562

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 623 CCTGGATTGAAGCGCAAGCTGAA 646

RESULT 13
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LOCUS 4109431 BARC 9BOV Bos taurus cDNA clone 9BOV37_106 5', mRNA
DEFINITION CN977984
VERSION CK977984.1 GI:45495958
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 672)
AUTHORS Sonstegard, T.S., Van Tasell, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gaabbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 37 row: I column: 06
Seg primer: CCCAGTCACGACGTTGTAAACG
High quality sequence stop: 672.
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/clone_lib="BARC 9BOV"
/notes="Organ: Abomasum; Vector: pagen-1; Site: 1: EcoRV;
Site 2: NotI; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks

```



of age, fundic and pyloric abomasum"

```

ORIGIN
Alignment Scores:
Pred. No.: 3,51e-101 Length: 672
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservatives: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CK977984 (1-672)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21
Db 105 GTTGTGGTACCTCTCTACTGGAGACATTAAGAAGCTGGAGTGGTGTGGTCCACG 164
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrLeuAla 41
Db 165 TTGTTCCTGCTGCTCTGCTGACGATTAACAGTGTGAGTGTAAAGCCCTACATGTC 224
QY 42 LeuAlaLeuLeuSerValThrLeuSerPheArgGlyLeuTyrLysGlyValLeuGlnAla 61
Db 225 TTGGCCCTGCTCTCTGTGACTATACGTTTAGATATATAAGGGTGTGATCCAGGCTATC 284
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLeuSer 81
Db 285 CAGAAATCTGATGAAGCCACCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 344
QY 82 GluGluLeuValGlnLysTyrSerLeuSerAlaLeuGlyHisValAsnSerThrLeuLys 101
Db 345 GAGGAGTGTGGTTCAGAGTACAGCAATCTGCTCTGTGTCATGTTAACTGCAATAAAA 404
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 405 GAACCTCAGACGCTCTCTCTAGTGTGATGTTAGTTGATCTCTGAAGTTTCAGGTG 464
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 465 ATGTGGGTATTTACCTATGTTGGTCTGTTCAATGGTCTGACACTACTAATTTTGGCT 524
QY 142 LeuLeuSerLeuPheSerLeuProValLeuTyrGluArgHisGlnValGlnLeuAspHis 161
Db 525 CTGATTTCACTCTTCAGTGTCTCTGTTATTGAACGGCATCAGCGGCAATATAGATCAT 584
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysileGlnAlaLysile 181
Db 585 TATCTGGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 644
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 645 CCTGGATTGAAGCGTAAAGCTGAA 668

RESULT 14
CB162885
LOCUS
DEFINITION K-EST0223580 L18POOLin1 Homo sapiens cDNA clone L18POOLin1-41-F04
5', mRNA sequence.
ACCESSION CB162885
VERSION CB162885.1 GI:28149011
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center

```

Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 41 row: F column: 04  
High quality sequence stop: 682.

# FEATURES

source  
1..682

location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="L18POOLin1-41-F04"  
/cell\_line="SNU-354+Cho-CK+Choi-CK+HLK-3"  
/lab\_host="Top10P"  
/clone\_lib="L18POOLin1"

/note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI;  
Site 2: NotI; The library was contributed by the Soares  
laboratory and it was constructed as described by Bonaldo,  
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research  
6(9): 791-806. RNA was prepared from harvested cell  
culture."

## ORIGIN

Alignment Scores: 3,58e-101 Length: 682  
Pred. No.: 904.00 Matches: 183  
Score: 98.94% Conservatives: 3  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB162885 (1-682)

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QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21
Db 115 GTTGTGGTACCTCTCTACTGGAGACATTAAGAAGCTGGAGTGGTGTGGTCCACG 174
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerLeuValThrAlaTyrLeuAla 41
Db 175 CTATTCCTGCTGCTTTCATTCACGATTAACAGTGTGAGCGTAAACAGCTTACATGTC 234
QY 42 LeuAlaLeuLeuSerValThrLeuSerPheArgGlyLeuTyrLysGlyValLeuGlnAla 61
Db 235 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATATAAGGGTGTGATCCAGCTATC 294
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLeuSer 81
Db 295 CAGAAATCAGATGAAGCCACCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 354
QY 82 GluGluLeuValGlnLysTyrSerLeuSerAlaLeuGlyHisValAsnSerThrLeuLys 101
Db 355 GAGGAGTGTGGTTCAGAGTACAGTAAATTCCTGCTCTGTGTCATGTGAACCTGCAGTAAAG 414
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 415 GAACCTCAGCGCTCTCTTAGTGTGATTTAGTGTGATTTCTCTGAAGTTTCAGTGTG 474
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 475 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGTTCTGACACTACTGATTTGGCT 534
QY 142 LeuLeuSerLeuPheSerLeuProValLeuTyrGluArgHisGlnValGlnLeuAspHis 161
Db 535 CTCAATTCCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGCGCAGATAGATCAT 594
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysileGlnAlaLysile 181
Db 595 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 654
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 655 CCTGGATTGAAGCGCAAAAGCTGAA 678

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RESULT 15
CK971318
LOCUS
DEFINITION 4087182 BARC 9BOV Bos taurus cDNA clone 9BOV3_J07 5', mRNA
CK971318 linear EST 16-MAR-2004
sequence.
ACCESSION CK971318
VERSION CK971318.1 GI:45489292
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 712)
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
TITLE Production of EST from cDNA libraries derived from immunologically
activated bovine gut
JOURNAL Unpublished (2004)
COMMENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@nri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.00925 using options -trim alt "-trim fasta. Vector identified
by cross match using options -minmatch 12 -minscore 12
Plate: 3-row: J column: 07
Seq primer: CCCAGTCACGACGTTGTAACAAG
High quality sequence stop: 712.
FEATURES
Location/Qualifiers
1..712
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV3_J07"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 9BOV"
/notes="Organ: Abomasum; Vector: pAgen-1; Site: 1: EcoRV;
Site 2: NotI; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Osteragia osteragi was initiated at 15 weeks
of age. fundic and pyloric abomasum"
ORIGIN
Alignment Scores:
Pred. No.: 3.81e-101 Length: 712
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 7 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x CK971318 (1-712)
Qy 2 ValValAspLeuLeuTyrrPheArgAspIleValSerThrGlyValValPheGlyValAspSer 21
Db 18 GTTGTGACCTCCCTACTCGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCCAGC 77
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAla 41
Db 78 TTGTTCTTCCTGCTCTCCCTGACAGTATTGACATTGTGAGTGTACGGCTCATTTGCC 137
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrrSerGlyValIleGlnAlaIle 61
Db 138 TTGGCCCTGCTCTCTGCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 197

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Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81
Db 198 CAGAAATCTGATGAGGCCACCCATTGAGGCATATTGGGAATCTGAAGTTGCTATATCT 257
Qy 82 GluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 258 GAGGAGTTGGTTTCAAGAGTACAGCAATCTCTCTTGGTTCATGTTAACTGCACATAAAA 317
Qy 102 GluLeuArgGluLeuPheLeuValAspIleValAspSerLeuLysPheAlaValLeu 121
Db 318 GAATCTAGAGCCCTCTTCTTAGTTGATTTAGTTAGTTCTCTGAAGTTTGCAGTGTG 377
Qy 122 MetTrpValPheThrTyrrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 378 ATGTGGGTATTACTATGTTGGTGGCTTGTTCATGGTCTGACACTACTAATTTGGCT 437
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrrGluArgHisGlnValGlnIleAspHis 161
Db 438 CTGATTTTCACTCTTCAGTGTCTCTGTTATTATTATGAACGGCATCAGGCGCAATAGATCAT 497
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 498 TATCTGGGACTTGCATAAAGATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAATC 557
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 558 CCTGGATTGAAGCGTAAAGCTGAA 581
RESULT 16
CK102817
LOCUS
DEFINITION AGENCOURT 14009211 NIH_MGC_186 Homo sapiens cDNA clone
IMAGE:30373271 5', mRNA sequence.
ACCESSION CK102817
VERSION CK102817.1 GI:30755991
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 743)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM166 row: m column: 24
High quality sequence stop: 617.
FEATURES
Location/Qualifiers
1..743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30373271"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_186"
/notes="Organ: Pooled-Skin; Vector: pDNR-LIB; Site: 1: SfiI
(ggcccattggcc); Site 2: SfiI (ggccgctggcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meninges, duramater, pia matter and choroid plexus.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATTTATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGCATG-dt(30)BN-3'
(where B = A, C, G, or T). Average

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insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library"

## ORIGIN

Alignment Scores: 4.05e-101 Length: 743  
 Pred. No.: 904.00 Matches: 183  
 Score: 904.00  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CD102817 (1-743)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 151 GTTGTGACCTCTGTTCTGGAGACATTAGAGACTGGAGTGGTGGTGGTGGTGGC 210  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 211 CTATTCTCTGCTTCTTCAATTGACAGTATTGACGATTTGAGCGTAAACGCTTACATTGCC 270  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 271 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTGATCCAAAGCTATC 330  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 331 CAGAAATCAGATGAGCGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGATATCT 390  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 391 GAGGAGTTGTTTTCAGAAATACAGTAATCTCTGCTTGGTTCATCTGAACTGCACGATAAAG 450  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 451 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGGTGTG 510  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 511 ATGTGGTATTTACCTATGTTGGTCTGTTGTTTAAATGCTCTACACTACTGATTTGGCT 570  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 571 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGCGATCAGGCACAGATAGATCAT 630  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 631 TATCTAGGACTTGCATAATGAAGATGTAAAGATGCTATGCTTAAATCCAAAGCAAAATC 690  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 691 CTGTGATGAGCGCAAAAGCTGAA 714

## RESULT 17

BG697436 758 bp mRNA linear EST 07-MAY-2001  
 LOCUS 602660623F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4804012 5',  
 DEFINITION mRNA sequence.

ACCESSION BG697436 GI:13963656

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 758)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10700 row: m column: 05  
 High quality sequence stop: 756.

## FEATURES

## source

1..758

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4804012"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.17e-101 Length: 758  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG697436 (1-758)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 132 GTTGTGACCTCTGTTCTGGAGACATTAGAGACTGGAGTGGTGGTGGTGGC 191  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 192 CTATTCTCTGCTTCTTCAATTGACAGTATTGACGATTTGAGCGTAAACGCTTACATTGCC 251  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 252 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTGATCCAAAGCTATC 311  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 312 CAGAAATCAGATGAGCGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGATATCT 371  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 372 GAGGAGTTGTTTTCAGAAATACAGTAATCTCTGCTTGGTTCATCTGAACTGCACGATAAAG 431  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 432 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGGTGTG 491  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 492 ATGTGGTATTTACCTATGTTGGTCTGTTTAAATGCTCTACACTACTGATTTGGCT 551  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 552 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGCGATCAGGCACAGATAGATCAT 611  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 612 TATCTAGGACTTGCATAATGAAGATGTAAAGATGCTATGCTTAAATCCAAAGCAAAATC 671  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 691 CTGTGATGAGCGCAAAAGCTGAA 714

Db 672 CCTGATTGAAGCCGCAAGCTGAA 695

RESULT 18  
AL533461 788 bp mRNA linear EST 24-MAR-2004  
LOCUS  
DEFINITION AL533461 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone  
CSODN004YJ08 5-PRIME, mRNA sequence.  
ACCESSION  
VERSION AL533461.3 GI:45708351  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 788)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 13, 2001 this sequence version replaced gi:31260542.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 1423.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CSODN004DE04QP1&c=1423.r.  
http://www.genoscope.cns.fr/cdna?s=CSODN004DE04QP1&c=1423.r.

FEATURES  
source  
1..788  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODN004YJ08"  
/tissue\_type="ADULT BRAIN"  
/dev\_stage="adult"  
/clone\_lib="Homo sapiens ADULT BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 4.4e-101 Length: 788  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 1 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AL533461 (1-788)

Qy 2 ValValAspLeuLeuThrValPheSerIleValSerValThrAlaValIleAlaSer 21  
Db 156 GTTGTGACCTCCGTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGGCCAGC 215  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
Db 216 CTATCTCTGCTGCTTTCATTGACAGTATTACGATTGTGAGCGTAACAGCTCAATTGCC 275  
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrIleValIleGlnAlaIle 61  
Db 276 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 335  
Qy 62 GlnIysSerAspGluGlyHisPropGheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 336 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 395

Qy 82 GluGluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnSerThrIleIys 101  
Db 396 GAGGAGTTGGTTCAGAAGTACAGTAATCTGCTCTTGGTCAATGTGAACGACGATAAG 455  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuIysPheAlaValLeu 121  
Db 456 GAACCTCAGGCGCCTCTTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTGCGAGTGTG 515  
Qy 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuIleAla 141  
Db 516 ATGGGGTATTACCTATGTTGGTCTTGTATGCTGACACTACTGATTTGGCT 575  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 576 CTCATTTCACTTTCAGTGTCTCTGTTATTATGAACGATCAGGCACACATAGATCAT 635  
Qy 162 TyrLeuGlyLeuAlaAsnIysSerValIysAspAlaMetAlaIleGlnAlaIle 181  
Db 636 TATCTAGGACTTGCAATAAGAATGTTAAAGATCTATGGCTAAATCCAGCAAAATC 695  
Qy 182 ProGlyLeuIysArgIysAlaAsp 189  
Db 696 CCTGGATTGAAGCCCAAGCTGAA 719

RESULT 19  
BG570231 843 bp mRNA linear EST 10-APR-2001  
LOCUS  
DEFINITION BG570231 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4717662 5',  
mRNA sequence.  
ACCESSION BG570231  
VERSION BG570231.1 GI:13577884  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 843)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-rc@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LUCM1567 row: 0 column: 07  
High quality sequence stop: 801.  
Location/Qualifiers  
1..843  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4717662"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATTTAGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGCGGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.85e-101 Length: 843

(Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp469C2134) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: <http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469C2134>. Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES	SOURCE
1. <b>High Accuracy:</b> The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. <b>High Accuracy:</b> The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.
2. <b>Scalability:</b> The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.	2. <b>Scalability:</b> The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.
3. <b>Interpretability:</b> The model's decisions are transparent and explainable, allowing users to understand the underlying reasoning.	3. <b>Interpretability:</b> The model's decisions are transparent and explainable, allowing users to understand the underlying reasoning.
4. <b>Robustness:</b> The model is highly resistant to adversarial attacks and data poisoning, ensuring reliable performance in real-world scenarios.	4. <b>Robustness:</b> The model is highly resistant to adversarial attacks and data poisoning, ensuring reliable performance in real-world scenarios.
5. <b>Efficiency:</b> The model is optimized for fast inference and low resource consumption, making it ideal for deployment on edge devices.	5. <b>Efficiency:</b> The model is optimized for fast inference and low resource consumption, making it ideal for deployment on edge devices.

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location/Qualifiers
1. 849
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFpZ469C2134"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym:
note=vector: pSPort1 SfiI

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## ORIGIN

Alignment Scores:	4.89e-101	Length:	849
Pred. No.:	Score:	Matches:	183
	904.00	Conservative:	3
Percent Similarity:	98.94%	Mismatches:	2
Best Local Similarity:	97.34%	Indels:	0
Query Match:	97.73%	Gaps:	0
DB:	7		

US-09-830-972-2 COPY 975 1163 (1-189) X CR765672 (1-849)

Qy	2	ValValAspLeuLeuTyTrpArgAspIleuLysLysThrGlyValValPheGlyAlaSer	21
Db	150	GTITGTTGACCTCTCTACTCGAGAGACATTAAAGAAGACTGGAGTGGTGTGGTGGCAGC	209
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla	41
Db	210	CTATTCTCGCTGCTTTCATTGACAGTATTGACGATTGTGAGTGTACAGCTACATTGCC	259
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlLysGlyValIleGlnAlaIle	61
Db	270	TTGGCCCTCTTTCITGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTATC	329
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSer	81
Db	330	CAGAAATCAGATGAAGGCCACCCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT	389
Qy	82	GluGluLeuValGlnLysTyTrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
Db	390	GAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGCTCATGTGAATCCACGATTAAG	449
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	450	GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTTC	509
Qy	122	MetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	510	ATGTGGGTATTTACCATATGTGGTGGCCCTGTGTTAATGGTCTGACGCTACTGATTTTGGCT	569
Qy	142	LeuIleSerLeuPheSerIleProValIleTyTrGluArgHisGlnValGlnIleAspHis	161
Db	570	CTCATTTCACTCTTCAGTGTTCCTGTTATTATTGACCGCATTCGGCACAGATGATCAT	629
Qy	162	TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	630	TATCTAGGACTTGCAAAATAAGAAATGTTAAAGATCTATGGCTAAATCCAAGCGAAATC	689
Qy	182	ProGlyLeuLysArgLysAlaAsp	189
Db	690	CCTGGATTTGAAGCGCAAAAGCTGAA	713

RESULT 21  
AL573494/c  
LOCUS

875 bp mRNA linear EST 06-APR-2004

Score:	904.00	Matches:	183
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.34%	Mismatches:	2
Query Match:	97.73%	Indels:	0
DB:	4	Gaps:	0

US-09-830-972-2 COPY 975 1163 (1-189) x BG570231 (1-843)

Qy	2	ValValAspLeuLeuTyrTrpArgAspIleIysIysThrGlyValValPheGlyAlaSer	21
Db	2	GTGTGTGACCTCTGCTACTGGAGAGACATTAAAGAAGACTCGAGTGGTGTGTGGTGCAGC	61
Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	62	CTATTCTGCTGCTCTTCATTGACAGTATTGAGCGTTAGCGGTAAACGCTACATTGCC	121
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle	61
Db	122	TTGGCCCTGCTCTGTGCACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	181
Qy	62	GlnIysSerAspGluGlyHisProPheArgAlaTyrIeuGluSerGluValAlaIleSer	81
Db	182	CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGAAGTTGCTATATCT	241
Qy	82	GluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValIleAsnSerThrIleLys	101
Db	242	GAGGAGTTGGTTTCAGAAGTACAGTAATTTCTCTCTTGGTCATGTGAACCTCCAGTAAGA	301
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuIysPheAlaValLeu	121
Db	302	GAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTCTGATTCCTGAAGTTTGCAGTGTG	361
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	362	ATGTGGGTATTTACCTATGTTGGTGCTTGTTTAATGGTCTGACACTACTGATTTTGGCT	421
Qy	142	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
Db	422	CTCATTTCACTCTTCAGTGTTCCTGTATTATTGAACGGCATCAGGCACAGATAGATCAT	481
Qy	162	TyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlaIysIleGlnAlaLysIle	181
Db	482	TATCTAGGACTTCGAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAGGCAAAATC	541
Qy	182	ProGlyLeuIysArgLysAlaAsp	189
Db	542	CCTGGATTGAAGCGCAAAAGCTGAA	565

RESULT 20	CR765672	849 bp	mRNA	linear	EST 23-SEP-2004
LOCUS	CR765672				
DEFINITION	DFKZP0469C2134_r1	469 (synonym: pkid1)	Pongo pygmaeus	cDNA clone	
	DFKZP0469C2134_5'			mRNA sequence.	

ACCESSION CR765672  
VERSION CR765672.1 GI:52605968  
KEYWORDS EST.

KEYWORDS	ESI.
SOURCE	Pongo pygmaeus (orangutan)
ORGANISM	Pongo pygmaeus

ORGANISM	<i>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.</i>
REFERENCE	1 (bases 1 to 849)

REFERENCE  
I (bases 1 to 849)  
OTTENVAELDER, B., OBERMAIER, B., DEUTSCHENBAUR, S., SCHAIPP, A.,  
MEWES, H. W., WEIL, B., AMID, C., OSANGER, A., FOBO, G., HAN, M. and  
WIEMANN, S.

TITLE	JOURNAL
Pongo pygmaeus mRNA (Ottenwaelder, B., Obermaier, B., Wiemann, S., Deutschenbaur, S., et al.)	Unpublished (2004)

Journal Comment  
Unpublished (2004)  
Contact: MIPS  
MIPS

**MIPS**  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

ingstaedt@med.uni-wuerzburg.de; 093764; neuherberg, Germany. This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix

```

DEFINITION  AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
              clone CSODI051YB11 3-PRIME, mRNA sequence.
ACCESSION   AL573494
VERSION     AL573494.3 GI:46246666
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 875)
            Li W.B., Gruber C., Jesse J., and Polayes D.
            Full-length cDNA libraries and normalization
            unpublished (2001)
            On Feb 16, 2001 this sequence version replaced gi:31294840.
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            1423.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CSODI051CA06NPl&c=1423.r.

FEATURES             Location/Qualifiers
     source           1..875
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CSODI051YB11"
                     /tissue type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA
                     digested with Not I and EcoR V sites of the pCMVSPORT 6
                     vector. Library was normalized."

ORIGIN
Alignment Scores:  5.11e-101      Length:      875
Pred. No.:        904.00          Matches:    183
Score:            98.94%          Conservative: 3
Percent Similarity: 97.34%        Mismatches:  2
Best Local Similarity: 97.34%     Indels:    0
Query Match:      97.73%         Gaps:      0
DB:               1

US-09-830-972-2_COPY_975_1163 (1-189) x AL573494 (1-875)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      875 GTTGTGGACCTCTCTGTACTGGAGACATTAAGAACTGGAGTGGTGGTGGTGGCCAGC 816

Qy      22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      815 CTATTCTCGTCTGCTTTCATTACAGTATTCAGCATTTGACGGTAACAGCCATCATTTGCC 756

Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      755 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 696

Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      695 CAGAAATCAGATGAAGGCCACCCATTAGGCCATATCTGGAATCTGAAGTTGCTATATCT 636

Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      635 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGGTCATGTGAACTGCACGATTAAG 576

Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      575 GAACTCAGCGCCCTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGCAAGTGTG 516

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Qy      122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db      515 ATGTGGGTATTACTATGTGGTGGCTTGTATTATGGTCTGACACTACTGATTTGGCT 456

Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      455 CTCATTTCACTCTTCACTGTTCCTGTGTTATTTATGAAGGCATCAGGCACAGATAGATCAT 396

Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      395 TATCTAGACTTGCAATAAGATGTTAAAGATCTATGGCTAAATCCAAGCAAAATC 336

Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      335 CCTGATTGAAGCCCAAGCTGAA 312

RESULT 22
CR611869
LOCUS    full-length cDNA clone CSODN004VJ08 of Adult brain of Homo sapiens
         (human).
DEFINITION  CR611869.1 GI:50492676
            HTC; CNSLT cDNA.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1540)
            Li W.B., Gruber C., Jesse J., and Polayes D.
            Full-length cDNA libraries and normalization
            Unpublished
            Contact: Peng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
            Genoscope.
            Direct Submission
            Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            Location/Qualifiers
            1..1540
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CSODN004VJ08"
            /tissue type="Adult brain"
            /plasmid="pCMVSPORT_6"

FEATURES             Location/Qualifiers
     source           1..1540
     Alignment Scores: 1.14e-100      Length:      1540
     Pred. No.:        904.00          Matches:    183
     Score:            98.94%          Conservative: 3
     Percent Similarity: 97.34%        Mismatches:  2
     Best Local Similarity: 97.73%     Indels:    0
     Query Match:      97.73%         Gaps:      0
     DB:               3

US-09-830-972-2_COPY_975_1163 (1-189) x CR611869 (1-1540)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      156 GTTGTGGACCTCTCTGTACTGGAGACATTAAGAACTGGAGTGGTGGTGGTGGCCAGC 215

Qy      22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

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216	CTATTCTGCTGCTTTCATTGACAGTATTGACGATTTGTGAGCGTTAACGCCCTACATTGCC	275
Qy	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	335
Qy	GlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	CAGAAATCAGATGAAGGCCGCCCATTTCAAGGCGATATCTGGAATCTGGAAGTTCCTATATCT	395
Qy	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
Db	GAGCAGTTGGTTTCAGAACTACAGTAATTTCTGCTCTTGGTCATGTCACTGCACGATAAAG	455
Qy	GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	GAATCTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTTCAGCTGTG	515
Qy	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	ATGTGGGTATTACCTATGTTGGTGCCCTGTTTANTGGTCTGACACTACTGATTTTGGCT	575
Qy	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
Db	CTCATTTTCACCTTTCAGTGTGTTCTCTTATTTATGAACGGCATCAGGCACAGATAGATCAT	635
Qy	TyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	TATCTAGACCTTGCNAATPAGAATGTTAAGATGCTATGGCTPAAATCCACGACAAATATC	695
Qy	ProGlyLeuLysArgLysAlaAsp	189
Db	CCTGGATTGAAGCGCAAGCTGAA	719

RESULT 23	AF077050	1785 bp	linear	HTC 21-NOV-2002		
LOCUS	AF077050	Homo sapiens neuroendocrine-specific protein C homolog mRNA,				
DEFINITION	complete cds.					
ACCESSION	AF077050					
VERSION	AF077050.1	GI:4689147				
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	1 (bases 1 to 1785)					
AUTHORS	Song,H., Peng,Y., Zhou,J., Huang,Q., Dai,M., Mao,Y., Yu,Y., Xu,X.,					
	Luo,B., Hu,R. and Chen,J.					
	Human neuroendocrine-specific protein C (NSP) homolog gene					
TITLE	Unpublished					
JOURNAL	2 (bases 1 to 1785)					
REFERENCE	Song,H.					
AUTHORS	Direct Submission					
	Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of					
	Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,					
JOURNAL						

## ORIGIN

<b>Alignment Scores:</b>					
Pred. NO.:	1.41e-100	Length:	1785		
Fred.	904.00	Matches:	183		
Percent Similarity:	98.94%	Conservative:	3		
Best Local Similarity:	97.34%	Mismatches:	2		
Query Match:	97.73%	Indels:	0		
DB:	3	Gaps:	0		
US-09-830-972-2_COPY_975_1163 (1-189) x AF077050 (1-1785)					
Qy	2	VaiValAspLeuLeuTyrrTtoArGAsPiLeLysThrGlyValValPheGlyAlaSer	21		
Dd	247	GTtTTGACCTCCTGACTCGAGAGACATTAAGAAGCTGGATGGTGTTGGTCGCAGC	306		
Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla	41		
Dd	307	CTATTCTGCTGCTTTTCATTGACAGTATTCCAGCATTTGTGAGCGCTAACAGCCTACATTGCC	366		
Qy	42	LeuAlaLeuSerValThrIleSerPheArgIleTyrllysGlyVallieGlnAlaIle	61		
Dd	367	T TGCCCTGCTCTCTGACCATCAGCTTTTAGGATATACAAGGGTGTGAATCCAAGCTATC	426		
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrrleuGluSerGluValAlaIleSer	81		
Dd	427	CAGAAATCAGATGNAAGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGTATATCT	486		
Qy	82	GluGluLeuValGlnLysTyrrSerAasnSerAlaLeuGlyHisValasnSerThrIleLys	101		
Dd	487	GAGGAGTTGGTTTCAGAAAGTACAGTAATCTTCCTCTTGGTCACTGAACTGCACGATAAAG	546		
Qy	102	GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121		
Dd	547	GAATCTCAGGCGCCTCTCTTAGTTAGTATGATTTATAGTTGATTTCTCTGAAGTTTCAGATGTTG	606		
Qy	122	MetTrpValPheThrTrValGlyAlaLeuPheAasnGlyLeuthrLeuLeulleLeuAla	141		
Dd	607	ATGCGGTATTAACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT	666		
Qy	142	LeulleSerLeuPheSerIleProValIleTyrrGluArgHisGlnValGlnIleAspHis	161		
Dd	667	CTCATTTCACTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCAT	726		
Qy	162	TyrLeuGlyLeuAlaLenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	181		
Dd	727	TATCTAGGACTTGCNAATAGAATGTTTAAAGATGCTATGGCTAAATCCAGCAAATTC	786		
Qy	182	ProGlyLeuLysArgLysAlaAsp	189		
Dd	787	CCTGGATTGAAGCGCAAAGCTGAA	810		
RESULT 24					
BIO79496					
LOCUS	602876306F1 NCI_CGAP_Mam2 Mus musculus cdna clone IMAGE:5008248 5'	781 bp	mRNA	linear	EST 20-JUN-2001
DEFINITION					
ACCESSION	BIO79496				
VERSION	BIO79496.1	GI:14497826			
KEYWORDS	Mus musculus				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 781)				
TITLE	NHL-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rcapbs-x@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cdna Library Preparation: Life Technologies, Inc. cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc.				

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: L1A11052 row: k column: 01  
 High quality sequence stop: 773.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /clone="IMAGE:5008248"  
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 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Mam2"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

# FEATURES source

## ORIGIN

Alignment Scores:  
 Pred. No.: 5.78e-101 Length: 781  
 Score: 903.00 Matches: 185  
 Percent Similarity: 98.40% Conservative: 0  
 Best Local Similarity: 98.40% Mismatches: 3  
 Query Match: 97.62% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BI079496 (1-781)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleYsValSerThrGlyValValPheGlyAlaSer 21  
 Db 213 GTTGTGGACCTCTCTGTGACATATAGAGACTGAGGAGTGGTGTGGTGGCCAGC 272  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 273 TTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAAGCGCTACATGGC 332  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 333 TTGGCCCTGCTCTCTGTGACATATAGAGACTGAGGAGTGGTGTGGTGGCCAGC 392  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 393 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTGGAATCTGAAAGTTGCCATATCA 452  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 453 GAGGAATTGGTTTCAGAAATATAGTAATTTCTGCTCTTGTGTCATGTGACAGCACATAAAA 512  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 513 GAATTGAGCGCTCTCTCTTGTAGTATGATGATTTAGTATTCCTTCAAGTTTGCAGTGTG 572  
 Qy 122 MetTrpValPheThrTyrValGlyValAlaLeuPheGlnGlyLeuThrLeuIleAla 141  
 Db 573 ATGGGGTATTTACTTACGTTGGGCGCTGTGTTCAATGGTTTGGACACTACTGATTTAGCT 632  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 633 CTGATCTCATTCTTTCAGTATTTCTGTTATATATGACGGGATCAGCGGCAGATCATCAT 692  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 693 TATCTAGGACTTGCAAAACAGAGCGTTAAGGATGCGATGCGCAAAATCCAAAGCAAAATC 752  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 753 CCTGGATTGAAGCGCAAGACGAT 776

RESULT 25

# AU297347

LOCUS AU297347 730 bp mRNA linear EST 08-MAY-2003  
 DEFINITION AU297347 female adult cerebrum, full-length enriched chimpanzee cDNA library Pan troglodytes versus cDNA clone PorA0834 5' similar to human RefSeq mRNA NM\_007008, mRNA sequence.  
 ACCESSION AU297347  
 VERSION AU297347  
 KEYWORDS EST.  
 SOURCE Pan troglodytes versus  
 ORGANISM Pan troglodytes versus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 730)  
 AUTHORS Sakate, R., Oeada, N., Hida, M., Sugano, S., Hayaaka, I., Shimohira, N., Yanagi, S., Suto, Y., Hashimoto, K. and Hirai, M.  
 TITLE Analysis of 5'-end sequences of chimpanzee cDNAs  
 JOURNAL Genome Res. 13 (5), 1022-1026 (2003)  
 MEDLINE 22612989  
 PUBMED 12727913  
 COMMENT Contact: Momoki Hirai  
 Department of Integrated Biosciences  
 The University of Tokyo, Graduate School of Frontier Sciences  
 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan  
 Tel: 81-4-7136-3688  
 Fax: 81-4-7136-3687  
 Email: mhiraik@u-tokyo.ac.jp.  
 Location/Qualifiers  
 1..730  
 /organism="Pan troglodytes versus"  
 /mol\_type="mRNA"  
 /sub\_species="verus"  
 /db\_xref="taxon:37012"  
 /clone="PorA0834"  
 /sex="female"  
 /tissue\_type="cerebrum"  
 /dev\_stage="adult"  
 /clone\_lib="female adult cerebrum, full-length enriched chimpanzee cDNA library"

# FEATURES source

## ORIGIN

Alignment Scores:  
 Pred. No.: 9.28e-101 Length: 730  
 Score: 901.00 Matches: 182  
 Percent Similarity: 98.94% Conservative: 4  
 Best Local Similarity: 96.81% Mismatches: 2  
 Query Match: 97.41% Indels: 0  
 DB: 1 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AU297347 (1-730)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleYsValSerThrGlyValValPheGlyAlaSer 21  
 Db 162 GTTGTGGACCTCTCTGTGACATATAGAGACTGAGGAGTGGTGTGGTGGCCAGC 221  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 222 CTATTCCTGCTGCTCTTTCAGCATTTTTCAGCATTTGAGTGTACAGCCTACATGCC 281  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 282 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCGTGTGATCCAAGCTATC 341  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 342 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATATCT 401  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 402 GAGGAGTGGTTTCAGAGTACAGTAATTTCTGCTTGTGTCATGTGAGTGCACGATAAG 461  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 462 GAACTCAGGCGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTGTAAGTTGTCAGTGTG 521



QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141  
 |||||  
 Db 522 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 581  
 |||||  
 QY 142 LeuLeuSerLeuPheSerileProValIleTyrGluAtrGHisGlnValGlnIleAspHis 161  
 |||||  
 Db 582 CTCATTTCACCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGCACAGATAGATCAT 641  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 642 TATCAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGCTTAAATCCACGGAATC 701  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 702 CCTGGATTGAAGCGCAAGCTGAA 725  
 |||||

## RESULT 26

CB067821 634 bp mRNA linear EST 21-JAN-2003  
 LOCUS ig38a06.y1 HR85 islet Homo sapiens cDNA clone IMAGE: 5, similar to  
 DEFINITION TR:Q9Y293 Q9Y293 FOOCEN-S. [1], mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

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## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB067821 (1-634)

## QY 2 ValValAspLeuLeuTyrTriArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

## Db 71 GTTGTGGACCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 130

## QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

## Db 131 CTATTCTGCTGCTTTCATTCACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTCGC 190

## QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

## Db 191 TTGGCCCTGCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 250

## QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

## Db 251 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGATCTGAAGTTGCTATATCT 310

## QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

## Db 311 GAGGAGTTGGTTCAGAACTACAGTAAATCTGCTCTTGGTCTCATGTGAACCTGACGATAAG 370

## QY 102 GluLeuArgArgLeuPheIleuValAspIleuValAspSerLeuLysPheAlaValLeu 121

## Db 371 GAACTCAGCGCCCTCTCTTATGATGATTTAGTTAGTATCTCTGAAGTTTGCAGTGTG 430

## QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141

## Db 431 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTATGCTGACACTACTGATTTGGCT 490

## QY 142 LeuLeuSerLeuPheSerileProValIleTyrGluArgHisGlnValGlnIleAspHis 161

## Db 491 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCGACAGATAGATCAT 550

## QY 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

## Db 551 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGCGCTAAATCCACGAANATC 610

## QY 182 ProGlyLeuLysArgLysAlaAsp 189

## Db 611 CCTGGATTGAAGCGCAAGCTGAA 634

## RESULT 27

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

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## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB067821 (1-634)

## QY 2 ValValAspLeuLeuTyrTriArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

## Db 71 GTTGTGGACCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 130

## QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

## Db 131 CTATTCTGCTGCTTTCATTCACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTCGC 190

## QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

## Db 191 TTGGCCCTGCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 250

## QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

## Db 251 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGATCTGAAGTTGCTATATCT 310

## QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

## Db 311 GAGGAGTTGGTTCAGAACTACAGTAAATCTGCTCTTGGTCTCATGTGAACCTGACGATAAG 370

## QY 102 GluLeuArgArgLeuPheIleuValAspIleuValAspSerLeuLysPheAlaValLeu 121

## Db 371 GAACTCAGCGCCCTCTCTTATGATGATTTAGTTAGTATCTCTGAAGTTTGCAGTGTG 430

## QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141

## Db 431 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTATGCTGACACTACTGATTTGGCT 490

## QY 142 LeuLeuSerLeuPheSerileProValIleTyrGluArgHisGlnValGlnIleAspHis 161

## Db 491 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCGACAGATAGATCAT 550

## QY 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

## Db 551 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGCGCTAAATCCACGAANATC 610

## QY 182 ProGlyLeuLysArgLysAlaAsp 189

## Db 611 CCTGGATTGAAGCGCAAGCTGAA 634

## RESULT 27

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

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## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB067821 (1-634)

## QY 2 ValValAspLeuLeuTyrTriArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

## Db 71 GTTGTGGACCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 130

## QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

## Db 131 CTATTCTGCTGCTTTCATTCACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTCGC 190

## QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

## Db 191 TTGGCCCTGCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 250

## QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

## Db 251 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGATCTGAAGTTGCTATATCT 310

## QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

## Db 311 GAGGAGTTGGTTCAGAACTACAGTAAATCTGCTCTTGGTCTCATGTGAACCTGACGATAAG 370

## QY 102 GluLeuArgArgLeuPheIleuValAspIleuValAspSerLeuLysPheAlaValLeu 121

## Db 371 GAACTCAGCGCCCTCTCTTATGATGATTTAGTTAGTATCTCTGAAGTTTGCAGTGTG 430

## QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141

## Db 431 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTATGCTGACACTACTGATTTGGCT 490

## QY 142 LeuLeuSerLeuPheSerileProValIleTyrGluArgHisGlnValGlnIleAspHis 161

## Db 491 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCGACAGATAGATCAT 550

## QY 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

## Db 551 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGCGCTAAATCCACGAANATC 610

## QY 182 ProGlyLeuLysArgLysAlaAsp 189

## Db 611 CCTGGATTGAAGCGCAAGCTGAA 634

## RESULT 27

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

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## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB067821 (1-634)

## QY 2 ValValAspLeuLeuTyrTriArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

## Db 71 GTTGTGGACCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 130

## QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

## Db 131 CTATTCTGCTGCTTTCATTCACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTCGC 190

## QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

## Db 191 TTGGCCCTGCTCTCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 250

## QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

## Db 251 CAGAAATCAGATGAAGGCCACCC



1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc\_Vidal@fci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

PCR Primers

FORWARD: ATGGACGGTCAAGAGAAAATTGG

BACKWARD: CATTGACGTTTGGCTTCAATC

Insert Length: 670 Std Error: 66.00

Plate: 11045 row: 02 column: B

Seq primer: ACTGGCCGCTGTTTACAACTGCTGACTGGGAAAC

High quality sequence start: 101

High quality sequence stop: 669

POLYA-No.

Location/Qualifiers

1. .670

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue type="mixed"

/clone\_lib="Full length cDNA from the Mammalian Gene

Collection"

/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

#### ORIGIN

Alignment Scores: 1.93e-100 Length: 670  
Pred. No.: 898.00 Matches: 182  
Score: 98.40% Conservative: 3  
Percent Similarity: 98.40% Mismatches: 3  
Best Local Similarity: 96.81% Indels: 0  
Query Match: 97.08% Gaps: 0  
DB: 7

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CV030029 (1-670)

Oy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 34 GTTGTGACCTCTGTTACTGAGAGACATTAGAGACTGGAGTGGTGTGGTCCAGC 93  
Oy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 94 CTATTCTGCTGCTTTTCATTGACAGATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 153  
Oy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCAAGCTATC 213  
Oy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 214 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTGTGCTATATCT 273  
Oy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 274 GAGGAGTGGTTTCAGAACTACAGTAATCTGCTCTGTGTCATGTGAACTGCACGATAAG 333  
Oy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 334 GAACTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 393  
Oy 122 MetTrpValPheThrTyrValGlyAlaLeuPheArgGlyLeuThrLeuLeuIleAla 141  
Db 394 ATGTGGGTATTACCTATGTTGGTCCCTGTTTAAATGCTCTGACACTACTGATTTGGCT 453  
Oy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 454 CTCATTTCACTCTTCAGTGTTCCTGTTATTATTATCAAGCGCATCAGGCACAGATGATCAT 513  
Oy 162 TrrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 514 TATCTAGACTTGCATAAATAAGATGTTAAAGATGCTATGCTAAATCCAAGCAAAATC 573  
Oy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 574 CCTGATTGAAGCGCANAGCTGAA 597  
RESULT 28  
CN646472  
LOCUS  
DEFINITION  
CN646472 960 bp mRNA linear EST 13-MAY-2004  
ILLUMIGEN MCQ 26335 Katze MBR Macaca mulatta cDNA clone IBUW:8548  
5' similar to Bases 129 to 958 highly similar to human RTN4  
(Hs.436349), mRNA sequence.  
ACCSSION  
CN646472 GI:47159915  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Macaca mulatta (rhesus monkey)  
Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecoidea; Macaca.  
REFERENCE  
1 (bases 1 to 960)  
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.  
Large-scale Rhesus Macaque cDNA Sequencing  
Unpublished (2003)  
JOURNAL  
COMMENT  
Contact: C. Magness  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagness@illumigen.com  
Sequenced on 2004.03.09. 743 Q20 bases.  
PCR Primers  
FORWARD: CCCTCACTAAAGGGAACAAAA  
BACKWARD: CACTATAGGCGGAATTGGGTA  
Insert Length: 960 Std Error: 0.00  
Plate: CL000173 row: H column: 11  
Seq primer: CCCTCACTAAAGGGAACAAAA  
POLYA-No.  
Location/Qualifiers  
1. .960  
/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/strain="Indian"  
/db\_xref="taxon:9544"  
/clones="IBUW:8548"  
/sex="female"  
/dev stage="adult"  
/lab\_host="E. coli SOLR"  
/clone\_lib="Katze\_MBR"  
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
kit (Catalog #200400) and ZAP-cDNA Gigapack III Gold  
Cloning Kit (Catalog #200450)"

#### FEATURES

source

#### ORIGIN

Alignment Scores:  
Pred. No.: 3.22e-100 Length: 960  
Score: 898.00 Matches: 181  
Percent Similarity: 98.40% Conservative: 5  
Best Local Similarity: 96.28% Mismatches: 2  
Query Match: 97.08% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN646472 (1-960)

Oy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 129 GTTGTGACCTCTCTACTGAGAGACATGAAGAAGACTGGAGTGGTGTGGTCCAGC 188

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 |||||  
 Db 189 CTATTCTCTGCTCTTCAATGACAGTATTACAGCATTTGTGAGTGTAAACAGCCTACATTCGCC 248  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 |||||  
 Db 249 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 308  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 309 CAGAAATCAGATGAAAGCCACCATTCAGGGCATATCTGGAATCTGGAAGTTCGATATCT 368  
 |||||  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 |||||  
 Db 369 GAGGAGTGTGTTTCAGAAATGACAGTAAATCTGCTCTGTGTCATGTGAACCTGCAGATAAG 428  
 |||||  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 429 GAATCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAGTTTCAGTGTG 488  
 |||||  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 |||||  
 Db 489 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGTTCTGACGCTACTGATTTGGCT 548  
 |||||  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 |||||  
 Db 549 CTCATTTCACTCTTCAGTGTCTCTTAGTTGATGATTTAGTTGATCTCTGAGTTTCAGTGTG 608  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 609 TATCTAGGACTTGCAAAATGAAATGTTAAAGATGCTATGGCTAAATCCAGCGAAATC 668  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 669 CCTGGATTGAAGCGCAAGCTGAA 692  
 |||||

## RESULT 29

CN803408 983 bp mRNA linear EST 26-MAY-2004  
 ILLUMIGEN MCQ 32945 Katze MMR Macaca mulatta cDNA clone  
 IBIUW:11396 5' similar to Bases 136 to 983 highly similar to human

RTN4 (Hs.436349), mRNA sequence.  
 CN803408 GI:47699384

VERSION CN803408.1

KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)

## ORGANISM

Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 Cercopitheciinae; Macaca.

## REFERENCE

AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.  
 TITLE Large-scale Rhesus Macaque cDNA Sequencing  
 JOURNAL Unpublished (2003)

## COMMENT

Contact: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2004.04.03. 731 Q20 bases.

PCR Primers

FORWARD: CCTCACTAAGGGGAACAAA

BACKWARD: CACTATAGGCGAATTGGTA

Insert Length: 983 Std Error: 0.00

Plate: CL000275 row: C column: 03

Seq primer: CCTCACTAAGGGGAACAAA

POLYA=No.

## FEATURES

source

1. .983

/organism="Macaca mulatta"

/mol\_type="mRNA"

/strain="Indian"

/db\_xref="taxon:9544"

/clone="IBIUW:11396"

/sex="female"

/dev\_stage="adult"

/lab\_host="E. coli SOLR"

/clone\_lib="Katze MMR"

/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
 kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold  
 Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.33e-100 Length: 983  
 Score: 898.00 Matches: 181  
 Percent Similarity: 98.94% Conservative: 5  
 Best Local Similarity: 96.28% Mismatches: 2  
 Query Match: 97.08% Indels: 0  
 Db: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN803408 (1-983)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 |||||  
 Db 136 GTTGTGACCTCCCTCTACTGAGAGACATGAGAGACTGGAGTGGTGTGGTCCAGC 195  
 |||||  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 |||||  
 Db 196 CTATTCTCTGCTCTTTCATTCAGCATTTGAGTGTAAACAGCCTACATTCGCC 255  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 |||||  
 Db 256 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 315  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 316 CAGAAATCAGATGAGGCGCACCCATTGAGGCATATCTGGAATCTGAGATTGCGATATCT 375  
 |||||  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 |||||  
 Db 376 GAGGAGTGGTTCAGAAATGACAGTAAATCTGCTCTGTGTCATGTGAACCTGCACGATAAG 435  
 |||||  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 436 GAATCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAGTTTCAGTGTG 495  
 |||||  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 |||||  
 Db 496 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTGACGCTACTGATTTGGCT 555  
 |||||  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 |||||  
 Db 556 CTCATTTCACTCTTCAGTGTCTCTTAGTTGATGATTTAGTAAAGATGCTATGGCTAAATCCAGCGAAATC 615  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 616 TATCTAGGACTTGCAAAATGAAATGTTAAAGATGCTATGGCTAAATCCAGCGAAATC 675  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 676 CCTGGATTGAAGCGCAAGCTGAA 699  
 |||||

## RESULT 30

CN647521

LOCUS

DEFINITION

ILLUMIGEN MCQ 28658 Katze MMR Macaca mulatta cDNA clone IBIUW:7529

5' similar to Bases 129 to 1018 highly similar to human RTN4

(Hs.436349), mRNA sequence.

ACCESSION CN647521

VERSION CN647521.1

KEYWORDS

EST.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

CN647521 1031 bp mRNA linear EST 13-MAY-2004  
 ILLUMIGEN MCQ 28658 Katze MMR Macaca mulatta cDNA clone IBIUW:7529  
 5' similar to Bases 129 to 1018 highly similar to human RTN4

(Hs.436349), mRNA sequence.

ACCESSION CN647521

VERSION CN647521.1

KEYWORDS

EST.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.

1 (bases 1 to 1031)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.

Large-scale Rhesus Macaque cDNA Sequencing

Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2004.03.24. 773 Q20 bases.

PCR Primers

FORWARD: CCCTCACTAAGGGAACAAA

BACKWARD: CACTATAGGCGAATGGGTA

Insert Length: 1031 Std Error: 0.00

Plate: CL000187 row: G column: 05

Seq primer: CCCTCACTAAGGGAACAAA

POLYA-No.

Location/Qualifiers

1..1031

/organism="Macaca mulatta"

/mol\_type="mRNA"

/strain="Indian"

/db\_xref="taxon:9544"

/clone="IBIUM.7529"

/sex="female"

/dev\_stage="adult"

/lab\_host="E. coli SOLR"

/clone\_lib="Katze MMRB"

/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;

Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis

kit (catalog #200400) and ZAP-cDNA Gigapack III Gold

Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,57e-100 Length: 1031  
Score: 998.00 Matches: 181  
Percent Similarity: 98.94% Conservative: 5  
Best Local Similarity: 96.28% Mismatches: 2  
Query Match: 97.08% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CM647521 (1-1031)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 129 GTTGTGACCTCTCTACTCGAGAGACATGAAGAAGACTGGAGTGTGTTGGTGCCAGC 188  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 189 CTATTCTCGTCTCTTCATTGACAGTATTGACGATTGTGAGTGTGAACAGCCTACATTGCC 248  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleClnAlaIle 61  
Db 249 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCAAGCTATC 308  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 309 CAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCATATCT 368  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 369 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTCTGTCATGTCAACTGCACGATAAAG 428  
Qy 102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121  
Db 429 GAATCAGGCCCTCTCTTCTAGTTAGTATGATTAGTTGATCTCTGAAAGTTTGCAGTTGTG 488  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141

Db 489 ATGTGGGTATTATCTATGTTGGTGCCTGTTTAAATGCTCTGACGCTACTGATTTGGCT 548  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 549 CTCAATTCACATCTTCAGTGTCTCTGTTTATTAATGAGCGCATGAGGACACATAGATCAT 608  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 609 TATCTAGGACTTGCATTAAGATGTTAAAGATCTATGGCTAAATCCAGCGGAATC 668  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 669 CCTGGATTGAAGCGCAAAAGCTGAA 692

## RESULT 31

AK034902.

LOCUS

DEFINITION

Mus musculus 12 days embryo embryonic body between diaphragm region

product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOCO PROTEIN)

(FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus

norvegicus], full insert sequence.

AK034902

VERSION

AK034902.1 GI:26084268

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Methods. Enzymol. 303, 19-44 (1999)

JOURNAL

MEDLINE

92279253

PUBMED

10349636

REFERENCE

2

11042159

REFERENCE

3

11042159

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

MEDLINE

20530913

PUBMED

11076861

REFERENCE

4

11076861

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the

PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

JOURNAL

REFERENCE

5

11076861

AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL

REFERENCE

6

11076861

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,





```

RESULT 34
AA986233      718 bp      mRNA      linear      EST 28-MAY-1998
LOCUS      uc73g12.y1 Sugano mouse liver mlia Mus musculus cDNA clone
DEFINITION      IMAGE:1431334 5' similar to TR:Q16801 Q16801
                NEUROENDOCRINE-SPECIFIC PROTEIN C. ; mRNA sequence.
ACCESSION      AA986233
VERSION
KEYWORDS
SOURCE
ORGANISM      Mus musculus (house mouse)
REFERENCE
AUTHORS      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
                Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
                Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                Theising, B., Wylie, T., Lennon, G., Soares, B., Wilton, R. and
                Waterston, R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
                WashU-HMI Mouse EST Project
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: mouseest@watson.wustl.edu
                This clone is available royalty-free through LNL; contact the
                IMAGE Consortium (info@image.lnl.gov) for further information.
                MGI:915402
                Possible reversed clone: similarity on wrong strand
                Seq primer: primer name ambiguous
                High quality sequence stop: 489.
                Location/Qualifiers
                1. .718
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL"
                /db_xref="taxon:10090"
                /clone="IMAGE:1431334"
                /sex="female"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="Sugano mouse liver mlia"
                /note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
                (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
                was primed with an oligo(dT) primer
                [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was
                ligated to a DraIII adaptor [TGTGGCTACTGG], digested
                and cloned into distinct DraIII sites of the pME18S-FL3
                vector [5' site CACTGTGTG, 3' site CACCATGTG]. XhoI should
                be used to isolate the cDNA insert. Size selection
                performed to exclude fragments <1.5kb. Library
                constructed by Dr. Sumio Sugano (University of Tokyo
                Institute of Medical Science). Custom primers for
                sequencing: 5' end primer CTCTGCTCTCTAAAGCTGG and 3' end
                primer GCACCTGCAGCTCGAGACA."
ORIGIN
Alignment Scores:
Pred. No.:      8,87e-100      Length:      718
Score:      893.00      Matches:      181
Percent Similarity: 97.8%      Conservative: 3
Best Local Similarity: 96.2%      Mismatches: 4
Query Match:      96.54%      Indels: 0
DB:      1      Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AA986233 (1-718)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      155 GTTGTGACCTCTCTGTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTCCGAGC 214

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Qy      22 LeupheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      215 TTATTCCTGCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAAGTGAACGGCCCTACATTGCC 274
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      275 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 334
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      335 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTTGAATCTGAAGTTGCCATATCA 394
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      395 GAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTCTTGTGTCATGTGAACAGCAATAAAA 454
Qy      102 GluLeuATGATGLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      455 GAATTCAGGGCTCTCTCTTTAGTTGATGATTTAGTTGATTCCTGAAAGTTTGCAGTGTG 514
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db      515 ATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATATGCTTTGACACTACTGATTTAGCT 574
Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      575 CTGATCTCACCTCTTCAGTATTCCTGTTATATATATGAACGGCATCAGCGGCAGATAGATCAT 634
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      635 TATCTAGGACTTGCAAACAGAGCGTTAAGATGCCATGCCATGCGCAANTCCAGCAAAATC 694
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      695 CTGGATTGAGCGCAGGCAGGACAA 718

RESULT 35
CN482802      592 bp      mRNA      linear      EST 26-APR-2004
LOCUS      hw24h12.y1 Human primary human ocular pericytes. Unamplified (hw)
DEFINITION      Homo sapiens cDNA clone hw24h12 5', mRNA sequence.
ACCESSION      CN482802
VERSION      CN482802.1 GI:46564306
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 592)
AUTHORS      Tsai, J.Y. and Wistow, G.
TITLE      Expressed sequence tag analysis of cultured primary human ocular
                pericytes
JOURNAL      Unpublished (2004)
COMMENT      Contact: Wistow G
                Section on Molecular Structure and Function
                National Eye Institute
                6/331, NIH, Bethesda, MD 20892-2740, USA
                Tel: 301 402 3452
                Fax: 301 496 0078
                Email: graeme@helix.nih.gov
                Plate: 24 row: h column: 12
                Seq primer: ML3RP1 reverse primer (ABI).
                Location/Qualifiers
                1. .592
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="hw24h12"
                /cell_type="pericytes"
                /dev_stage="Adult"
                /lab_host="EMDH10B"
                /clone_lib="Human primary human ocular pericytes."
FEATURES
source

```





QY 122 MetTropValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThriLeuLeuLeuAla 141  
 |||||  
 Db 540 ATGTGGGATTATACCTATGTTGGTCTGTTCAATGGTCTGACACTACTGATTTGGCT 599  
 |||||  
 QY 142 LeuLeuSerLeuPheSerileProValileTyrrGluArgHisGlnValGlnleAspHis 161  
 |||||  
 Db 600 CTGATTTACCTCTTCAGTGTTCTCTGTTATTACGAAACGGCATCAGGCACAAATAGATCAC 659  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysileGlnAlaLysile 181  
 |||||  
 Db 660 TATCTAGGACTTGTCATATAAGAAATGTTAAAGATGCTATGGCTAAATCAAGCAAAATTT 719  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 720 CCTGGATTGAAGCGCAAGCTGAA 743  
 |||||

RESULT 37  
 BM801698  
 LOCUS  
 DEFINITION AGENCOURT\_6458941 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:5558493  
 5', mRNA sequence.

ACCESSION BM801698  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 958)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM12281 row: i column: 22  
 High quality sequence start: 25  
 High quality sequence stop: 579.  
 High quality Location/Qualifiers

1..958

FEATURES  
 source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5558493"  
 /tissue\_type="duodenal adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC 88"  
 /note="Organ: small intestine; Vector: pCMV-SPORT6;  
 Site 1: NotI; Site 2: SalI; Cloned unidirectionally;  
 oligo-dT primed. Average insert size 1.767 kb. Library  
 enriched for full-length clones and constructed by Life  
 Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
 Pred. No.: 1.78e-99 Length: 958  
 Score: 892.00 Matches: 181  
 Percent Similarity: 97.8% Conservative: 3  
 Best Local Similarity: 96.28% Mismatches: 4  
 Query Match: 96.43% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BM801698 (1-958)

QY 2 ValValAspLeuLeuTyrrPheArgAspLeuLysLysThryGlyValValPheGlyAlaSer 21  
 |||||  
 Db 66 GTTGTGACCTCTCTACTGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 125  
 |||||

QY 22 LeuPheLeuLeuLeuSerLeuThrrValPheSerileValSerValThAlaTyrrileAla 41  
 |||||  
 Db 126 CTATTCCTGCTGCTTTTCATTGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTCG 185  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrileSerPheArgileTyrrLysGlyValileGlnAlaile 61  
 |||||  
 Db 186 TTGGCCCTGCTCTCTGTGACCANTAGCTTTTAGGATATACAAGGGTGTGATCCAGCTATC 245  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaileSer 81  
 |||||  
 Db 246 CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGAAGTTGCTATATCT 305  
 |||||  
 QY 82 GluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnSerThrileLys 101  
 |||||  
 Db 306 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTGTGTCATGTGAACCTGCACGATAAG 365  
 |||||  
 QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 366 GAATCAGCGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTGCGATGTTG 425  
 |||||  
 QY 122 MetTropValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrrLeuLeuLeuAla 141  
 |||||  
 Db 426 ATGTGGGATTATACCTATGTTGGTCTGTTTAAATGTTGCTGACACTACTGATTTGGCT 485  
 |||||  
 QY 142 LeuLeuSerLeuPheSerileProValileTyrrGluArgHisGlnValGlnleAspHis 161  
 |||||  
 Db 486 CTCATTTTCACTCTTCAGTGTTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 545  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysileGlnAlaLysile 181  
 |||||  
 Db 546 TATCTACGACTTGCAATPAAGATGCTAAAGATGCTATGGCTTAATCCAGCAAAATC 605  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 606 CCTGGATTGAAGCGCAAGCTGAA 629  
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RESULT 38  
 BG296048  
 LOCUS

DEFINITION 602393712F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4505499 5',  
 mRNA sequence.

ACCESSION BG296048

VERSION BG296048.1 GI:13058293

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 749)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10379 row: 9 column: 04

High quality sequence stop: 745.

FEATURES

Location/Qualifiers

1..749

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:4505499"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_94"



/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dt primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.67e-99 Length: 749  
Score: 891.00 Matches: 183  
Percent Similarity: 98.39% Conservativity: 0  
Best Local Similarity: 98.39% Mismatches: 3  
Query Match: 96.32% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG296048 (1-749)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 125 GTTGTGACCTCTCTGACTGAGACATTAAGAAGACTGGAGTGTGTTGGTGCAGC 184  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 185 TTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCCATCATTCGC 244  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 245 TTGGCCCTGCTCTCTGACTATCAGCTTTAGGATATATAGGTTGATCAAGCTATC 304  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 305 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTGGAATCTGAAGTTGCCATATCA 364  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 365 GAGGAATGGTGTTCAGAAATATAGTAATCTGCTCTGTGTCATGTGAACAGCACATAAAA 424  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 425 GAATGTAGGCGCTCTCTTAGTGTGATGATTTAGTTGATTCCTCCCTGAAGTTGCGAGTTG 484  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 485 ATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTGACACTACTGATTTAGCT 544  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 545 CTGATCTCACCTTCCTGATTCCTGTTATATATGACGGCATCAGCGCGCAGATAGATCAT 604  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 605 TATCTAGGACTTGCANACAGAGCGTTAAGATGCCATGGCCAAATCCAAAGCAAAATCC 664  
Qy 182 ProGlyLeuLysArgLys 187  
Db 665 CTTGGATTGAAGCGCAAG 682

## RESULT 39

BG715173 757 bp mRNA linear EST 08-MAY-2001  
LOCUS 602675631P1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4798279 5',  
DEFINITION mRNA sequence.

ACCESSION BG715173

VERSION BG715173.1 GI:13994106

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 757)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: ccapbs@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LHAM10685 row: n column: 08  
High quality sequence stop: 757.  
Location/Qualifiers  
source  
1. 757

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:4798279"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_96"  
/note="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
(gtcgag); Oligo-dt primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NHGRI/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.69e-99 Length: 757  
Score: 891.00 Matches: 181  
Percent Similarity: 97.87% Conservativity: 3  
Best Local Similarity: 96.28% Mismatches: 4  
Query Match: 96.32% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG715173 (1-757)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 179 GTTGTGACCTCTCTGACTGAGACATTAAGAAGACTGGAGTGTGTTGGTGCAGC 238  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 239 CTATTCCTGCTGCTTCATTCAGCATTTTCAGCATTCGAGCGTAACAGCCTACATGCC 298  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 299 TTGGCCCTGCTCTCTGAGCATTCAGCTTTAGGATATATCAAGGGTGTGATCAAGCTATC 358  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 359 CAGAAATCAGATGAAGGCCACCCATTCGGCGCATTCGGAATCTGAAGTTGCTATATCT 418  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 419 GGGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTTCATGTCATGTGAACCTGCCGATAAG 478  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 479 GAACCTCAGGGCGCTCTCTTAGTTGATGATTTAGTTGATTCCTCTGAAGTTTGCAGTGTG 538  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 539 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTTGGCT 598  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

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Db      599 CTCATTTCAGTCTTCTGCTGTTATTTATGAAGGCATCAGGCACAGATAGATCAT 658
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      659 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAATC 718
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      719 CCTGGATTGAAGCGCAAAAGCTGAA 742

RESULT 40
BU845601
LOCUS   BU845601
DEFINITION AGENCOURT_10414454 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE: 6579264 5', mRNA sequence.
ACCESSION BU845601
VERSION   BU845601.1 GI:24030042
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 924)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone Distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L16W2782 row: e column: 24
          High quality sequence stop: 696.
          Location/Qualifiers
            1..924
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:6579264"
              /tissue_type="teratocarcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH MGC_109"
              /note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:
              XhoI; cDNA made by oligo-dT priming. Directionally cloned
              into EcoRI/XhoI sites using the following 5' adaptor:
              GGCACGAG(G). Library constructed by Ling Hong in the
              laboratory of Gerald M. Rubin (University of California,
              Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
              Superscript II RT (Life Technologies). Note: this is a
              NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 2,99e-99 Length: 924
Score: 890.00 Matches: 180
Percent Similarity: 97.87% Conservative: 4
Best Local Similarity: 95.74% Mismatches: 4
Query Match: 96.22% Indels: 0
DB: 5 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BU845601 (1-924)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyValAsp 21
Db      244 GTGTGTGACCTCTCTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 303
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      304 CTATTCTCTGCTGCTTCTTCACTTGACAGTATTACGACATTGTGAGCGTAACAGCCTACATTGCC 363

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Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      364 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 423
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      424 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAAATCTGAAGTTGCTATATCT 483
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      484 GAGGAGTTGGTTCAAGAGTACAGTAATCTCTGCTCTTGGTCATGTGAACCTGCACGATAAG 543
Qy      102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121
Db      544 GAACTCAGGCGCCTCTTCTTAGTTGATGATTAGTTAGTTGATTCTCTGAAGTTTGCAGTGTG 603
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAla 141
Db      604 ATGTGGGTATTACTATGTTGGTGCCCTGTTTAAATGGTCTGACACTACTGATTTTGGCT 663
Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      664 CTCAATTCACCTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 723
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      724 TATCTAGGACTTGCAAAATGAAGATGTTNAAGATGCTATGGCTAAANATCCAAGCAAAATC 783
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      784 CCTGGATGAAGCGCAAAAGCTGAA 807

RESULT 41
BU805577
LOCUS   BU805577
DEFINITION ILLUMIGEN MQC_36873 Katze_MBR Macaca mulatta cDNA clone
IBIUM:12670 5' similar to Bases 138 to 1022 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
ACCESSION BU805577
VERSION   BU805577.1 GI:47701553
KEYWORDS EST.
SOURCE    Macaca mulatta (rhesus monkey)
ORGANISM  Macaca mulatta
REFERENCE 1 (bases 1 to 1042)
AUTHORS   Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
TITLE     Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL   Unpublished (2003)
COMMENT   Contact: C. Magness
          Illumigen Biosciences Inc.
          2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
          Tel: 2063780400
          Fax: 2063780408
          Email: cmagness@illumigen.com
          Sequenced on 2004.05.12. 633 Q20 bases.
          PCR Primers
          FORWARD: CCCTCACTAAAGGGAACAAAA
          BACKWARD: CACTATAGGCGAATTGGGTA
          Insert Length: 1042 Std Error: 0.00
          Plate: CL000243 row: C column: 03
          Seq primer: CCCTCACTAAAGGGAACAAAA
          POLYA=Yes.
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            1..1042
              /organism="Macaca mulatta"
              /mol_type="mRNA"
              /strain="Indian"
              /db_xref="taxon:9544"
              /clone="IBIUM:12670"
              /sex="female"
          FEATURES
            source

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/dev stage="adult"
/lab host="E. coli SOLR"
/clone lib="Katze.MMR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Strategene ZAP-cDNA Synthesis
Kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3.54e-99 Length: 1042
Score: 890.00 Matches: 180
Percent Similarity: 98.40% Conservative: 5
Best Local Similarity: 95.74% Mismatches: 3
Query Match: 96.22% Indels: 0
DB: 7 Gaps: 0

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US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN805577 (1-1042)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 138 GTTGTGACCTCTCTACTGAGAGACATGAAGAGACTGGTGGTGTGGTGGCCAGC 197
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 198 CTATTCCTGCTGCTTTCATTCACAGTATTCAGCATTTGAGTGTGAACAGCCTACATTGCC 257
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 258 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCAAGCTATC 317
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 318 CAGAAATCAGATGAGGCCACCCATTTCAGGCATATCTGGAAATCTGAAGTTGCCATATCT 377
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 378 GAGGAGTGGTTCAGAACTACAGTAATCTCTCTCTGTCATGTGAACTGCACGATTAAG 437
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 438 GAATCTCAGGCCCTCTCTCTAGTTAGTATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 497
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 498 ATGTGGGTATTTACTATGTGGTGGCTTTGTTTAAATGCTCTGACGCTACTGATTTGGCT 557
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 558 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 617
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIleAla 181
Db 618 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCGAAATC 677
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 678 CTGGATTTGAAGCGCATAGCTGAA 701

```

## RESULT 42

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CD110203
LOCUS CD110203
DEFINITION AGNCOURT_13994940 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30331865 5', mRNA sequence.
ACCESSION CD110203
VERSION CD110203.1 GI:30754412
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/

```

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Straubeberg, Ph.D.  
 Email: csapsb@mail.nih.gov  
 Tissue Procurement: Dr. Stefan Hansson  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
 and advice from Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDAM347 row: p column: 18  
 High quality sequence stop: 630.

## FEATURES

source

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1..871
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30331865"
/tissue_type="pre-eclatptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/notes="Organ: placenta; Vector: pBluescriptR; Site 1:
ali-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

```

## ORIGIN

## Alignment Scores:

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Pred. No.: 3.65e-99 Length: 871
Score: 889.00 Matches: 182
Percent Similarity: 98.41% Conservative: 4
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.11% Indels: 1
DB: 6 Gaps: 0

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US-09-830-972-2\_COPY\_975\_1163 (1-189) x CD110203 (1-871)

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Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 187 GTTGTGACCTCTCTGTTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 246
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 247 CTATTCCTGCTGCTTTCATTCAGCAGTATTCAGCATTTGAGCCTAACAGCCTACATTGCC 306
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 307 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCAAGCTATC 366
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 367 CAGAAATCAGATGAGGCCACCCATTTCAGGCATATCTGGAAATCTGAAGTTGCTATATCT 426
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 427 GAGGAGTGGTTCAGAACTACAGTAATCTGCTCTTGGTCAATGTAAGTGCACGATAAG 486
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 487 GAATCTCAGGCCCTCTCTCTAGTTAGTATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 546
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 547 ATGTGGGTATTTACTATGTTGGTGGCTTGTAAATGCTGTCGACACTACTGATTTGGCT 606

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QY 142 LeuileSerLeuPheSerileProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 607 CTCATTCTACTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 666  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 667 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCNAATC 726  
 QY 182 ProGlyLeu-LysArgLysAlaAsp 189  
 Db 727 CCTGGAATCAAAAGCGCAAGCTGAA 751

RESULT 43  
 BU503291  
 LOCUS AGENCOURT\_8933519 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6490526  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BU503291  
 VERSION BU503291.1 GI:22809480  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 921)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
 http://image.llnl.gov  
 Plate: LLAM14040 row: h column: 15  
 High quality sequence stop: 627.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6490526"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

FEATURES  
 source  
 1..921  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6490526"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 6,99e-99 Length: 921  
 Score: 887.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 1  
 Query Match: 95.89% Indels: 1  
 DB: 5 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU503291 (1-921)

QY 2 ValValAspLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGACCTCTGCTGACAGACATTAAGAGACTGGAGTGGTGTGGTCCAC 215  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraIleAla 41  
 Db 216 TTATTCTGCTGCTGCTGACAGTGTTCAGCATTTGTCAGTGTAAACGGCTACATTGCC 275

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 335  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAGAANTCAGATGAAGCCACCCATTACGGCATATTTGGAAATCTGAAGTTCCTCCATATCA 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 396 GAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTCTTGTTCATGTGAACAGCAATAAAA 455  
 QY 102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAAATTGAGCGCTCTCTTCTTAGTTAGTATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 515  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 516 ATGTGGGTATTTACTTACGTGGTCCCTTGTTCAATGGTTTGACACTACTGATTTAGCT 575  
 QY 142 LeuLeuSerLeuPheSerileProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 576 CTGATCTCCTCTTCAGTATTTCTGTTATATATGAACGGCATCAGGCGCAGATAGATCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 636 TATCTAGGACTTGCAACACAGAGCGTTAAGGATGCCATGGCCCAATCCAGCAAAATC 695  
 QY 182 Pro-GlyLeuLysArgLysAla 188  
 Db 696 CCTGGATTGAAGCCCAAGC 717

RESULT 44  
 CO048918  
 LOCUS ILLUMIGEN\_MCO\_38898 Katze.MBR Macaca mulatta cDNA clone  
 DEFINITION IBIUW:16203 5', similar to Bases 112 to 991 highly similar to human  
 RTN4 (hs.436349), mRNA sequence.  
 ACCESSION CO048918  
 VERSION CO048918.1 GI:48688540  
 KEYWORDS EST.  
 SOURCE Macaca mulatta (rhesus monkey)  
 ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 Cercopithecinae; Macaca.  
 1 (bases 1 to 1013)  
 Katze.M.G., Thomas.M., Korth.M., Iadonato.S.P. and Magness,C.L.  
 Large-scale Rhesus Macaque cDNA Sequencing  
 Unpublished (2003)  
 Contact: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com  
 Sequenced on 2004.05.13. 609 Q20 bases. Library Preparation: Prof.  
 Michael Katze Lab at University of Washington DNA Sequencing:  
 Illumigen Biosciences Inc. For further information, see  
 http://www.macaque.org  
 PCR Primers  
 FORWARD: CCTCCTAAAGGGAACAAA  
 BACKWARD: CACTATAGGCGGAATGGTA  
 Insert Length: 1013 Std Error: 0.00  
 Plate: CLO00160 row: G column: 08  
 Seg primer: CCCTCACTAAAGGGAACAAA  
 POLYA=Yes.  
 Location/Qualifiers  
 1..1013  
 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
 /strain="Indian"  
 /db\_xref="taxon:9544"

FEATURES  
 source  
 1..1013  
 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
 /strain="Indian"  
 /db\_xref="taxon:9544"

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/clone="IBIUW:16203"
/sex="female"
/dev stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MBR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

```

## ORIGIN

## Alignment Scores:

```

Pred. No.:      1,41e-98      Length:      1013
Score:          885.00        Matches:      181
Percent Similarity: 98.41%    Conservative: 5
Best Local Similarity: 95.77% Mismatches: 2
Query Match:     95.68%      Indels: 1
DB:              7          Gaps: 0

```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x C0048918 (1-1013)

```

Qy  2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db  112 GTTGTTCACCTCCCTACTCGAGACATGAGAGACTGGAGTGGTGTGGTCCAGC 171
Qy  22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db  172 CTATTCCTGCTGCTTTCATGACAGTATTACGCAATTGGAGTGTAAACGCTCATTTGCC 231
Qy  42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db  232 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGTATC 291
Qy  62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db  292 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGGAATTTGGCATATCT 351
Qy  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db  352 GAGAGTGGTTCAGAGTACAGTAATCTGCTTTGGTCAATGTAAGTGCACGATTAAG 411
Qy  102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db  412 GAACCTCAGGCCCTCTCTTAGTTGATGATTAGTTGATTTGATTCTCTGAAATTTGCAGTGTG 471
Qy  122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db  472 ATGTGGGTATTACCTATGTTGGTCCCTGTTTAATGCTCTGACGCTACTGATTTGGCT 531
Qy  142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db  532 CTCAATTCACCTCTTCAGTGTCTCTGTTATTATGACGGCATCAGGCACAGATAGATCAT 591
Qy  162 TyrLeuGlyLeuAlaAsnLysSer-ValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db  592 TATCTAGGACTTGCATAAAGATGGTTAAAGATGCTATGCTAAATCCAAAGCGAAT 651
Qy  181 eProGlyLeuLysArgLysAlaAsp 189
Db  652 CCCTGGATTGAAGCGCAAGCTGAA 676

```

## RESULT 45

```

CN801888      1018 bp      mRNA      linear      EST 26-MAY-2004
LOCUS      ILLUMIGEN MCQ 37222 Katze_MBR Macaca mulatta cDNA clone
DEFINITION      IBIUW:16016 5' similar to Bases 146 to 1018 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
ACCESSION      CN801888
VERSION      CN801888.1 GI:47697864
KEYWORDS      EST.
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM      Macaca mulatta
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopitheciinae; Macaca.

REFERENCE  
1 (bases 1 to 1018)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Katze, M.C., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.  
Large-scale Rhesus Macaque cDNA Sequencing  
Unpublished (2003)  
Contact: C. Magnus  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagnus@illumigen.com  
Sequenced on 2004.05.14. 594 Q20 bases.  
PCR Primers  
FORWARD: CCCTCACTAAAGGGAACAAAA  
BACKWARD: CACTATAGGGCGAATGGGTA  
Insert Length: 1018 Std Error: 0.00  
Plate: CL000272 row: E column: 10  
Seq primer: CCCTCACTAAAGGGAACAAAA  
POLYA=No.

FEATURES  
source

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1..1018
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:16016"
/sex="female"
/dev stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MBR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

```

## ORIGIN

## Alignment Scores:

```

Pred. No.:      1,42e-98      Length:      1018
Score:          885.00        Matches:      181
Percent Similarity: 98.41%    Conservative: 5
Best Local Similarity: 95.77% Mismatches: 2
Query Match:     95.68%      Indels: 1
DB:              7          Gaps: 0

```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN801888 (1-1018)

```

Qy  2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db  146 GTTGTTCACCTCCCTACTCGAGACATGAGAGACTGGAGTGGTGTGGTCCAGC 205
Qy  22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db  206 CTATTCCTGCTGCTTTCATTCAGCATATTCAGCATTTGAGTGTAAACGCTCATATTGCC 265
Qy  42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db  266 TTGSCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTATCCAAAGCTATC 325
Qy  62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db  326 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGGAATTTGGCATATCT 385
Qy  82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db  386 GAGAGTGGTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTAAGTGCACGATTAAG 445
Qy  102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db  446 GAACCTCAGGCCCTCTCTTAGTTGATGATTAGTTGATTTGATTCTCTGAAATTTGCAGTGTG 505
Qy  122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

```

Db 506 ATGTGGTATTACCTATGTTGGTGGCTTTGTTAATAGTCTGACGCTACTGATTTGGCT 565  
 QY 142 LeuileSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHis 161  
 Db 566 CTATTTCACTCTTCAGTGTCTCTGTTATTTATGAAGCGCATCAGGCACAGATAGATCAT 625  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnIleLysIle 181  
 Db 626 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCCGAAAT 685  
 QY 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 686 CCTGTGATTGAAGCGCAAGCTGAA 710

## RESULT 46

LOCUS BG623462 747 bp mRNA linear EST 18-APR-2001  
 DEFINITION 602648520F1 NIH\_MGC\_79 Homo sapiens cDNA clone IMAGE:4770077 5',  
 mRNA sequence.

ACCESSION BG623462.1 GI:13674833

VERSION EST.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM1636 row: g column: 06

High quality sequence stop: 742.

## FEATURES

source

1..747

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4770077"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH MGC 79"

/note="Organ: placenta; Vector: pDNR-LIB (Clontech);

Site 1: Sfil (ggccgctcgcc); Site 2: Sfil

(ggccattatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence:

5'-ATTCTAGCGCGGCGCGCACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.3

Kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:

Pred. No.: 1.62e-98 Length: 747

Score: 883.00 Matches: 179

Percent Similarity: 96.81% Conservative: 3

Best Local Similarity: 95.21% Mismatches: 6

Query Match: 95.46% Indels: 0

DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG623462 (1-747)

QY 2 ValValAspLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

Db 133 GTTGTGACCTCCCTGCTACTGGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 192  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAla 41  
 Db 193 CTATTCCTGCTGCTTCATTCACAGTATTCAGCATTTGAGCGTAACAGCCTACATGGC 252  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAla 61  
 Db 253 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCTATC 312  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSer 81  
 Db 313 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAAATCTGAAGTTGCTATATCT 372  
 QY 82 GluGluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 373 GAGGAGTTGGTTCAGAACTACAGTAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 432  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 433 GAACCTCAGCGCCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTGTG 492  
 QY 122 MetTrpValPheThrTyValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 493 ATGTGGGTATTTACCTATGTTGGGCCCTGTTTATGTTCTGACACTGACTGATTTGGCT 552  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHis 161  
 Db 553 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAAGCGCATCAGGCACAGATAGATCAT 612  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 613 TATCTAGGACTTGCAAAATGAAGATGTTTACAGATGCTTATGGTAAATCCAGCAAAATC 672  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 673 CCTGATTGAAGCGCAAGTGAAT 696

## RESULT 47

LOCUS BG740561

DEFINITION

602633075F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4778131 5',

mRNA sequence.

ACCESSION BG740561

VERSION BG740561.1 GI:14051214

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 758)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM10633 row: f column: 20

High quality sequence stop: 743.

Location/Qualifiers

1..758

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4778131"

/lab\_host="DH10B (T1 phage-resistant)"

/clone.lib="NCI\_CGAP\_Skn3"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.93e-98 Length: 758  
 Score: 881.00 Matches: 181  
 Percent Similarity: 97.35% Conservative: 3  
 Best Local Similarity: 95.77% Mismatches: 4  
 Query Match: 95.24% Indels: 1  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG740561 (1-758)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 130 GTTGTTCACCTCTCTGACGACATTAAGAAGACTGGAGTGGTGTGGTCCGACG 189  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 190 CTATTCTCTGCTCTTTCATTGACAGTATTGACGATTTGAGCGTAACAGCCTACATTGCC 249  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 250 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 309  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 310 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGGAATGCTATATCT 369  
 Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 370 GAGGAGTNGGTTTCAGAGTACAGTAATTCCTCTTGGTCAATGTAAGTGCACGATAAG 429  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 430 GAATCAGCGCCCTCTTCTTAGTGTAGTATTAGTTGATTTCTGAAAGTTGCGAGTTG 489  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 490 ATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGCTGACACTACTGATTTGGCT 549  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 550 CTCATTTTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 609  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLys-AspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 610 TATCTAGGACTTGCATATAGAAATGTTTACAGATGCTATGCTAAATCCAGCAAAAT 669  
 Qy 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 670 CCCTGGATTGAAGCGCAAGCTGAA 694

## RESULT 48

NC641703 1081 bp mRNA linear EST 12-MAY-2004  
 ILLUMIGEN MCQ 5216 Katze.MBR Macaca mulatta cDNA clone IBIUM:6014  
 5' similar to Bases 156 to 1013 highly similar to human RTN4  
 (Hs.436349), mRNA sequence.

NC641703 GI:47152713

## ACCESSION

VERSION NC641703.1

KEYWORDS EST.

## SOURCE

ORGANISM Macaca mulatta (rhesus monkey)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecoidea; Cercopithecoidea; Cercopithecoidea;

## REFERENCE

1 (bases 1 to 1081)  
 Katze.M.G., Thomas.M., Korth.M., Iadonato.S.P. and Magness.C.L.

Large-scale Rhesus Macaque cDNA Sequencing

## JOURNAL

COMMENT

Unpublished (2003)  
 Contact: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2003.12.04. 735 Q20 bases.

PCR Primers

FORWARD: CCCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGGGCGAATTTGGTGA

Insert Length: 1081 Std Error: 0.00

Plate: CL000043 row: H column: 10

Seq primer: CCCTCACTAAAGGGAACAAA

POLYA-Yes.

## FEATURES

source

1..1081

/organism="Macaca mulatta"

/mol\_type="mRNA"

/strain="Indian"

/db\_xref="taxon:9544"

/clones="IBIUM:6014"

/sex="female"

/dev\_stage="adult"

/lab\_host="E. coli SOLR"

/clone\_lib="Katze MBR"

/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: Ecor I;

Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis

kit (catalog #200400) and ZAP-CDNA Gigapack III Gold

Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.85e-98 Length: 1081  
 Score: 881.00 Matches: 180  
 Percent Similarity: 97.88% Conservative: 5  
 Best Local Similarity: 95.24% Mismatches: 3  
 Query Match: 95.24% Indels: 1  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN641703 (1-1081)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTTCACCTCTCTGACGACATTAAGAAGACTGGAGTGGTGTGGTCCGACG 215  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 216 CTATTCTCTGCTCTTTCATTGACAGTATTGACGATTTGAGCGTAACAGCCTACATTGCC 275  
 Qy 42 LeuAlaLeuLeuSerValThrIle-SerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 335  
 Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
 Db 336 CCAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGAGTTGGATATC 395  
 Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLy 101  
 Db 396 TGAGGAGTTGGTTCAGAAATACAGTAATTCCTCTCTGGTTCATGTGAACATGCACGATAA 455  
 Qy 101 sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLe 121  
 Db 456 GGAATCTCAGCGCCCTCTTCTTAGTGTAGTATTTAGTTGATTTCTGAAAGTTTGAGTGT 515  
 Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 516 GATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGCTGACGCTACTGATTTGGC 575  
 Qy 141 aLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161



Db 576 TCTATTCTCCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACACATAGATCA 635  
 QY 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 636 TTATCTAGGACTGCAATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCGAAAT 695  
 QY 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 696 CCTGGATTGAAGCGCAAGCTGAA 720

RESULT 49  
 CO259245  
 LOCUS 4130644 BARC 8BOV Bos taurus mRNA linear EST 23-JUN-2004  
 DEFINITION 4130644 BARC 8BOV Bos taurus cDNA clone 8BOV\_51K20 5', mRNA

ACCESSION CO259245  
 VERSION CO259245.1 GI:49144047  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 585)  
 AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and Matukumalli,L.K.  
 TITLE Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle

JOURNAL Unpublished (2004)  
 COMMENT Contact: Richard G. Baumann  
 Bovine Functional Genomics Lab  
 ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604  
 Fax: 3015048744

Email: rbaumann@nri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim\_alt '- -trim\_fasta. Vector identified by cross\_match using options -minmatch 12 -minscore 12

Plate: 51 row: K column: 20

Seq primer: CCTATTAGTGCACACTATAGAAC

High quality sequence stop: 585.

FEATURES  
 source

1..585  
 Location/Qualifiers  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /strain="Holstein"  
 /db\_xref="taxon:9913"  
 /clone="8BOV\_51K20"  
 /sex="Female"

/tissue\_type="Epithelial, Muscle"  
 /dev\_stage="Lactating, Neonatal"  
 /lab\_host="DH10B Tona"  
 /clone\_lib="BARC 8BOV"  
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site\_1: Notri; Site\_2: EcoRI; Normalized cow cDNA intestinal library in pCMVSPORT6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"

ORIGIN

Alignment Scores:

Pred. No.: 2,69e-98 Length: 585  
 Score: 880.00 Matches: 179  
 Percent Similarity: 98.37% Conservative: 2  
 Best Local Similarity: 97.28% Mismatches: 3  
 Query Match: 95.14% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CO259245 (1-585)

QY 2 ValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 32 GTTGTGTACCTCCCTCTACTGAGAGACATTAAAGAACTGGAGTGGTGTCCGGTCCAGC 91  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 92 TTGTTCTCTGCTGCTCTGCTGACAGTATTACGATTTGAGTGTAAACGGCTACATTGCC 151  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 152 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGGTGTGATCCAGGCTATC 211  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 212 CAGAAATCTGATGAAGGCCACCCATTCAGGCGATATTTGGAATCTGAAGTTGCTATATCT 271  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 272 GAGGAGTTGGTTTCAGAGTACAGCAATCTCTGCTCTTGGTCACTGTTAACTGCACATAAAA 331  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuPheAlaValLeu 121  
 Db 332 GAATCAGACGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 391  
 QY 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 392 ATGTGGGTATTTACCTATGTTGGTGCCTTGTCTCAATGGTCTGACACTACTAATTTTGGCT 451  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 452 CTGATTTCACTCTTCAGTGTTCTGTTATTATGAACGGCATCAGGCCCAATAGATCAT 511  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 512 TATCTGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAATC 571

QY 182 ProGlyLeuLys 185  
 Db 572 CTGTGATTGAAG 583

RESULT 50

BI838242

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 742)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgsbbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: L1AM11559 row: k column: 15

High quality sequence stop: 734.

Location/Qualifiers

1..742

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5222534"

FEATURES

source



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/lab host="DH10B"
/clone lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3,78e-98 Length: 742
Score: 880.00 Matches: 181
Percent Similarity: 97.35% Conservativeness: 3
Best Local Similarity: 95.77% Mismatches: 4
Query Match: 95.14% Indels: 1
DB: 4 Gaps: 0

```

```

US-09-830-972-2_COPY_975_1163 (1-189) x BF838242 (1-742)

```

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPhe-GlyAlaSe 21
Db 135 GTTGTGACCTCTCTGACCATCAGATTAAAGACCTGAGTGGTGTGGTGGCCAG 194
Qy 21 rLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAl 41
Db 195 CCTATTCCTGCTCTTTCATTGACAGTATTGAGCAATGTCGCGTAACAGCCTACATTGC 254
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaI 61
Db 255 CTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTAT 314
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 315 CCAGAAATCAGATGAAGCCACCCATTTCAGGCGATATCTGGAATCTGAAGTTGCTATATC 374
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLy 101
Db 375 TGAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTGCTCATGTAACCTGCACGATAA 434
Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 121
Db 435 GGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGAGTGT 494
Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl 141
Db 495 GATGGGTATTTACCTATGTTGGTCTGTTGTTAAATGCTGACACTTACTGATTTTGGC 554
Qy 141 aLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161
Db 555 TCTCATTTTCATCTTTCAGTGTCTCTGTTTATTTATGAACGGATCAGGCACAGATAGATCA 614
Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIl 181
Db 615 TTATCTAGACTTTCGAAATAGATGTTTAAAGATGCTATGCTAAATCCAGCAAAAT 674
Qy 181 eProGlyLeuLysArgLysAlaAsp 189
Db 675 CCCTGGATTGAAGCGCAAGTGAAT 699

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RESULT 51
CN219472
LOCUS CN219472 821 bp mRNA linear EST 08-APR-2004
DEFINITION WLA006H01.ab1 Wlbrain Gallus gallus cdna 5', mRNA sequence.
ACCESSION CN219472
VERSION CN219472.1 GI:46298814
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
AUTHORS Savolainen,P., Fitzsimmons,C.J., Arvestad,L., Andersson,L. and
Lundeberg,J.
TITLE EST analysis of brain and testis cDNA libraries from White leghorn
and Red Jungle Fowl
JOURNAL Unpublished (2004)
COMMENT Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5537 8481
Fax: +46 (0)8 5537 8335
Email: Peter.Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.
FEATURES
source
1..821
/organism="Gallus gallus"
/mol type="mRNA"
/strain="White Leghorn"
/db xref="taxon:9031"
/sex="female"
/lab host="Electromax DH10B (Invitrogen)"
/clone lib="Wlbrain"
/note="Organ: brain; Vector: pSPORT-1; Site 1: Hind III;
Site 2: EcoRI; The cDNA libraries were created with the
Superscript Plasmid System (Invitrogen)."
```

## ORIGIN

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Alignment Scores:
Pred. No.: 3,21e-97 Length: 821
Score: 873.00 Matches: 173
Percent Similarity: 97.31% Conservativeness: 8
Best Local Similarity: 93.01% Mismatches: 5
Query Match: 94.38% Indels: 0
DB: 7 Gaps: 0

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US-09-830-972-2_COPY_975_1163 (1-189) x CN219472 (1-821)

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```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db 177 GTTGTGACCTCTCTTACTGCGGACATTAAGAAGACAGGAGTGGTGTGGTGGCCAGC 236
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 237 TTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTCGCGTACAGCTTACATGCC 296
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
Db 297 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCAATC 356
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 357 CAAAGTCCGATGAAGCCATCCATTAGGCTTACTTGGAGTCTGTAGTGTAGTGTGTCT 416
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 417 GAAGAGCTGATTCAGAAATACAGAGTGTGTGCTTCATCATCAACGGCACAGTCAAG 476
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 477 GAGCTGAGAGCCCTCTTCCCTCGTTGATGACTTGTGTTGATTTCTCTGAGTTTGCAGTGTG 536
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 537 ATGTGGTGTTCATCTACCTGTTGGTCCCTGTTTAAATGCTCTGACATTACTACTGGCT 596
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 597 TTGATTTTCGCTGTTCAGTGTTCCTGTTATTTATCAGAGACATCAGGCCCATGACCAT 656
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

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|||||
657 TATTGGGACTAGTACAGACGCTCAAGATGCGGCAAGATCCAGCAAGATC 716
|||||
182 ProGlyLeuLeuArgLys 187
|||||
717 CCTGGGCTGAAGCGCAA 734

RESULT 52
BG699748 784 bp mRNA linear EST 07-MAY-2001
602681431F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4814382 5',
mRNA sequence.
ACCESSION BG699748
VERSION BG699748.1 GI:13968365
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10709 row: m column: 07
High quality sequence stop: 747.
FEATURES
Location/Qualifiers
1..784
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4814382"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 4e-97 Length: 784
Score: 872.00 Matches: 182
Percent Similarity: 97.88% Conservative: 3
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 94.27% Indels: 2
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BG699748 (1-784)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 169 GTTGTGACCTCTGTACTGGAGACATTAGAGACTGGAGTGGTGTGGTGGCCAGC 228
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 229 CTATTCTCTGCTTTTCATTGACAGTATTTCAGCATTTGAGCGGTAAACAGCTACATTGCC 288

```

```

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 289 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAAGCTATC 348
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 349 CAGAAATCAGATGAGGCCACCCATTAGGGCATATCTGGAAATCTGAAGTTGCTATATCT 408
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 409 GAGGAGTTGGTTTCAGAACTACAGTAATCTGCTCTTGGTTCATGTCAACTGCACGATAAAG 468
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 469 GAACCTCAGCGCCCTCTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTGCAAGTTG 528
Qy 122 MetTrpValPheThrTyrValGlyAla-LeuPheAsnGlyLeuThrLeuLeuAla 141
Db 529 ATGTGGGTATTTACCTAATGTTGGTCCCTTTGTTTAATGCTGTGACACTACTGATTTTGGC 588
Qy 141 AleuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161
Db 589 TCTCATTTCACTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCA 648
Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
Db 649 TTATCTAGGACTTGCAAAATAAGAAATGTTCAAGATGCTATGGCTAAATATCCAAAGCAAAAT 708
Qy 181 eProGly-LeuLysArgLysAla 188
Db 709 CCTGGATTGAAGCGCAAGCT 731

RESULT 53
CA322433 817 bp mRNA linear EST 09-JUL-2003
LOCUS UI-M-FX0-cck-n-21-0-UI.r1 NIH_BMAP_FX0 Mus musculus cDNA clone
CA322433 IMAGE:6820918 5', mRNA sequence.
ACCESSION CA322433
VERSION CA322433.1 GI:24540531
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1..817
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6820918"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpb"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FX0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;

```

Site 2: Not 1; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.24e-97 Length: 817  
 Score: 872.00 Matches: 186  
 Percent Similarity: 97.40% Conservative: 1  
 Best Local Similarity: 96.88% Mismatches: 2  
 Query Match: 94.27% Indels: 3  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CA322433 (1-817)

Qy 1 SerValValAspLeuLeu-TyrTrp-ArgAspIleLysLysThrGlyValValPheGlyA 20  
 Db 41 TCAGTTGTGACCTCTGTTACTGGGAGACATTAAGACCTGGAGTGTGTGTG 100  
 Qy 20 laSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrI 40  
 Db 101 CCAGCTTATCTGCTGCTCTCTGACAGTGTTCAGCATTTGTTCAGTGAAGCCATCA 160  
 Qy 40 leAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnA 60  
 Db 161 TTGGCTTTGGCCCTGCTCTCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAG 220  
 Qy 60 laIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaI 80  
 Db 221 CTATCCAGAAATCAGATGAAGCCACCATTTCAGGCATATTTGGAACTCGAAGTTCGCA 280  
 Qy 80 leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI 100  
 Db 281 TATCAGAGGAATTGGTTCCAGAAATATAGTAAATCTGCTCTTGGTCATGTGAACAGCACAA 340  
 Qy 100 leLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 341 TAAAGAAATTCAGGCGTCTCTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTTCGAG 400  
 Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL 140  
 Db 401 TGTGATGTGGGTATTTACTTACGTGTGGTGGTCTTGTTCATGATGTTGACACTACTGATTT 460  
 Qy 140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160  
 Db 461 TAGCTCTGATCTCACTCTTCACTATCTCTGTTATATATGACCGCATCAGCGCAGATAG 520  
 Qy 160 spHisTyrLeuGlyLeuAlaHisLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180  
 Db 521 ATCATATTATAGGACTTGCACAAACAGAGCGTTAAGGATGCCATGCCCAAAATCCAAGCAA 580  
 Qy 180 ysIlePro-GlyLeuLysArgGlyAlaAsp 189  
 Db 581 AAATCCCTGGGATTTGAAGCGCANAGCAGAA 610

## RESULT 54

BI872386

## LOCUS

603397035F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5400584 5',

## DEFINITION

mRNA sequence.

## ACCESSION

BI872386

## VERSION

BI872386.1 GI:16046048

## KEYWORDS

SOURCE EST. Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)

## AUTHORS

Unpublished (1999)

## JOURNAL

Contact: Robert Strausberg, Ph.D.

## COMMENT

Email: cga@remail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM2021 Row: f Column: 09  
 High quality sequence stop: 754.

## FEATURES

## source

1..857  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5400584"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_94"  
 /notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.53e-97 Length: 857  
 Score: 872.00 Matches: 186  
 Percent Similarity: 97.89% Conservative: 0  
 Best Local Similarity: 97.89% Mismatches: 1  
 Query Match: 94.27% Indels: 3  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BI872386 (1-857)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 130 GTTGTTCACCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGTGTGTGTCGCCAGC 189  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 190 TTATTCCTGCTGCTGCTCTGACAGAGTGTTCAGCATTTGTCAGTGTGAACGGCTCATTTGCC 249  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 250 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCATATC 309  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 310 CAGAAATCAGATGAAGCCACCCCATTCAGGCGCATTTTGAATCTGAAGTTGCCATATCA 369  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 370 GAGGAATTTGGTTCCAGAAATATAGTAAATCTGCTCTTGGTCATGTGAACAGCACCAATAA 429  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 430 GAATTGAGGGGTCTCTCTTAGTTGATGATTTAGTTAGTTCCCTGAAGTTTGCAGTGTG 489  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 490 ATGTGGGTATTTACTTACGTGTGGTGGTCTTGTCAATGGTTGTGACACTACTGATTTAGCT 549

QY 142 Leu1SerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 550 CTGATCTCACTCTTCAGTATTCTCTGTATATATGAACGGCATCAGCGCGAGATAGATCAT 609  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla-LysIleGlnAla-LysI 181  
 Db 610 TATCTAGGACTTGCAAAACAGAGCGTTAAGGATGCCATGGCCAAATAATCCAGCAAAAA 669  
 QY 181 LeProGlyLeu-LysArgLysAla 188  
 Db 670 TCCCTGGATTGGACGGCAAGCA 693

RESULT 55  
 C0504431  
 LOCUS  
 DEFINITION  
 clone GGEZCB1023A09, chicken breast muscle - CB1 Gallus gallus cdna

ACCESSION  
 C0504431  
 VERSION  
 EST.  
 SOURCE  
 Gallus gallus (chicken)

ORGANISM  
 Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE  
 1 (bases 1 to 647)  
 Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,  
 Patricio,M., Ledur,M.C. and Coutinho,L.L.  
 Discovery of new genes expressed in the chicken breast muscle  
 Unpublished (2004)

AUTHORS  
 Contact: Helena J. Alves  
 Laboratory of Animal Biotechnology, Dep. of Animal Production  
 ESAUQ - University of Sao Paulo  
 Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
 Tel: 55 19 3429 4434  
 Fax: 55 19 3429 4285  
 Email: hjalves@esauq.usp.br and llcoutin@esauq.usp.br

PCR Primers  
 BACKWARD: T7.

FEATURES  
 source

Location/Qualifiers  
 1..647  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="GGEZCB1023A09"  
 /tissue\_type="breast muscle"  
 /dev\_stage="1 and 21 days old"  
 /lab\_host="DH5 alpha"  
 /clone\_lib="chicken breast muscle - CB1"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This  
 cdna library was constructed with the SuperScript plasmid  
 System with Gateway Technology kit (Invitrogen), following  
 manufacturer's protocols. Plasmid DNA was purified using a  
 modified alkaline lysis method. Sequencing reactions were  
 conducted using the DYNamic Cycle Sequencing Kit for  
 MegabACE (Amersham Biosciences) according to the  
 manufacturer's recommendations. Clones were sequenced by  
 the 5' end with T7 primer. Sequencing reactions were  
 analyzed on MegabACE1000 DNA Sequencer (Amersham  
 Biosciences). The quality and clustering of the ESTs were  
 analyzed using the softwares Phred/Cap3. Only EST  
 sequences with Phred quality greater than 20 and at least  
 150 bp were considered for clustering."

ORIGIN

Alignment Scores:  
 Pred. No.: 4,048-97 Length: 647  
 Score: 871.00 Matches: 172  
 Percent Similarity: 96.81% Conservative: 10  
 Best Local Similarity: 91.49% Mismatches: 6  
 Query Match: 94.16% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x C0504431 (1-647)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 54 GTTGTGGACCTCCCTTACTGCGGAGACATTAAAGACAGAGTGGTGTGGTCCAGC 113

QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 114 TTGTTCTCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTCGC 173

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 174 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC 233

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 234 CAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTTGGAGTCTGTAGTGTAGCTGTGCT 293

QY 82 GluGlnLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 294 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTTGTGTGCATCATCAACGGCAGCAGTCAAG 353

QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 354 GAGCTGAGACGCCCTCTCTCGTTGATGACTTGGTTGATTTCTGAAAGTTTGCAGTGTG 413

QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 414 ATGTGGGTGTTCACTTACGTTGGTGGCTTGTATTAATGCTGTGACATTACTGATCTGGCT 473

QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 474 TTGATTTCTGCTGTTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCCATCGACCAT 533

QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 534 TATTTGGGAGCTAGTGACACAGACGTCAAGATGCGATGGCAAGATCCAAAGCAAGATC 593

RESULT 56

BG699274

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

BG699274

VERSION

BG699274.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 774)

AUTHORS

NIH-MGRC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILLNL at:

http://image.llnl.gov

Plate: L1AM10702 row: 1 column: 11

High quality sequence stop: 774.

FEATURES

Location/Qualifiers

1..774

SOURCE

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4811674"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/notes="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTATTTTATTTTATTTN-3', size-selected for average insert size 2.5 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 6,94e-97 Length: 774
Score: 870.00 Matches: 181
Percent Similarity: 97.37% Conservative: 4
Best Local Similarity: 95.26% Mismatches: 3
Query Match: 94.05% Indels: 2
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BG699274 (1-774)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db 169 GTTGTGACCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 348

Qy 22 LeupheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 229 CTATTCTCGCTGCTTTCATTGACAGATTCAGCATTTGTGAGCGTAACAGCCCTACATTGCC 288

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 289 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 348

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 349 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGATATCT 408

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 409 GAGGAGNTGGTTTCAGAGATACAGTAATCTCTGCTCTGTCATGTGAACCTGCACGATAAG 468

Qy 102 GluLeuArgArgLeuPheLeu-LeuValAspLeuValAspSerLeuLysPheAlaValLe 121
Db 469 GAACCTCAGCGCCCTCTCTTAGCTTGATTTAGTTAGTTCTCTGGAAGTTGAGTGT 528

Qy 121 uMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141
Db 529 GATGTGGGTATTTACCTATGNTGGTGCCTCTGTTAATGCTCTGACACTACTGATTTGGC 588

Qy 141 aLeuIleSerLeuPheSer-IleProValIleTyrGluArgHisGlnValGlnIleAspH 161
Db 589 TCTCATTTTCATCTCTTCAGTTGCTTCTGTTATTTATGAACGGCATCAGGCACAGATG 648

Qy 161 iSfYrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
Db 649 ATTATCTAGGACTTGCATTAAGATGTTAAGATGCTATGGCTTAATCCACGACAAA 708

Qy 181 leProGlyLeuLysArgLysAlaAsp 189
Db 709 TCCCTGGATTGAAGCGCAAGCTGAA 734

RESULT 57
CK305449
LOCUS
DEFINITION SB02029A2B02.f1 normalized Keck-Tagu Library SB02 Taeniopygia

```

```

guttata cDNA clone SB02029A2B02.f1 5, mRNA sequence.
ACCESSION CK305449
VERSION CK305449.1 GI:44815023
KEYWORDS EST.
SOURCE Taeniopygia guttata
ORGANISM Taeniopygia guttata
REFERENCE 1 (bases 1 to 736)
AUTHORS Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M., Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A. and Liu,L.
TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior
JOURNAL Unpublished (2004)
COMMENT Contact: David F. Clayton
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University Genome Center.
Vector Trimming: Cross match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'
PCR Primers
FORWARD: TAATACGACTCAGCTATAGGG (T7)
BACKWARD: TAATACCCCTCAGCTAAAG (T3)
Insert Length: 736 Std Error: 0.00
Plate: SB02029A2 row: B column: 02
Seq primer: TAATACGACTCAGCTATAGGG (T7)
High quality sequence stop: 736.
FEATURES
source
1..736
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="SB02029A2B02.f1"
/tissue_type="brain"
/dev_stage="late embryo, post-hatch days 1, 10, 20, 45, and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized Keck-Tagu Library SB02"
/notes="Organ: brain; Vector: pBS II SK(+); Site 1: EcoRI(5' side of insert); Site 2: NotI (3' side of insert); The library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. An identifying tag was added at the 3'during cDNA synthesis: insertAAAAAAAAAAAAAAAAAATGCCA."
ORIGIN
Alignment Scores:
Pred. No.: 2.02e-96 Length: 736
Score: 866.00 Matches: 171
Percent Similarity: 96.28% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 7
Query Match: 93.62% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CK305449 (1-736)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db 125 GTTGTGACCTCTCTTCTGCGGAGACATTAAGAGACCGGGTGTGTTGGACGACC 184

Qy 22 LeupheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 185 TTGTTCTGCTGCTCTCATTAACAGTCTTCAGCATCGTGAGTGTGCACAGCCCTACATTGCC 244

```

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLe 61  
 Db 245 CTGGCCCTGCTCTCTGTACCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCAATC 304  
 QY 62 GlnLysSerAspGluClyHisProPheArgAlaTyrLeuGluSerClyValAlaLeSer 81  
 Db 305 CAGAAGTCTGATGAGGGCCACCCCTTACGGGCTTACCTGGATCGGATGTCGGCTGTCG 364  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 365 GAGGAGCTCATCCAGAGTACAGCAACGTCGCTGGGCCACGCTGAACGGCACCTCCGG 424  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 425 GAGCTGGCGGCTCTCTCTCGTCGATGACCTGGTGGATTCCTCAAGTTCGAGTATTG 484  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 485 ATGTGGTCTTTCACCTTACGCTGGTGGCTTGTCAATGGTCTGACATTACTGATCTGGCT 544  
 QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 545 TTGATTTCGCTCTTCTAGTCTCTCTGTTATTATGAGACATCAGGCCCAATCGACCAT 604  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 605 TACCTGGGACTTGTGAACAAGAACCTCAAGATGCCATGGCAAGATCCAAAGCAAGATC 664  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 665 CCTGGTGAAGCGCAAACTGAA 688

## RESULT 58

CK303615

LOCUS

DEFINITION SB02018A1G04.f1 normalized Keck-Tagu Library SB02 Taeniopygia guttata cDNA clone SB02018A1G04.f1 5, mRNA sequence.  
 CK303615  
 CK303615.1 GI:44813189

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Taeniopygia guttata  
 Taeniopygia guttata  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Estrilidae; Taeniopygia.

REFERENCE

AUTHORS

1 (bases 1 to 765)  
 Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M., Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A. and Liu, L.

The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior  
 Unpublished (2004)

JOURNAL

COMMENT

Contact: David F. Clayton  
 University of Illinois  
 B107 CUSL, 601 S. Goodwin, Urbana, IL 61801, USA  
 Tel: 217 244 3668  
 Fax: 217 244 1648  
 Email: dclayton@uiuc.edu  
 Base Calling/Quality Scores: PHRED from Washington University Genome Center.

Vector Trimming: Cross\_match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'

PCR Primers

FORWARD: TAATACGACTACTATAGG(T7)

REVERSE: ATTAACCTCTACTAAG(T3)

Insert Length: 765 Std Error: 0.00

Plate: SB02018A1 row: G column: 04

Seq primer: TAATACGACTACTATAGG (T7)

High quality sequence stop: 765.

## FEATURES

source

## Location/Qualifiers

1..765  
 /organism="Taeniopygia guttata"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:59729"  
 /clone="SB02018A1G04.f1"  
 /issue\_type="brain"  
 /dev\_stage="late embryo, post-hatch days 1, 10, 20, 45, and adult (pooled)"  
 /lab\_host="DH10B"  
 /clone\_lib="normalized Keck-Tagu Library SB02"  
 /note="Organ: brain; Vector: pBS II SK(+); Site: 1; EcoRI(5' side of insert); Site 2: NotI (3' side of insert); The library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. An identifying tag was added at the 3' during cDNA synthesis:  
 insertAAAAAAAAAAAAAAAAATGCGA."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.13e-96 Length: 765  
 Score: 866.00 Matches: 171  
 Percent Similarity: 96.28% Conservative: 10  
 Best Local Similarity: 90.96% Mismatches: 7  
 Query Match: 93.62% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CK303615 (1-765)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 119 GTTGTTCACCTCTCTTTCGCGAGACATTAAAGACCGGGGTGTGTTGGAGCCAGC 178  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 179 TTGTTCTGCTGCTCTCAATTACAGTGTTCAGCATCGTGTGAGTGTACAGCTTACATGCC 238  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLe 61  
 Db 239 CTGGCCCTGCTCTCTGTCCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC 298  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLeSer 81  
 Db 299 CAGAAGTCTGATGAGGGCCACCCCTTACGGGCTTACCTGGACTCGGATGTGGCCGTGTCG 358  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 359 GAGGAGCTCATCCAGAGTACAGCAACGCTGCTGGGCCACGCTGAACGGCACCTCCGG 418  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 419 GAGCTGGCGGCTCTCTCTCGTCGATCAGCTGGTGGATTCCCTCAAGTTCGAGTATTG 478  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 479 ATGTGGTCTTTCACCTACGTTGGTGGCTTGTTCATGTGCTGACATTACTGATCTGGCT 538  
 QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 539 TTGATTTCGCTCTTTCAGTGTTCCTGTTATTATGAGACATCAGGCCCAATCGCCAT 598  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 599 TACCTGGGACTTGTGAACAAGAACCTCAAGATGCCATGGCAAGATCCAAAGCAAGATC 658  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 659 CCTGGTGAAGCGCAAACTGAA 682

## RESULT 59

CK306874

LOCUS

793 bp mRNA linear EST 01-MAR-2004

DEFINITION SB02042A1A11.f1 normalized Keck-Tagu Library SB02 Taeniopygia  
guttata cdna clone SB02042A1A11.f1 5, mRNA sequence.

ACCESSION CK306874  
VERSION CK306874.1 GI:44816448  
KEYWORDS EST.  
SOURCE Taeniopygia guttata  
ORGANISM Taeniopygia guttata  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
Estrilinae; Taeniopygia.  
1 (bases 1 to 793)  
Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,  
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.  
and Liu,L.  
The Songbird Neurogenomics Initiative: An Evolving Public Resource  
for Study of Genes, Brain, and Behavior  
Unpublished (2004)  
Contact: David F. Clayton  
University of Illinois  
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA  
Tel: 217 244 3668  
Fax: 217 244 1648  
Email: dclayton@uiuc.edu  
Base Calling/Quality Scores: PHRED from Washington University  
Genome Center.  
Vector Trimming: Cross match from Washington University Genome  
Center PHRAP suite. Low quality bases (Phred score < 20) were  
trimmed from both ends of the sequence by an in-house script.  
This sequence is vector free and at least 200 bp in length. Funded  
by PHS grant # R01 NS045264, 'Songbird Neurogenomics Initiative.'  
PCR Primers  
FORWARD: TAATACGACTCACTATAGG(T7)  
BACKWARD: ATTAACCTCCTCAATAAG(T3)  
Insert Length: 793 Std Error: 0.00  
Plate: SB02042A1 row: A column: 11  
Seq primer: TAATACGACTCACTATAGG (T7)  
High quality sequence stop: 793.  
Location/Qualifiers  
1..793  
/organism="Taeniopygia guttata"  
/mol\_type="mRNA"  
/db\_xref="taxon:59729"  
/clone="SB02042A1A11.f1"  
/tissue\_type="brain"  
/dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,  
and adult (pooled)"  
/lab\_host="DH10B"  
/clone\_lib="normalized Keck-Tagu Library SB02"  
/note="Organ: brain; Vector: pBS II SK(+); Site 1:  
EcoRI(5' side of insert); Site 2: NotI (3' side of  
insert); The library was constructed and normalized as  
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.  
(1996), Genome Research 6(9): 791-806. An identifying tag  
was added at the 3' during cdna synthesis:  
insertAAAAAAAAAAAAAAAAATGCCA."

ORIGIN

Alignment Scores:  
Pred. No.: 2.25e-96 Length: 793  
Score: 866.00 Matches: 171  
Percent Similarity: 96.28% Conservative: 10  
Best Local Similarity: 90.96% Mismatches: 7  
Query Match: 93.62% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CK306874 (1-793)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
|||||  
Db 89 GTTGTGACCTTCCTTTCTGGCGAGACATTAGAGACCGGGGGTGTGGAGCAGC 148  
|||||  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIleAla 41  
|||||

Db 149 TTGTTCTGCTGCTCTCATTAACAGAGTGTTCAGCATCGTAGTGTACAGCCCTACATTCGCC 208  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
|||||  
Db 209 CTGGCCCTGCTCTCTGTCCACCATCAGCTTTAGGATATACAGGGAGTTATCCAGCAATC 268  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
|||||  
Db 269 CAGAAGTCTGATGAGGCCACCCCTTCAGGGCTTTACCTGGACTCGGATGTGGCGTGTGCG 328  
Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
|||||  
Db 329 GAGGAGCTCATCCAGAAAGTACAGCAACGTCGTGCTGGGCCACAGTCGAACGCGTCCGG 388  
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValPheAlaValLeu 121  
|||||  
Db 389 GAGCTGGCGGCCCTTCCTCGTCGATGACCTGGTGGATTCCTCAAGTTCGAGTATGTG 448  
Qy 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
|||||  
Db 449 ATGTGGTTCCTTCACTTACGTTGGTGGCTTGTTCATGTCTGACATTACTGATCTGGCT 508  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
|||||  
Db 509 TTGATTTTCGCTCTTTCAGTGTCTCTGTTATTATGAGAGACATCAGGGCCCAATCGACCAT 568  
Qy 162 TyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaTyrIleGlnAlaIleVal 181  
|||||  
Db 569 TACCTGGGACTTGTGAACAAGACGTCAAAGATGCCATGCCAAAGATCCAAAGCAAGATC 628  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
|||||  
Db 629 CCTGGTGTGAAGCCCAAACTGAA 652

RESULT 60  
CK304164  
LOCUS  
DEFINITION SB02022B2C10.f1 normalized Keck-Tagu Library SB02 Taeniopygia  
guttata cdna clone SB02022B2C10.f1 5, mRNA sequence.

ACCESSION CK304164  
VERSION CK304164.1 GI:44813738  
KEYWORDS EST.  
SOURCE Taeniopygia guttata  
ORGANISM Taeniopygia guttata  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
Estrilinae; Taeniopygia.  
1 (bases 1 to 852)  
Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,  
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.  
and Liu,L.  
The Songbird Neurogenomics Initiative: An Evolving Public Resource  
for Study of Genes, Brain, and Behavior  
Unpublished (2004)  
Contact: David F. Clayton  
University of Illinois  
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA  
Tel: 217 244 3668  
Fax: 217 244 1648  
Email: dclayton@uiuc.edu  
Base Calling/Quality Scores: PHRED from Washington University  
Genome Center.  
Vector Trimming: Cross match from Washington University Genome  
Center PHRAP suite. Low quality bases (Phred score < 20) were  
trimmed from both ends of the sequence by an in-house script.  
This sequence is vector free and at least 200 bp in length. Funded  
by PHS grant # R01 NS045264, 'Songbird Neurogenomics Initiative.'  
PCR Primers  
FORWARD: TAATACGACTCACTATAGG(T7)  
BACKWARD: ATTAACCTCCTCAATAAG(T3)  
Insert Length: 852 Std Error: 0.00  
Plate: SB02022B2 row: C column: 10  
Seq primer: TAATACGACTCACTATAGG (T7)  
High quality sequence stop: 852.  
Location/Qualifiers  
1..852  
/organism="Taeniopygia guttata"  
/mol\_type="mRNA"  
/db\_xref="taxon:59729"  
/clone="SB02022B2C10.f1"  
/tissue\_type="brain"  
/dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,  
and adult (pooled)"  
/lab\_host="DH10B"  
/clone\_lib="normalized Keck-Tagu Library SB02"  
/note="Organ: brain; Vector: pBS II SK(+); Site 1:  
EcoRI(5' side of insert); Site 2: NotI (3' side of  
insert); The library was constructed and normalized as  
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.  
(1996), Genome Research 6(9): 791-806. An identifying tag  
was added at the 3' during cdna synthesis:  
insertAAAAAAAAAAAAAAAAATGCCA."

ORIGIN

Alignment Scores:  
Pred. No.: 2.25e-96 Length: 852  
Score: 866.00 Matches: 171  
Percent Similarity: 96.28% Conservative: 10  
Best Local Similarity: 90.96% Mismatches: 7  
Query Match: 93.62% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CK306874 (1-793)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
|||||  
Db 89 GTTGTGACCTTCCTTTCTGGCGAGACATTAGAGACCGGGGGTGTGGAGCAGC 148  
|||||  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIleAla 41  
|||||



```

High quality sequence stop: 852.
Location/Qualifiers
1. .852
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="SB02022B2C10.f1"
/tissue_type="brain"
/dev_stage="late embryo, post-hatch days 1, 10, 20, 45, and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized keck-tagu library SB02"
/note="Organ: brain; Vector: pBS II SK(+); Site_1: EcoRI(5' side of insert); Site_2: NotI (3' side of insert); The library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. An identifying tag was added at the 3' during cDNA synthesis: insertAAAAAAAAAAAAAAAAAATGCGA."

ORIGIN
Alignment Scores:
Pred. No.: 2,49e-96 Length: 852
Score: 866.00 Matches: 171
Percent Similarity: 96.2% Conserv: 10
Best Local Similarity: 90.9% Mismatches: 7
Query Match: 93.6% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CK304164 (1-852)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 109 GTTGTGACCTCTTCTGTCGACCATGCTTACGATATACAGGGAGTGTATCCAGCAATC 168
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 169 TTGTTCTCTGCTCTCTATTACAGTTTCAGATCGTGGAGTGTACAGCCCTACATTGCC 228
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 229 CTGGCCCTGCTCTCTGTCCACCATGCTTACGATATACAGGGAGTGTATCCAGCAATC 288
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 289 CAGAAAGTCTGATGAGGGCCACCCCTTCAGGGCTTACCTGGACTCGGATGTGGCCGTGCG 348
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 349 GAGGAGCTCATCCAGAGTACAGCAACGTCGTCGTCGGCCACGTCGACGGACCGTCGCG 408
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 409 GAGTGGCGGCGCTCTTCTCGTATGATGACCTGGTGGATTCCCTCAAGTTCGAGTATTG 468
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141
DB 469 ATGTGGTGTTCCTCACTTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 528
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 529 TTGATTCGCTCTTCAGTGTCTCTGTTATTTATGAGACATCAGGCCCAATTCAGCAT 588
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 589 TACCTGGGACTTGTGAACAAGACGTCAAAGATGCCATGGCAAGATCCCAAGCAAGATC 648
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 649 CTGGGTGTTGAGCGCAAACTGAA 672

RESULT 61
CR548792
LOCUS CR548792 683 bp mRNA linear EST 12-JUL-2004
DEFINITION DKFZp469H1132_r1 469 (synonym: pkidl) Pongo pygmaeus CDNA clone
ACCESSION DKFZp469H1132 5', mRNA sequence.
VERSION CR548792
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
REFERENCE 1 (bases 1 to 683)
AUTHORS Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Pongo, G., Han, M. and Wiemann, S.
TITLE Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS
MIPS Incoltaeder Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
(Hilden/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp469H1132) is available at
the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email:
clone@rzd.de Further information about the clone and the
sequencing project is available at
http://mips.gsf.de/projects/cdna/
http://mips.gsf.de/projects/cdna/
FEATURES
Location/Qualifiers
1. .683
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469H1132"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkidl)"
/note="vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN
Alignment Scores:
Pred. No.: 2,41e-96 Length: 683
Score: 865.00 Matches: 176
Percent Similarity: 97.7% Conserv: 1
Best Local Similarity: 97.24% Mismatches: 4
Query Match: 93.51% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CR548792 (1-683)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 140 GTTGTGACCTCTCTCTGAGAGACATTAAGAGACTGGAGTGTGTGGTCCGACG 199
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 200 CTATTCTTCGCTGCTTTCATTGACAGTATTCAGCATTTGAGTGTAAACAGCCCTACATTGCC 259
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 260 TTGGCCCTGCTTCTGTCGCCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 319
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 320 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGCTATCT 379
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 380 GAGGAGTGTGGTTTCAGAGTACAGTAATTTCTGCTTCTGTCATGTGTAATCTGCAATGCA 439
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

```



Db 440 GAACCTAGCGGCTCTTCTTAGTGTGATTTAGTTGATTTCTCTGAAGTTTCCAGTGTG 499

Qy 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141

Db 500 ATGTGGTATTACCTATTGTTGGTCCCTTTTATGATGCTGTGACGCTACTGATTTGGCT 559

Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 560 CTCATTTTCACTCTTTCAGTGTCTCTCTTATTTATGAACGGCATCAGGCACAGATGATCAT 619

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 620 TATCTAGGACTTGCAATGAAGATTTAAAGATGCTATGGCTAAATTCGAAGCGGAAATC 679

Qy 182 Pro 182

Db 680 CCT 682

RESULT 62

CO503803

LOCUS

DEFINITION GGEZCB1022G02.g chicken breast muscle - CB1 Gallus gallus cdna

ACCESSION CO503803

VERSION CO503803.1 GI:50273989

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE

AUTHORS Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,

TITLE Discovery of new genes expressed in the chicken breast muscle

JOURNAL Unpublished (2004)

COMMENT Contact: Helena J. Alves

Laboratory of Animal Biotechnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434

Fax: 55 19 3429 4285

Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br

PCR Primers

BACKWARD: T7.

FEATURES

source

1..685

Location/Qualifiers

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="GGEZCB1022G02"

/tissue\_type="breast muscle"

/dev\_stage="1 and 21 days old"

/lab\_host="DH5 alpha"

/clone\_lib="chicken breast muscle - CB1"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This

cDNA library was constructed with the SuperScript plasmid

System with Gateway Technology kit (Invitrogen), following

manufacture's protocols. Plasmid DNA was purified using a

modified alkaline lysis method. Sequencing reactions were

conducted using the DYEnamic Cycle Sequencing Kit for

MegaBACE (Amersham biosciences) according to the

manufacturer's recommendations. Clones were sequenced by

the 5' end with T7 primer. Sequencing reactions were

analyzed on MegaBACE1000 DNA Sequencer (Amersham

bio sciences). The quality and clustering of the ESTs were

analyzed using the softwares Phred/Cap3. Only EST

sequences with Phred quality greater than 20 and at least

150 bp were considered for clustering."

ORIGIN

Alignment Scores:

Pred. No.: 2.42e-96 Length: 685

Score: 865.00 Matches: 171

Percent Similarity: 96.28% Conservative: 10

Best Local Similarity: 90.96% Mismatches: 7

Query Match: 93.51% Indels: 0

DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CO503803 (1-685)

Qy 2 ValValAspLeuLeuTyrTTPArgAspIleLysValThrGlyValValPheGlyAlaSer 21

Db 72 GTTGTGTACCTCTTCTTACTGCGAGACATTAAAGACAGAGGTGTGTTGGTCCAGC 131

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 132 TTGTTCTCTGCTCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC 191

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 192 TTGGCCCTGCTTCTGTGACCATCAGCTTTTAGGATATATACAAGGGAGTTTATCCAGGCAATC 251

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 252 CAAAAGTCCGATGAAGCCATCCATTTAGGCTTACTTTGGAGTCTGTAGTGTGTGTCT 311

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

Db 312 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTTGGTCACTCAACGGCACAGTCAAG 371

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 372 GAGCTGAGAGCGCTCTTCTCGTGTGATGACTTGTGTTGATTCTCTCAAGTTTGCAGTGTG 431

Qy 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141

Db 432 ATGGGGTGTTCACCTACGTTGGTGGCTTGTATATGTCGTGACATTAATGCTGCTGCT 491

Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 492 TTGATTTTCGCTGTTTCAGTGTCTCTGTTTATTATGAGAGACATCAGGCCAGATCGACCAT 551

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 552 TATTGGGACTAGTGAACAAGACGTCAGATCGATGGCCAAAGATCCCAAGATCCCAAGATC 611

Qy 182 ProGluLeuLysArgLysAlaAsp 189

Db 612 CCTGGGCTGAAGCGGCAAACTGAG 635

RESULT 63

AF125103 1798 bp mRNA linear HTC 22-MAY-2001

LOCUS Homo sapiens neuroendocrine specific protein c homolog mRNA,

DEFINITION complete cds.

ACCESSION AF125103

VERSION AF125103.1 GI:5107001

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 1798)

1 Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G.,

Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W.,

Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J., and Chen,Z.

Cloning and functional analysis of cDNAs with open reading frames

for 300 previously undefined genes expressed in CD34+ hematopoietic

stem/progenitor cells

Genome Res. 10 (10), 1546-1560 (2000)

JOURNAL

MEDLINE 20499367

PUBMED 11042152

REFERENCE

2 (bases 1 to 1798)

Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H.,

Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Human neuroendocrine specific protein c homolog mRNA, complete cds  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1798)  
AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H., Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Direct Submission  
JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China

## FEATURES

Location/Qualifiers  
1..1798  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="CD34+ hematopoietic stem/progenitor cells"  
215..814  
/codon\_start=1  
/product="neuroendocrine specific protein c homolog"  
/protein\_id="AAD39920.1"  
/db\_xref="GI:5107002"  
/translation="MDGQKQKWKDVLLYWRDIIKTVGVFGASFLLLSLTVFSIV  
SVYIALALSLVTFSPRIYGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSA  
LHVNCTIKELRFLVDLDVSLKFAVLMVFTVVGALFNLGLLILALISLQCS  
YLERHQADIDHYLGLANKNVKDAKIQAKPLGRKAE"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.27e-95 Length: 1798  
Score: 864.00 Matches: 182  
Percent Similarity: 97.88% Conservative: 3  
Best Local Similarity: 96.30% Mismatches: 3  
Query Match: 93.41% Indels: 2  
DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AFI25103 (1-1798)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 248 GTTGTGACCTCTCTGCTGAGAGACATTAGAGAGCTGGAGTGGTGTGGTCCAGC 307  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 308 CTATTCTGCTGCTTTCATTGACAGTATTCACATTGTGAGCGTAACAGCTACATTGCC 367  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 427  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 428 CAGAAATCAGATGAAGGCCACCCTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 487  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 488 GAGGAGTTGGTTCAGAGGTACAGTAATCTCTGCTTGTGTCATGCACTGACGATAAG 547  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 548 GAACTCAGCGCGCTCTCTTCTAGTATGATTTAGTTGATCTCTGAAAGTTGCACTGTTG 607  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB 608 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTGGCT 667  
QY 142 LeuIleSerLeu-PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161  
DB 668 CTCATTTCACTCTCTCAGTGTTCCTGTTATTTA-GAAGCGCATCAGGCACAGATAGTCA 726  
QY 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIl 181  
DB 727 TTATCTAGGACTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAAT 786  
QY 181 eProGlyLeuLysArgLysAlaAsp 189

Db 787 CCTGGATTGAAGCGCAAAAGCTGAA 811

## RESULT 64

BU950008

LOCUS

DEFINITION

in33d05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6126776 5'

similar to TR:Q9Y2Y7 Q9Y2Y7 FOCEN-M. [2] TR:O94962 ;, mRNA

sequence.

ACCESSION

BU950008

VERSION

BU950008.1

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 569)

AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lenishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,

Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,

Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other\_ESTs: in63d05.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence stop: 488.

Location/Qualifiers

1..569

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6126776"

/tissue type="Purified pancreatic islet"

/lab host="DH10B"

/clone lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:

NotI; Site\_2: XhoI; cDNA made by oligo-dr priming.

Size-selected on agarose gel. Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD,

Metabolism Div. (Alan Permutt Lab), Washington University

School of Medicine, Box 8127, 660 South Euclid Ave., St.

Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:

314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:

Pred. No.: 3.29e-96 Length: 569

Score: 863.00 Matches: 175

Percent Similarity: 97.80% Conservative: 3

Best Local Similarity: 96.15% Mismatches: 4

Query Match: 93.30% Indels: 0

DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU950008 (1-569)

QY 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSer 27

DB 12 TGGAGAGACATTAAGAGATTGGAGTGGTGTGGTCCAGCCTATTCTCTGCTGCTTCA 71

Qy 28 LeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerVal 47  
 Db 72 TTGACAGTATTTCAGCATTTGTGGGTACACGCTACATGCTTGGCCCTCTCTGTG 131  
 Qy 48 ThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIleGlnLysSerAspGluGly 67  
 Db 132 ACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGCC 191  
 Qy 68 HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLys 87  
 Db 192 CACCATTTCAGGGCATATCTGGAATCTGAAGTGTCTATATCTGAGGAGTTGGTTCAAG 251  
 Qy 88 TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPhe 107  
 Db 252 TACAGTAATCTCTCTCTGTCATGTGACATGACGATTAAGGAATCAGCGGCTCTTC 311  
 Qy 108 LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyr 127  
 Db 312 TTAGTTGATGATTTAGTTGATTTCTGAAATTTGCAAGTTTGCAGTGTGATGTTACCTAT 371  
 Qy 128 ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSer 147  
 Db 372 GTTGGTGGCTTTGTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGT 431  
 Qy 148 IleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsn 167  
 Db 432 GTTCTGTTATTTATGAACGCATCAGGCACAGATAGATCATATTTAGGACTTGCAT 491  
 Qy 168 LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLys 187  
 Db 492 AAGAATGTTAAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAA 551  
 Qy 188 AlaAsp 189  
 Db 552 GCTGAA 557

RESULT 65  
 BI544917  
 LOCUS 60324368F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5284672 5',  
 DEFINITION mRNA sequence.

ACCESSION BI544917  
 VERSION BI544917.1 GI:15432229  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 731)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiruki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLM11719 row: h column: 17  
 High quality sequence stop: 724.  
 Location/Qualifiers

1..731  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5284672"  
 /tissue type="hippocampus"  
 /lab\_host="DH10B"

FEATURES  
 source

/clone lib="NIH\_MGC\_95"  
 /notes=Organ: brain; Vector: pBluescriptR (modified  
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
 (gtcggg); Oligo-dT primed using primer  
 5'-TTTTTTTTTTTTTNN-3', size-selected for average  
 insert size 2.5 kb and normalized to ROT 5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NIH/NHGRI, National Institutes of Health). Note: this  
 is a NIH\_MGC Library."

# ORIGIN

Alignment Scores:  
 Pred. No.: 6,25e-96 Length: 731  
 Score: 862.00 Matches: 175  
 Percent Similarity: 98.33% Conservative: 2  
 Best Local Similarity: 97.22% Mismatches: 3  
 Query Match: 93.19% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BI544917 (1-731)

Qy 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 191 GTTGTTCACCTCTCTGTACTCGAGAGACATTAAAGAAGACTCGAGTGGTGTGGTGCACG 250  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 251 CTATTCCTGCTGCTTCATTTGACAGATATTGACGATTTGAGCGTAACAGCGCTACATGCCC 310  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 311 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 370  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 371 CAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGGAATGCTATATCT 430  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 431 GAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTGCTCATGTGAACCTGCACGATAAG 490  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 491 GAATCAGGCGCTCTCTTAGTTAGTATGATTTAGTTGATTTCTCTGAGGTTGCGAGTTG 550  
 Qy 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 551 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 610  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 611 CTCATTTCACTCTTCAGTGTCTCTGTTTATTATGAACGCGCATCAGGCACAGATAGATCAT 670  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 671 TATCTAGACTTTCGCAATATAGATTTAAAGATGCTATGTTAAATAATCCAGCAAAATC 730

## RESULT 66

BU364240

LOCUS

DEFINITION 603585074F1 CSEQCHN72 Gallus gallus cDNA clone CHES1539d19 5', mRNA

ACCESSION BU364240

VERSION BU364240.1 GI:25872241

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 820)

BU364240 820 bp mRNA linear EST 28-NOV-2002

603585074F1 CSEQCHN72 Gallus gallus cDNA clone CHES1539d19 5', mRNA

sequence.

ACCESSION BU364240

VERSION BU364240.1 GI:25872241

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 820)

**AUTHORS** Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
**TITLE** A Comprehensive Collection of Chicken cDNAs  
**JOURNAL** Curr. Biol. 12 (22), 1965-1969 (2002)  
**MEDLINE** 22335534  
**PUBMED** 12445392  
**COMMENT** Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 0161212008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

**FEATURES**

source  
 1. 820  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"  
 /clone="CHST539d19"  
 /sex="Female"  
 /tissue\_type="cerebrum"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSPQCHN72"  
 /note="Organ: brain; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

**ORIGIN**

Alignment Scores:  
 Pred. No.: 7,368-96 Length: 820  
 Score: 862.00 Matches: 173  
 Percent Similarity: 96.30% Conservative: 9  
 Best Local Similarity: 91.53% Mismatches: 6  
 Query Match: 93.19% Indels: 1  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU364240 (1-820)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGACCTCTTACTTGGGAGACATTAAAGACAGAGTGTGTGTGTCAGC 215  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
 Db 216 TTGTTCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC 275  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTATTCAGGCAATC 335  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAAAGTCGATGAAGGCCCATCTTAGGCTTACTTGGAGTCTGATGCTGTGCT 395  
 Qy 82 GluGluLeuValGlnLysTyrSerIleSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 396 GAAGAGCTGATTACAGAAATACAGCAGTGTGTGCTTGTGTCATCATCAACGGCAGCTCAAG 455  
 Qy 102 GluLeuArgAlaLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 456 GAGCTGACAGCCCTCTTCTCGTGTGACATGGTGTGATTCTCTGAAGTTTGCAGTTTG 515  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 516 ATGTGGGTGTTTCACTTACGTGGTGGCTTGTATTAATGCTGTGACATTACTGATCGCT 575  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 576 TTGATTTCTGCTGTTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCAGATCGACCAT 635  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 636 TATTGGGAGCTAGTGAACAAGACGTCAAGATGGATGGCAAGATCCAAAGCAAGATC 695  
 Qy 182 Pro-GlyLeuLysArgLysAlaAsp 189  
 Db 696 CCTGGCCTGAAGCGCAAAACTGAG 720  
 RESULT 67  
 BU848611  
 LOCUS  
 DEFINITION AGNCOURT 10276498 NIH\_MGC 144 Mus musculus cDNA clone  
 IMAGE:6596409 5', mRNA sequence.  
 ACCESSION BU848611  
 VERSION BU848611.1 GI:24033573  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Michael Brownstein Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LCM2825 row: p column: 09  
 High quality sequence stop: 160.  
 Location/Qualifiers  
 1. 813  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6596409"  
 /lab\_host="DH10B (T1-phage-resistant)"  
 /clone\_lib="NIH\_MGC\_144"  
 /note="Organ: Brain; Vector: pDNR-LIB; Site\_1: SfiI  
 (ggccatagggcc); Site\_2: SfiI (ggccgcctggcc); cDNA made  
 by oligo-dT priming and directionally cloned. 5' and 3'  
 adaptors were used in cloning as follows:  
 5'-AAGCAGTGTGATCAACGAGATGCGCATACGCGCGG-3' and  
 5'-ATTCTAGAGCGGCGCGCATG-dt(30)NN-3'. Full-length  
 enriched library was constructed using the Clontech  
 Creator SMART kit and size-selected to contain the 0.2-0.5  
 kb size fraction (other fractions present in NIH\_MGC\_143).  
 Library created in the laboratory of M. Brownstein (NIMH,  
 NIH). Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,27e-95 Length: 813  
 Score: 858.00 Matches: 178  
 Percent Similarity: 97.28% Conservative: 1  
 Best Local Similarity: 96.74% Mismatches: 4  
 Query Match: 92.76% Indels: 1

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DB:
US-09-830-972-2_COPY_975_1163 (1-189) x B0848611 (1-813)
  5      Gaps: 0

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 159 GTTGTGTGACCTCCCTGCTACTGAGAGACATTAAGAACTGGAGTGGTGTGGTGCCAGC 218
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 219 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTACGGCTTACATGCC 278
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 279 TTGGCCCTGCTCTCTGCTACTATCAGCTTTAGGATATATTAAGGGTGTGATCCAAGTATC 338
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 339 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 398
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 399 GAGGAATGGTTTCAGAAATATAGTAATTTCTGCTCTGTGTCATGTGAACAGCACATATAA 458
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 459 GAAATTGAGCGTCTCTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTGCAGTGTG 518
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAla 141
Db 519 ATGTGGGTATTTACTTACGTGGTGGCTTGTTCATATGATGGTGTGACACTACTGGATTTAGCT 578
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 579 CTGATCTCACCTCTTCAGTATTTCTGTGTATATATGAACGGCATGCCATGCCAGGCGACATAGATCAT 638
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 639 TATCTAGGACTTGCAAAACAGAGCGTAAGGATGCCATGCCATGNNCAAAATCCCAAGCAAAAT 698
Qy 181 eProGlyLeu 184
Db 699 CCCTGGATTG 708

RESULT 68
LOCUS BG427864 713 bp mRNA linear EST 14-MAR-2001
DEFINITION 602501551F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614924 5',
mRNA sequence.
ACCESSION BG427864
VERSION BG427864.1 GI:13334370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN1367 row: f column: 13
High quality sequence stop: 712.
Location/Qualifiers
1. 713

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4614924"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccattggcc); Site_2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGCGGCGGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 4,44e-95 Length: 713
Score: 855.00 Matches: 178
Percent Similarity: 96.28% Conservative: 3
Best Local Similarity: 94.68% Mismatches: 7
Query Match: 92.43% Indels: 1
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BG427864 (1-713)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 146 GTTGTGTGACCTCCCTGCTACTGAGAGACATTAAGAACTGGAGTGGTGTGGTGCCAGC 205
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 206 CTATTCCTGCTGCTCTTCATTCAGCAGTATTCAGCATTGTGACGTAACAGCCCTACATTGCC 265
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 266 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGTATC 325
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 326 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGTATATCT 385
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 386 GAGAGTGTGGTTTCAGAACTACAGTAATTCGCTCTTGGTCAATGTAACCTGCACGATAAAG 445
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 446 GAACTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTCCTCTGAAAGTTGCAGTGTG 505
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 506 ATGTGGGTATTTACTATGTTGGTGC-CTGTTTAATGGTCTGACACTACTGATTTGGCT 564
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 565 CTCATTTTCACCTTCAGTGTCTCTGTCATTTATGAACGGCATCAGGCGACATAGATCAT 624
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 625 TATCTAGGACTTGCAAAATAGAAGTTTACAGATGCTTAATGGTAAATCCCAAGCAAAATC 684
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 685 CCTGGATTGAAGCGCAAGGTGAAT 708

RESULT 69
LOCUS CD511521 758 bp mRNA linear EST 06-JUN-2003
DEFINITION AGENCOURT 14353136 NIH_MGC 187 Homo sapiens cDNA clone
IMAGE:30405928 5', mRNA sequence.

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ACCESSION CD511521
VERSION CD511521.1 GI:31443239
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 758)
          NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-re@mail.nih.gov
          Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
          CDNA Library Preparation: CLONTECH Laboratories, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: NDCM193 row: n column: 17
          High quality sequence: 614.
          Location/Qualifiers
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              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:30405928"
              /lab_host="DH10B (T1 phage-resistant)"
              /clone_lib="NIH_MGC_187"
              /note="Organ: Blood vessels - aorta, basilar and artery;
              Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2:
              SfiI (ggccgctcgcc); 5' and 3' adaptors were used in
              cloning as follows: 5' adaptor sequence:
              5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
              5'-ATTCTAGAGCGGAGCGGCCGACATG-dt(30)BN-3' (where B = A,
              C, or G and N = A, C, G, or T). Average insert size 1.4 kb
              (range 0.5-4.0 kb). 14/15 colonies contained inserts by
              PCR. This library was enriched for full-length clones and
              was constructed by Clontech Laboratories (Palo Alto, CA).
              Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 5.58e-95 Length: 758
Score: 854.50 Matches: 178
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 95.70% Mismatches: 3
Query Match: 92.38% Indels: 2
DB: 6 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x CD511521 (1-758)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21
Db 148 GTTGTGACCTCCTCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCAGC 207
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrIleAla 41
Db 208 CTATTCTCTGCTCTTCATTGACGATTTACGATTTGGAGCGTACACGCTTACATTGCC 267
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 268 TTGGCCCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGGTATC 327
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 328 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATCT 387
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

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Db 388 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTCTTGGTTCATGTAACCTGCAGTAAG 447
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 448 GAACCTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTGTG 507
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 508 ATGTGGGTATTACCTATGTTGGTCCCTTGTATTATGCTGACACTACTGATTTGGCT 567
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 568 CTCATTTCACCTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATGATCAT 627
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMet-AlaLysIleGlnAlaLysI 181
Db 628 TATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGGCTAAATCCAAAGCAAAA 687
QY 181 ePro---GlyLeuLys 185
Db 688 TCCCTCGGATTTGAA 703

RESULT 70
LOCUS BI394814
DEFINITION BI394814 646 bp mRNA linear EST 06-AUG-2001
          pgpin.pk009.15 Normalized Chicken Pituitary/Hypothalamus/Pineal
          Library Gallus gallus cDNA clone pgpin.pk009.15 5' similar to
          gi|5902016 ref|NP_008939.1| reticulon 4; neuroendocrine-specific
          protein C like (foccon) [Homo sapiens] gi|13637055 ref|XP_002439.3|
          neuroendocrine-specific protein C like (foccon) [Homo sapiens]
          GI|AAD27783.1|AF077050.1 (AF077050) neuroendocri, mRNA sequence.
ACCESSION BI394814
VERSION BI394814.1 GI:15088096
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 646)
          Porter,T.E. and Cogburn,L.A.
AUTHORS ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
          Library USDA/IRAFS Animal Genome Project
TITLE Unpublished (2001)
JOURNAL Contact: Larry A. Cogburn
          University of Delaware
          Townsend Hall, Newark, DE 19717, USA
          Tel: 302-831-1335
          Fax: 302-831-2822
          Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES Location/Qualifiers
          1..646
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            /mol_type="mRNA"
            /strain="Commercial broiler chicken"
            /db_xref="taxon:9031"
            /clone="pgpin.pk009.15"
            /sex="Male and Female"
            /tissue type="Pituitary Gland/Hypothalamus/Pineal Gland"
            /dev stage="Embryonic (dl2,dl4,dl9); post-hatch
            (w1,w3,w5,w7,w9)"
            /lab host="E. Coli EMDH10B"
            /clone_lib="Normalized Chicken
            Pituitary/Hypothalamus/Pineal Library"
            /note="Vector: pCMVSPORT6; Library made from equivalent
            pools of total RNA isolated from each tissue at different
            ages. Single pass sequencing from 5'-end"

ORIGIN
Alignment Scores:
Pred. No.: 6.82e-95 Length: 646
Score: 853.00 Matches: 170

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Percent Similarity: 95.21% Conservatives: 9  
 Best Local Similarity: 90.43% Mismatches: 9  
 Query Match: 92.22% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x B1394814 (1-646)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 51 GTTGTGACCTCTTACTGCGGAGACATTAAAGACAGGAGTGGTGTGGTCCAGC 110  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 111 TTGTTCTCGTCTCTCAATTAACAGTGTTCAGCATCGTGGAGCGTACAGCTTACATGGC 170  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 171 TTGGCCCTGCTTCTGTGACCATCAGCTTTTAGGATATACAAAGGAGTATCCAGGCAATC 230  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 231 CAAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTGGAGTCTGTAGTGTGTCT 290  
 Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 291 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTTGTGTCATCAACGGCACAGTCAAG 350  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 351 GAGCTGAGAGCCCTCTTCTCGTGTGAGTGTGGTGTGATCTCTGAAAGTTTGGAGTGTG 410  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 411 ATGTGGGTGTTCACTAGTGTGGCTGTGTTTAAATGCTGACATTAATGATGCTGCT 470  
 Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 471 TTGATTTTCGCTGTTTCAGTGTCTGTTATTATGAGAGACATCAGGCGCCAGATCCAGCAN 530  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 531 TATTGGGACTTNTGAAACAAGACGTCAAGATCGGATGCGAAGATCCAAAGCAAGATC 590  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 591 CCNNNTGAAGCGCANNACTGAG 614

## RESULT 71

BUI39629  
 LOCUS 603134795F1 CSEQCHL24 1028 bp mRNA linear EST 25-NOV-2002  
 DEFINITION 603134795F1 CSEQCHL24 Gallus gallus CDNA clone ChEST117m23 5', mRNA  
 sequence.  
 BUI39629  
 BUI39629.1 GI:25354039  
 VERSION EST.  
 KEYWORDS Gallus gallus (chicken)  
 SOURCE Gallus gallus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 1028)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken CDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 MEDLINE  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

FEATURES  
source

Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..1028  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="ChEST117m23"  
 /dev\_stage="16 day embryo"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHL24"  
 /note="Organ: brain; Vector: pBluescript II KS(+); Site 1:  
 [EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
 [Stratagene] vector to accommodate cDNA produced with the  
 T-trimmed protocol (Construction of uni-directionally  
 cloned cDNA libraries from messenger RNA for improved 3'  
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
 Ligate in double stranded adaptor containing BspI and  
 BamHI sites [5'ggccggtgcagcccgatcgaaaaaag]  
 [5'aattcttttttcggatccggggtcgacgc]"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.32e-94 Length: 1028  
 Score: 853.00 Matches: 174  
 Percent Similarity: 95.81% Conservative: 9  
 Best Local Similarity: 91.10% Mismatches: 6  
 Query Match: 92.22% Indels: 2  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BUI39629 (1-1028)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 186 TCAGTTGTCACCTCTTACTGCGGAGACATTAAAGACAGGAGTGGTGTGGTCC 245  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 246 AGCTTGTGCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGGCGTGACAGCTTACATT 305  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 306 GCCTTGGCCCTGCTTCTGTGACCATCAGCTTAGGATATACAAAGGAGTATCCAGGCA 365  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 366 ATCCAAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTGGAGTCTGTAGTGTG 425  
 Qy 81 SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 426 TCTGAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGTGTCATCAACGGCACAGTC 485  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 486 AAGAGCTGAGAGCCCTCTTCTCGTGTGAGTACTTGGTGTGATCTCTGAAGTTGCAAGT 545  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 546 TTGATGTGGGTGTTCACTACGTTGGTGGCTTGTGTTAATGCTGTCGACATTAATGACTG 605  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 606 GCTTTGATTTTCGCTGTTTCAGTGTCTGTTATTATGAGAGACATCAGGCGCCAGATCGAC 665  
 Qy 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla-LysIleGlnAlaLys 180  
 Db 666 CATTATTTGGGACTAGTGAACAAGACGTCAAGATCGGATGCGAAGATCCAAAGATCCAGCAA 725  
 Qy 180 silePro-GlyLeuLysArgLysAlaAsp 189  
 Db 726 GATCCCTGGGCTTGAAGCGCAAAACTGAG 754



```

RESULT 72
BG109465          819 bp  mRNA  linear  EST 30-JAN-2001
LOCUS             602280543F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368011 5',
DEFINITION        mRNA sequence.
ACCESSION         BG109465
VERSION           BG109465.1 GI:12602971
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1 (bases 1 to 819)
                  NIH-MGC http://mgs.nci.nih.gov/.
                  National Institutes of Health, Mammalian Gene Collection (MGC)
                  Unpublished (1999)
                  Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-r@mail.nih.gov
                  Tissue Procurement: ATCC
                  cDNA Library Preparation: Life Technologies, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLAM10021 row: f column: 12
                  High quality sequence stop: 647.
FEATURES          Location/Qualifiers
                  1..819
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4368011"
                     /tissue_type="osteosarcoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC 86"
                     /note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.533 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:       1..le-94          Length:      819
Score:           852.50           Matches:    180
Percent Similarity: 96.8%         Conservative: 3
Best Local Similarity: 95.24%     Mismatches:  5
Query Match:     92.16%          Indels:     2
DB:              4               Gaps:       0

US-09-830-972-2_COPY_975_1163 (1-189) x BG109465 (1-819)

QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB      19 GTGTGTGACCTCCTCTACTGGAGACATTAAAGACTGGAGTGGTGTGTGGTCCAGC 78

QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB      79 CTATTCTCTGCTTTCATTGACAGTATTACGATTGTGAGCGTAACAGCCTACATTGCC 138

QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB      139 TTGGCCCTGCTCTGTGACCATCATCAGTTTAGGATATACAAGGGGTGTGATCCAGCTATC 198

QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB      199 CAGAATCAGATGAAGGACCCCATTCAGGCATATCTGGATCTGAAGTGTCTATATCT 258

QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB      259 GAGGAGTTGGTTTCAGAAGTACAGTAATCTCTGCTCTTGTGTGATGTGAAGTGCACGATAAG 318

```

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QY      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB      319 GAACCTCAGCGCCCTCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCAGG--TTG 376

QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
DB      377 ATGTGGGTATTTACCTATGTTGGTCCCTGTGTTTATGTTCTGACACTCTACTGATTTGGCT 436

QY      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValIleGlnIleAspHis 161
DB      437 CTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 496

QY      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla-LysIle 181
DB      497 TATCTAGACTTGCAATTAAGAATGTTAAAGATGCTATGGTAAATCCAAAGCCAAAAT 556

QY      181 eProGlyLeuLysArgLysAlaAsp 189
DB      557 CCTGGATTGAAGCGCAAGCTGAA 581

RESULT 73
COS81452          960 bp  mRNA  linear  EST 20-JUL-2004
LOCUS             ILLUMIGEN MCO_47216 Katze_MMLV Macaca mulatta cDNA clone
DEFINITION        IBIUW:17799 5' similar to Bases 83 to 959 highly similar to human
                  RTN4 (Hs.436349), mRNA sequence.
ACCESSION         COS81452
VERSION           COS81452.1 GI:50412806
KEYWORDS          EST.
SOURCE            Macaca mulatta (rhesus monkey)
ORGANISM          Macaca mulatta
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
                  Cercopithecinae; Macaca.
REFERENCE         1 (bases 1 to 960)
                  Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
                  Large-scale Rhesus Macaque cDNA Sequencing
                  Unpublished (2003)
                  Contact: C. Magness
                  Illumigen Biosciences Inc.
                  2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
                  Tel: 2063780400
                  Fax: 2063780408
                  Email: cmagness@illumigen.com
                  Sequenced on 2004.06.24. 532 Q20 bases. Library Preparation: Prof.
                  Michael Katze Lab at University of Washington DNA Sequencing:
                  Illumigen Biosciences Inc. For further information, see
                  http://www.macaque.org
                  PCR Primers
                  FORWARD: CCTCACTAAAGGGAACAAA
                  BACKWARD: CACTATAGGCGGAATTGGTA
                  Insert Length: 960 Std Error: 0.00
                  Plate: CL000396 row: H column: 08
                  Seg primer: CCTCACTAAAGGGAACAAA
                  POLYA-Yes.
FEATURES          Location/Qualifiers
                  1..960
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9544"
                     /clone="IBIUW:17799"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze_MMLV"
                     /note="Organ: liver; Vector: pDONR 222; Site 1: BsrG I;
                     Site 2: BsrG I; created from CloneMiner cDNA Library
                     Construction kit (catalog #18249-029)"
ORIGIN
Alignment Scores:

```



Pred. No.: 1.59e-94 Length: 960  
 Score: 852.00 Matches: 175  
 Percent Similarity: 96.28% Conservative: 6  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 92.11% Indels: 1  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CO581452 (1-960)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSerLeu 22  
 Db 84 GTTGACCTCTCTAGTGAGAGACTTGAAGAATAATGGAGTGGTGTGGCGCAGCCTA 143  
 Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 144 TTCCTGCTCTTCTTTCGACAGTATTCAGCATTTGTAGTGTAACAGCTACATTCCTTG 203  
 Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrIleValysGlyValIleGlnAlaLeu 62  
 Db 204 GCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGCTATCCAG 263  
 Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIleSerGlu 82  
 Db 264 AAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCCATATCTGAG 323  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 324 GAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCACGATAAGGAA 383  
 Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 384 CTCAGGCCCTCTCTTCTAGTTGATGATTTAGTTGATCTCTGAAGTTTGCAGTGTTCATG 443  
 Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
 Db 444 TGGGTATTTACCTATGTTGGTGGCTTGTATTAATGGTCTGACGCTACTGATTTGGCTCTC 503  
 Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 504 ATTTCACTCTTCAGTGTCTGTTATTTATGACGGCATGACGGCAGACAGATAGATCATAT 563  
 Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 564 CTAGGACTTGCAATAGAATGTTAAAGATGCTATGGCTAAATCCCGAGGAAATCC 623  
 Qy 182 cGlyLeuLysArgLysAlaAsp 189  
 Db 624 TGGATTGAAGCGCCAAGCTGAA 645

RESULT 74  
 BG400408  
 LOCUS BG400408 905 bp mRNA linear EST 12-MAR-2001  
 DEFINITION 60246428F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4592670 5',  
 mRNA sequence.

ACCESSION BG400408

VERSION BG400408.1 GI:13293856

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: LUCM1331 row: g column: 07  
 High quality sequence stop: 708.

FEATURES

source

1. .905  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4592670"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCCGCGCGGCATG-3' (where B = A, C,  
 G, or T). Average insert size 1.65  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
 Pred. No.: 2.59e-94 Length: 905  
 Score: 850.00 Matches: 177  
 Percent Similarity: 95.79% Conservative: 5  
 Best Local Similarity: 93.16% Mismatches: 6  
 Query Match: 91.89% Indels: 2  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG400408 (1-905)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21  
 Db 153 GTTGTGGACCTCTCTGTAACGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCAGC 212  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 213 CTATTCCTGCTCTTTCATTTGACAGTATTCAGCATTTGTGAGCGTAACAGCTACATGCC 272  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleValysGlyValIleGlnAlaIle 61  
 Db 273 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAAGCTATC 332  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIleSer 81  
 Db 333 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 392  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 393 GAGAGTGGTTCAGAGTACAGTATTCCTGCTCTTGGTCTATGTGAAGTGCACGATAAG 452  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 453 GAACTCAGGGCGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 512  
 Qy 122 Met-TrpValPheThrTyrValGlyAlaLeuPheAsn-GlyLeuThrLeuLeuLeuAla 141  
 Db 513 ATCGTGGGTATTTACCTATGTTGGTGGCTGTTTACTGGGTCTGACACTCTGATTTGGG 572  
 Qy 141 laLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspH 161  
 Db 573 CTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAAACGGCATCAGGCACAGATAGTC 632  
 Qy 161 isTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 633 ATTATCTAGGACTTGCAATAAAGAAATGTTAAAGATGCTATGGGTAAATCCAAAGAAAA 692  
 Qy 181 leProGlyLeuLysArgLysAlaAsp 189  
 Db 693 TCCTGGATTGAAGCGCCAAGTTGAA 718



## Alignment Scores:

Pred. No.: 4,74e-94 Length: 759  
 Score: 847.00 Matches: 172  
 Percent Similarity: 96.28% Conservatives: 9  
 Best Local Similarity: 91.49% Mismatches: 7  
 Query Match: 91.57% Indels: 1  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU138907 (1-759)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 137 GTTGTTCACCTCTTACTGCGGAGACATTAAGAAGACAGAGTGTTGTGTGCAGC 196  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 197 TTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACGTTACATTGCC 256  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 257 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCATC 316  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 317 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGCTGTCT 376  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 377 GAAGAGCTGATTCAGAAATACAGCAGGTGTGTCTGCTGCATCAACGGCAGTCAGC 436  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 437 GAGCTGAGAGCCCTCTCTCTGTTGATGACTTGGTGAATCTCTGAAGTTTGCAGTTG 496  
 Qy 122 MetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 497 ATGTGGGTGTTCACCTACGTGTGGTCTGTTAAATGGTCTGCATTTACTGATCTGGCT 556  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 557 TTGAATTCGCTGTTCAGTGTCTCTGTTATTTATGAGAGACATCAGGCCCATCGACCAT 616  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 617 TATTTGGACTAGTGAACAGAACCTCAA-GATGCGATGCCAAGATCCAGGCAAGATC 675  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 676 CTTGGGCTGAAGCGCAAAACTGAG 699

## RESULT 77

CK791443  
 LOCUS  
 DEFINITION 826 bp mRNA linear EST 25-FEB-2004  
 AGENCOURT 18667576 NIH MGC 230 Mus musculus CDNA clone  
 IMAGE:30848940 5', mRNA sequence.

ACCESSION CK791443

VERSION CK791443.1 GI:42803439

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 826)

NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

CONTACT: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: Shioko Kimura/Atsushi Yamada, (NCI,CCR)

## CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM1156 row: a column: 13

High quality sequence stop: 680.

## FEATURES

## source

1..826  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30848940"  
 /tissue\_type="Pooled thyroids from 5 mice"  
 /lab\_host="DH10B Tona"  
 /clone\_lib="NIH\_MGC\_230"  
 /notes="Organ: thyroid; Vector: pExpress-1; Site 1: NotI;  
 Site 2: NotI; RNA obtained from 5 normal wild-type mice  
 thyroid. CDNA was primed using oligo-dT primer:  
 5'-pGACTAGTTCTAGATCGAGCGCGCC(T)25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection 1.4 kb  
 resulted in an average insert size of 1.2 kb. Normalized  
 version of this library is NIH\_MGC\_189library constructed  
 by Express Genomics (Frederick, MD). Note: this is a  
 NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,17e-94 Length: 826  
 Score: 846.50 Matches: 179  
 Percent Similarity: 98.36% Conservatives: 1  
 Best Local Similarity: 97.81% Mismatches: 2  
 Query Match: 91.51% Indels: 2  
 DB: 7 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CK791443 (1-826)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 171 GTTGTTCACCTCTTACTGCGGAGACATTAAGAAGACTGGAGTGTGTGTGTGCAGC 230  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 231 TTATTCCTGCTGCTCTCGACAGTGTTCAGCATTTGTCAGTGAACGGCTCATTTGCC 290  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 291 TTGGCCCTGCTCTCTGCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 350  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 351 CAGAAATCAGATGAAGGCCACCATTCAGGCATATTTGGAATCTGAAGTTGCCATATCA 410  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 411 GAGGAATTTGGTTCAGAAATATAGTAACTCTGCTCTTGGTCATCTGAACACACATAAAA 470  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 471 GAATTGAGCGCTCTCTCTTCTAGTTGATGATTAGTTAGTTCCCTGAGGTTTGCAGTTTG 530  
 Qy 122 MetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 531 ATGTGGGTATTTACTTACGTGTGGTCTGTTCAATGGTTTGACACTACTGATTTAGCT 590  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 591 CTGATCTCACTCTTCTAGTATTCCTGTTATATATATGAACGGCATCAGCGCGCAGATAGATCAT 650  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 651 TATCTAGGACTTGC-AACAAGAGCGTTAAGGATGCCATGGCCAAATCCAG---CAAATC 706



```

Db 366 TTTAATGCTGACACTACTGATTGCTGCTCATTTTCACTCTTCAAGTGTCTCTGTTATT 425
Qy 152 TyrgluarhlglnvalglnleasphistyrleuGlyLeuAlaAenLysSerVallyls 171
Db 426 TATGACGGCATCAGCCACATGATATATCTAGGACTTGCATAATGAAGTTGATAA 485
Qy 172 AspAlaMetAlaLyslleGlnAlaLyslleProGlyLeuLysArgLysAlaAasp 189
Db 486 GATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 539

RESULT 80
BE733819 716 bp mRNA linear EST 15-SEP-2000
LOCUS 601569133P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843729 5',
DEFINITION mRNA sequence.
ACCESSION BE733819 GI:10147721
VERSION BE733819.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 716)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at: image.llnl.gov
Plate: LUCM539 row: a column: 10
High quality sequence stop: 716.
FEATURES
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3843729"
/tissue type="choriocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_21"
/note="Organ: placenta; vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

```

Alignment Scores:
Pred. No.: 5.81e-94 Length: 716
Score: 846.00 Matches: 181
Percent Similarity: 96.84% Conservative: 3
Best Local Similarity: 95.26% Mismatches: 4
Query Match: 91.46% Indels: 3
DB: 2 Gaps: 0
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x BE733819 (1-716)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyValAsp 21
Db 142 GTTGTCACCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 201
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLysIleAla 41
Db 202 CTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCGCTACATTGCC 261
```

```

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 262 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 321
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 322 CAGAAATCAGATGAAGGCCACCCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 381
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 382 GAGGAGTGGTTTCAAGATACAGTAATCTGCTCTTGGTCAATGTAAGTGCACGATAAAG 441
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 442 GAATCAGGCGCCTCTTCTTAGTTGATGATTAGTTAGTCTCTCTGAAGTTGTCAGTGTG 501
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 502 ATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGGTCTGACACTACTGAT-TTGGCT 560
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 561 CTATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 620
Qy 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGln-AlaLysIl 181
Db 621 TATCTAGGACTTGCAATAGAATGTTAAAGTGTCTATGCTAAATCCAAAGCAGAAAAT 680
Qy 181 e-ProGlyLeuLysArgLysAlaAasp 189
Db 681 CCCCTGGATTGAAGCGCAAGTGAAT 706
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## RESULT 81

CR755232/c

LOCUS

DEFINITION

CR755232 Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus

cDNA clone GP0AAA15ZC09, mRNA sequence.

ACCESSION

CR755232

VERSION

CR755232.1

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

Rattus norvegicus

ORGANISM

Rattus norvegicus

REFERENCE

1 (bases 1 to 1054)

AUTHORS

Cros,N., Tkatchenko,A.V., Pisani,D.F., Leclerc,L., Leger,J.J.,

Marini,J.F. and Dechesne,C.A.

TITLE

Analysis of altered gene expression in rat soleus muscle atrophied

by disuse

JOURNAL

J. Cell. Biochem. 83 (3), 508-519 (2001)

MEDLINE

21479502

PUBMED

11596118

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Genoscope sequence ID: GP0AAA15ZC09RPL.

FEATURES

Location/Qualifiers

1..1054

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="GP0AAA15ZC09"

/sex="Female"

/tissue type="muscle"

/clone lib="Rattus norvegicus muscle Sprague-Dawley"

/note="Vector: pCRII-TOPO; Pietu G., Cros N., Leger J.J.,

Dechesne C.A. Subtracted library from atrophied and

control soleus muscles Subtraction was performed

according to Diatchenko et al. (Diatchenko L, Lau YF,



```

Qy 110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTTPValPheThrTyrValGly 129
Db 301 GATGATTAGTTGATCTCTGAGTTTGCAAGTTTGATGGTATTTACCTAATGTTGGT 360
Qy 130 AlaLeuPheAnGlyLeuThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 149
Db 361 GCCTTGTGTTAATGCTGACACTACTGATTGCTGCTCTCACTTCACTTCACTTCACTT 420
Qy 150 ValTleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSer 169
Db 421 GTTATTATTATGAACGCGCATCAGCGCAGATAGATCATTTATCTAGGACTTGCAGAAAT 480
Qy 170 VallysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
Db 481 GTTAAAGATGCTATGGCTAAATCCAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 540

RESULT 83
CD000871
LOCUS
DEFINITION AGENCOURT 13650322 NIH MGC 186 Homo sapiens cDNA clone
IMAGE:30321390 5', mRNA sequence.
ACCESSION CD000871
VERSION CD000871.1 GI:30295402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: c3apbb-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM120 row: 1 column: 07
High quality sequence stop: 530.
FEATURES
Location/Qualifiers
1..735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30321390"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_186"
/notes="Organ: Pooled-Skin; Vector: pNIR-LIB; Site 1: Sfil
(ggcatatggcc); Site 2: Sfil (ggcgctcgcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meninges, dura mater, pia mater and choroid plexus.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTAGAGCGCGGCGGCAGATG-RT(30)BN-3'
(where B = A, C, G or N = A, C, G, or T). Average
insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library"

Alignment Scores:
Pred. No.: 2,51e-93 Length: 735
Score: 841.00 Matches: 176
Percent Similarity: 97.27% Conservative: 2
Best Local Similarity: 96.17% Mismatches: 3

```

```

Query Match: 90.92% Indels: 2
DB: 6 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x CD000871 (1-735)
Qy 2 ValValAspLeuLeuTyrTipArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 189 GTTGTTCACCTCCTGTTACTCGAGAGACATTAAAGAAGACTGGAGTGGTGGTGGTGGCAGC 248
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 249 CTATTCTCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGGTAAACAGCCCTACATTGCC 308
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaTle 61
Db 309 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 368
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 369 CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 428
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 429 GAGGAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTTCATGTGTAACATGCACGATAAG 488
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 489 GAATCTAGGCGCTCTCTTCTAGTTGATGATTAGTTAGTTCTCTGAAAGTTTGCAGTGTG 548
Qy 122 MetTrpValPheThrTyrVal-GlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141
Db 549 ATGTGGGTATTACCTATGTTTGGTGGCTGCTTGTAAATGGTCTGACACTACTGATTTTGGC 608
Qy 141 AleuLeuSerLeuPheSer-IleProValIleTyrGluArgHisGlnValGlnIleAspH 161
Db 609 TCTCATTTCACTCTTCAGTGGTTCCTGTTATTTATGAACGCGCATCAGGCACAGATAGTC 668
Qy 161 istYrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
Db 669 ATTATCTAGGACTTGCATATAAATGTTAAAGATGCTATGGCTTAAATCCAGCCANAA 728
Qy 181 lePro 182
Db 729 TCCCT 733
RESULT 84
BUI09449
LOCUS
DEFINITION BUI09449 915 bp mRNA linear EST 25-NOV-2002
603126259F1 CSRQCHL13 Gallus gallus cDNA clone CHEST95f15 5', mRNA
sequence.
ACCESSION BUI09449
VERSION BUI09449.1 GI:25312699
KEYWORDS EST.
ORGANISM Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 915)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

```



FEATURES  
source

Location/Qualifiers  
1. .915  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHS795f15"  
/dev\_stage="22"  
/lab\_host="DH10B"  
/clone\_lib="CSQCHL13"  
/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
[Stratagene] vector to accommodate cDNA produced with the  
T-trimmed protocol (Construction of uni-directionally  
cloned cDNA libraries from messenger RNA for improved 3'  
end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
Ligate in double stranded adaptor containing BspI and  
BamHI sites [5'ggcgcgctgcagcccgatccgaaaaaag]  
[5'aattcttttttcggatccgggctgcacgc]"

## ORIGIN

Alignment Scores:  
Pred. No.: 4,55e-93 Length: 915  
Score: 840.00 Matches: 171  
Percent Similarity: 95.77% Conservative: 10  
Best Local Similarity: 90.48% Mismatches: 8  
Query Match: 90.81% Indels: 1  
DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU109449 (1-915)

QY 1 SerValAlaLeuLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAla 20  
DB 127 GCGGTTGTGTACCTCTTACTGGCGGACATTAAGAACAGCAGGAGTGGTGTTCGTGCC 186  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 187 AGCTTGTTCCTGCTCTCTCAATTAACAGTGTTCAGCATCGTGAGCGGTGACAGCTTACATT 246  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 247 GCCTTGGCCCTGTTCTGTGACCATCAGCTTAGATATACAGGGAGTATCCAGGCA 306  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 307 ATCCAAAAGTCGATGAAGGCCATCCATTAGGCGCTTACTTGGAGCTCTGATGTAGCTGTG 366  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 367 TCTGAAGAGCTGATTACAGAAATACAGCAGTGTGTGTGTCATCAACGGCACAGTC 426  
QY 101 LysGluLeuArgArgLeuPheLeuValAlaAspLeuValAspSerLeuLysPheAlaVal 120  
DB 427 AAGGAGCTGAGACGCTCTCTCTGTGATGCTTGTGTGATCTCTGAGTT-CCAGTG 485  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 486 TTGATGTGGGTTCACCTTACGTGGTGGCTTGTGTTTAATGGTCTGACATTACTGATCTG 545  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 546 GCTTTGATTTCCTGTTCTGAGTTCCTGTTATTTATGAGAGACATCAGGCCAGATCGAC 605  
QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 606 CATTATTGGGACTAGTGAACAAGACGTCAAAGATGCGATGGCAAGATCCAAACCAAG 665  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 666 ATCCCTGGGCTGAAGCGCAAAATTGAG 692

RESULT 85

## CN791158

LOCUS 4125836 BARC 8BOV Bos taurus cDNA clone 8BOV\_41013 5', mRNA  
DEFINITION linear  
sequence.  
ACCESSION CN791158  
VERSION CN791158.1 GI:47687138  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
REFERENCE 1 (bases 1 to 677)  
AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and Matukumalli,L.K.  
TITLE Intestinal Muscle and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Unpublished (2004)  
JOURNAL  
COMMENT Contact: Richard G. Baumann  
ANRI Bovine Functional Genomics Lab

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim alt -trim fasta. Vector identified  
by cross match using options -minmatch 12 -minscore 18  
Plate: 41 row: O column: 13

Seq primer: CCTATTAGGTGACACTATAGAAC

High quality sequence stop: 677.

## FEATURES

Location/Qualifiers  
source

1. .677  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Holstein"  
/db\_xref="taxon:9913"  
/clone="8BOV\_41013"  
/sex="Female"  
/tissue type="Epithelial, Muscle"  
/dev stage="Lactating, Neonatal"  
/lab\_host="DH10B Tona"  
/clone\_lib="BARC 8BOV"  
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site\_1:  
NotI; Site\_2: EcoRI; Normalized cow cDNA intestinal  
library in pCMVSPORT6.1, constructed from equimolar mRNA  
pools derived from 5 sources, 4 lactating intestinal, 1  
neonatal intestinal 4/5 Lactating, Proximal Duodenum,  
Jejunum, distal ileum, Colon, 1/5 Neonatal, Proximal  
Duodenum, Jejunum, distal ileum"

## ORIGIN

## Alignment Scores:

Pred. No.: 3.94e-93 Length: 677  
Score: 839.00 Matches: 170  
Percent Similarity: 98.85% Conservative: 2  
Best Local Similarity: 97.70% Mismatches: 2  
Query Match: 90.70% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN791158 (1-677)

QY 2 ValValAlaLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 156 GTTGTGACCTCCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTTCGTGCCAGC 215  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 216 TTGTTCCTGCTCTCTGCTGACAGTATTGACATTGTGAGTGTAAACGGCTTACATTGCC 275  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 276 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 335



QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAGAAATCTGATGAGGCCACCCATTGAGGCATATTGGAACTGGAAGTGTCTATATCT 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 396 GAGGAGTTGGTTTCAGAAAGTACAGCAATCTGCTCTTGCTCATGTTAACTGACCAATAAAA 455  
 QY 102 GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAATCTAGAGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTGTG 515  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 516 ATGTGGGTATTACCTATGTTGGTCCCTTGTCAATGGTCTGACACTACTAAATTTGGCT 575  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 576 CTGATTTCACTCTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCGCAATAGATCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175  
 Db 636 TATCTGGACTTGCANATAAGAAATGTTAAAGATCTATGGCT 677  
 RESULT 86  
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 LOCUS CR753971 1057 bp mRNA linear EST 02-SEP-2004  
 DEFINITION cDNA clone GP0AAA15ZC09, mRNA sequence.  
 ACCESSION CR753971  
 VERSION CR753971.1 GI:51865928  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 1057)  
 CROS.N., Tkatchenko,A.V., Pisani,D.F., Leclerc,L., Leger,J.J.,  
 Marini,J.F. and Dechesne,C.A.  
 Analysis of altered gene expression in rat soleus muscle atrophied  
 by disease  
 J. Cell. Biochem. 83 (3), 508-519 (2001)  
 21479502  
 11596118  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Genoscope sequence ID : GP0AAA15ZC09Cp1.  
 Location/Qualifiers  
 1.1057  
 /organism="Rattus norvegicus"  
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 /clone="GP0AAA15ZC09"  
 /sex="Female"  
 /tissue\_type="muscle"  
 /clone\_lib="Rattus norvegicus muscle Sprague-Dawley"  
 /note="Vector: pCRII-TOPO; Pietu G., Cros N., Leger J.J.,  
 Dechesne C.A. Subtracted library from atrophied and  
 control soleus muscles Subtraction was performed  
 according to Diatchenko et al. (Diatchenko L, Lau YF,  
 Campbell AP, Chenchik A, Moqadam F, Huang B, Lukyanov S,  
 Lukyanov K, Gurskaya N, Sverdlov ED, Siebert PD.  
 Suppression subtractive hybridization: a method for  
 generating differentially regulated or tissue-specific  
 cDNA probes and libraries. Proc Natl Acad Sci U S A. 1996;  
 93 :6025-30) Rats were female Sprague Dawley between 200  
 and 220g. Soleus muscle atrophy was performed by 14 days  
 of hindlimb suspension."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,68e-92 Length: 1057  
 Score: 834.50 Matches: 178  
 Percent Similarity: 95.31% Conservative: 5  
 Best Local Similarity: 92.71% Mismatches: 5  
 Query Match: 90.22% Indels: 4  
 DB: 7 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x CR753971 (1-1057)  
 QY 2 ValValAspLeu-LeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaLase 21  
 Db 136 GTTGTGGACCTCATCTACTTGGAGAGACATTAAAGAGACTGGAGTGGTGTAGTGCAG 195  
 QY 21 rLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaLysIleAl 41  
 Db 196 CTTATTCTCTGCTGCTCTAAACAGTGTTCAGCATTTATCAGTGTAAACGGCTACATTGC 255  
 QY 41 aLeuAla---LeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
 Db 256 CTTGGCCCATAGACTCTCGGTAATAATATAGCTTTAGGATATATAGGGCGGTGATACAGGC 315  
 QY 60 alIeGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 316 TATCCAGAAATCAGATGAGCGCCACCCATTTCAGGGCATATTTAGAATCTCGAAGTTGCTAT 375  
 QY 80 eSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 376 ATCAGAGGAATTTGGTTCAAAAATACAGTAATCTCTGCTCTTGGTCAATGTGAACAGCAAT 435  
 QY 100 eLysGluLeuArgArgPheLeuValAspAspLeuValAspSerLeuLysPhe-Alav 120  
 Db 436 AAAGAACTCAGGCGGCTTTTCTTAGTTAGTATGATTTAGTTGATTCCTCGACACTACTGATT 495  
 QY 120 alLeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL 140  
 Db 496 TGTGATGTTGGTGTCTTACTTATGTTGGTCCCTTTGTTCAATGGTCTGACACTACTGATT 555  
 QY 140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAl 160  
 Db 556 TAGCTCTGATCTCACTCTTCAGTATTCTCTGTTATTTATGAACGGCATCAGGTGCAGATAG 615  
 QY 160 spHisTyr-LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 179  
 Db 616 ATCATTTATCATAGGACATTCGAACAGAGATTATTAAGGATGCCATGGCCAAATCCAAGCA 675  
 QY 180 LysIleProGlyLeuLysArgLysAlaAsp 189  
 Db 676 AAAATCCTGGATTGAAGCGCAAGCAGAT 705  
 RESULT 87  
 CR771568  
 LOCUS CR771568 684 bp mRNA linear EST 23-SEP-2004  
 DEFINITION DKFZp469C2337.r1.469 (synonym: pkid1) Pongo pygmaeus cDNA clone  
 DKFZp469C2337-5', mRNA sequence.  
 ACCESSION CR771568  
 VERSION CR771568.1 GI:52614841  
 KEYWORDS EST.  
 SOURCE Pongo pygmaeus (orangutan)  
 ORGANISM Pongo pygmaeus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.  
 1 (bases 1 to 684)  
 REFERENCES  
 AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schapp,A.,  
 Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
 Wiemann,S.  
 TITLE Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,  
 Deutschenbaur,S., et al.)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: MIPS  
 MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert. Clone from S. Wiemann,  
Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix  
(Martinsried/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFZp469C2337) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneid=DKFZp469C2337  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/

FEATURES  
source  
1..684  
/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
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/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="469 (synonym: pkid1)"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 1..668-92 Length: 684  
Score: 834.00 Matches: 169  
Percent Similarity: 98.28% Conservative: 2  
Best Local Similarity: 97.13% Mismatches: 3  
Query Match: 90.16% Indels: 0  
Gaps: 0  
DB: 7

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CR771568 (1-684)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuTyrGlyValValPheGlyAlaSer 21  
DB 162 GTTNTTGACCTCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAGC 221  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 222 CTATTCTCGCTCTTTCATTGACATGTTACAGCATTTGAGTGTAAACAGCCTACATTGCC 281  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 282 TTGGCCCTCTCTCTGACCATCAGCTTAGATATACAGGGTGTATCAAGCTATC 341  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 342 CAGAAATCAGATGAAGCCACCATTCAGGCATATCTGGAATCTGAACTGCTATATCT 401  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 402 GAGGAGTGGTTTCAGAGTACAGTAAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 461  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 462 GNACTCAGCCGCTCTCTTAGTGTATGATTTAGTTGATTTCTGAAAGTTGTCAGTGTG 521  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 522 ATGGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGTCAGCCTACTGATTTGGCT 581  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 582 CTCATTTCACCTTCAGTGTCTCTGCTATTTATGAACGGCATCAGGCCACAGATAGATCAT 641  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175  
DB 642 TATCTAGGACTTGCAGAAATGAAGATGTTAAAGTGTATGGCT 683

RESULT 88  
BG428512 906 bp mRNA linear EST 14-MAR-2001  
LOCUS

DEFINITION 602501030F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4614679 5',  
mRNA sequence.  
ACCESSION BG428512  
VERSION BG428512.1 GI:13335018  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ULNL at:  
http://image.llnl.gov  
Plate: LCM1366 row: 1 column: 08  
High quality sequence stop: 730.

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4614679"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_75"  
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggccgcctcgcc); Site\_2: SfiI (ggccattatggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATATGCCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGGCGGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.39e-92 Length: 906  
Score: 832.00 Matches: 180  
Percent Similarity: 96.83% Conservative: 3  
Best Local Similarity: 95.24% Mismatches: 5  
Query Match: 89.95% Indels: 3  
Gaps: 0  
DB: 4  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG428512 (1-906)  
QY 2 ValValAspLeuLeuTyrTrpArgAspLeuTyrGlyValValPheGlyAlaSer 21  
DB 103 GTTGTGACCTCTCTGACTGGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAGC 162  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 163 CTATTCTCGCTCTTTCATTGACAGTATTCAGCATTTGAGCGTAAACAGCCTACATTGCC 222  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 223 TTGGCCCTCTCTCTGACCATCAGCTTAGGATATACAGGGTGTGATCAAGCTATC 282  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 283 CAGAAATCAGATGAAGCCACCATTCAGGCATATCTGGAATCTGAACTGCTATATCT 342  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 343 GAGGAGTGGTTTCAGAGTACAGTAAATCTGCTCTTGGTTCATGTGAACTGCACGATAAG 402

```

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 403 GAATCAGCCGCTCTTCTTAGTGATGATTAGTTCCTGAGATTTCAGTGTG 462
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheArgLeuThrLeuLeuAla 141
Db 463 ATGTGGGTATTACTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTGGT- 521
Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGlu-ArgHisGlnValGlnIleAspHi 161
Db 522 CTCATTTCACCTTCCTAGTGTTCCCTGTTATTATGAACGGCATCAGGCACAGATAGATCA 581
Qy 161 sTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysII 181
Db 582 TTATCTAGGACTTCGNAATAGATGTTAAAGATGCTATGCT-AAAATCCAGCAAAAT 640
Qy 181 eProGlyLeuLysArgLysAlaAsp 189
Db 641 CCCTGGATTGAAGCGCAAGTGAAT 665

RESULT 89
BUI16200
LOCUS BUI16200 961 bp mRNA linear EST 25-NOV-2002
DEFINITION 603002628F1 CSEQCHL15 Gallus gallus cDNA clone CHEST1198 5', mRNA
sequence.
ACCESSION BUI16200
VERSION BUI16200.1 GI:25322885
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 961)
Boardman,P.E., Sanz-Exquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1..961
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST1198"
/sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHL15"
/note="Organ: brain; Vector: pBluescript II KS(+); Site.1:
EcoRI; Site.2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BglI and
BamHI sites [5'-ggccgcgtgcagcccgatccgagaaaaag
[5'aattcttttttcgattccggggctgcgc]".
FEATURES
source

```

## Alignment Scores:

Pred. No.: 9,73e-92 Length: 961  
 Score: 829.50 Matches: 171  
 Percent Similarity: 95.74% Conservative: 9  
 Best Local Similarity: 90.96% Mismatches: 8  
 Query Match: 89.68% Indels: 2  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BUI16200 (1-961)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 175 GTTGTTCACCTCTTACTGCGGAGACATTAAAGAAGACAGAGTGGTGTGGTCCAGC 234
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 235 TTGTTCCTGCTGCTCTCATTAACACAGTGTTCAGCATCGTGAGCGTGAGCAGCTTACATTGCC 294
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 295 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAAGGAGTTATCCAGGCAATC 354
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 355 CAAAAGTCCGATGAAGGCCATCCATTTAGGCTTTACTTTGAGTCTGATGTAGCTGTGTCT 414
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 415 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTTGTGTCATCAACGCGCACAGTCAAG 474
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 475 GAGCTGAGACGCTCTTCTCTGTTGATGACTTGGTTGATTTCTGAGAGTTTGCAGTGTG 534
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 535 ATGTGGGTGTTCATTCACGTGGTGGCTTGTAAATGGTCTGACATTTACTGATCTGGCT 594
Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 595 TTGATTTTCGCTGTTTCAGTGTCTCTGTTATTATGAGAGACATCAGGCCCATCGACCAT 654
Qy 162 TyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 655 TATTGGGACTAGTGAACAGAGACGTCAGAGATGCGATGGC-AGATCCAGCAAGAT- 712
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 713 CCTGGGCTGAAGCGCAAAACTGAG 736

```

## RESULT 90

BQ807975

LOCUS

DEFINITION

NIHSC k121d10.Y1 NCI CGAP Brn72 Macaca mulatta cDNA clone

INWAS:5331139 5', mRNA sequence.

ACCESSION

BQ807975

VERSION

BQ807975.1 GI:22032184

KEYWORDS

EST.

SOURCE

Macaca mulatta (rhesus monkey)

ORGANISM

Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecoidea; Macaca.

REFERENCE

1 (bases 1 to 619)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

cDNA Library Preparation:

cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: info@image.llnl.gov  
Plate: LLM11840 row: H column: 20  
Seq primer: M13Rpl reverse primer (ABI).  
Location/Qualifiers

## FEATURES

source  
1..619  
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/clone\_lib="NCI CGAP Brn72"  
/note="Organ: brain; Vector: pCMV-SPT6.1; Site 1: NotI; Site 2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Invitrogen. Note: this is a NCI CGAP Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 6e-92 Length: 619  
Score: 829.00 Matches: 167  
Percent Similarity: 98.84% Conservatve: 4  
Best Local Similarity: 96.53% Mismatches: 2  
Query Match: 89.62% Indels: 0  
DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BQ807975 (1-619)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysLysThrGlyValValPheGlyAlaSer 21  
DB 100 GTTGTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 159  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 160 CTAATTCCTGCTCTTCATTCAGCATATTCAGCATGTGAGTGTGAACAGCTTACATGCC 219  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 220 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 279  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerLeuValAlaIleSer 81  
DB 280 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGGAAGTTGCCATATCT 339  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 340 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTCTGTGTCATGTGAACCTGCACGATAAAG 399  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 400 GAACCTCAGCGCCCTCTCTAGTTCATCATTTAGTTAGTTGATTCTCTGAAGTTGCCAGTGTG 459  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 460 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTATGCTCTGACGCTACTGATTTGGCT 519  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 520 CTAATTCACCTCTTCAGTGTCTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCAT 579  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMet 174  
DB 580 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATG 618

## RESULT 91

CO505196  
LOCUS  
DEFINITION  
GGEZEB1026A09, g embryo breast muscle - B61 Gallus gallus cdna clone  
GGEZEB1026A09, mRNA sequence.  
ACCESSION  
CO505196

CO505196.1 GI:50275382  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

AUTHORS  
1. (Bases 1 to 669)  
Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B.,  
Patrício, M., Ledur, M.C. and Coutinho, L.L.  
Discovery of new genes expressed in the chicken breast muscle  
Unpublished (2004)

## TITLE

JOURNAL  
COMMENT  
Contact: Helena J. Alves  
Laboratory of Animal Biotechnology, Dep. of Animal Production  
ESALQ - University of Sao Paulo  
Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434

Fax: 55 19 3429 4285

Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br

PCR Primers

BACKWARD: T7.

## FEATURES

source

Location/Qualifiers

1..669  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
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/tissue\_type="breast muscle"  
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/clone\_lib="embryo breast muscle - B61"  
/note="Vector: pSPORI1; Site 1: NotI; Site 2: SalI; This  
cDNA library was constructed with the SuperScript Plasmid  
System with Gateway Technology kit (Invitrogen), following  
manufacturer's protocols. Plasmid DNA was purified using a  
modified alkaline lysis method. Sequencing reactions were  
conducted using the DYEnamic Cycle Sequencing kit for  
MegABACE (Amersham Biosciences) according to the  
manufacturer's recommendations. Clones were sequenced by  
the 5' end with T7 primer. Sequencing reactions were  
analyzed on MegABACE1000 DNA Sequencer (Amersham  
Biosciences). The quality and clustering of the ESTs were  
analyzed using the softwares Phred/Cap3. Only EST  
sequences with Phred quality greater than 20 and at least  
150 bp were considered for clustering."

## ORIGIN

Alignment Scores:  
Pred. No.: 6.7e-92 Length: 669  
Score: 829.00 Matches: 171  
Percent Similarity: 95.74% Conservatve: 9  
Best Local Similarity: 90.96% Mismatches: 7  
Query Match: 89.62% Indels: 2  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CO505196 (1-669)

QY 3 ValAspLeuLeuTyrTrp-ArgAspIleLysLysThrGlyValValPheGlyAlaSerLe 22  
DB 43 GTTGACCTCTTTACTGNCAGACATTAAGACAGGAGTGTGTGTT-GGTGCCAGCTT 101  
QY 22 uPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLe 42  
DB 102 GTTCCTGCTCTCTCATTAACAGTGTTCAGCATCGTCGAGCTTACATTCGCTT 161  
QY 42 uAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleG 62  
DB 162 GGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGTTATCCAGGCATCCA 221  
QY 62 nLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerLeuValAlaIleSerG 82  
DB 222 AAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTGGAGTCTGATGTAGTGTCTGA 281

Qy 82 uGluLeuValGlnLysTyrSerAasnSerAlaLeuGlyHisValAasnSerThrIleLysG1 102  
 Db 282 AGAGCTGATTTCAGAAATACAGCAGTGTGTCTTGGTCAACATCAACGCCAGTCAAGGA 341  
 Qy 102 uLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMe 122  
 Db 342 GCTGAGACGCCCTCTCCCTCGTGTGATGACTTGGTGTGATCTCTGAAGTTTGCAGTGTGAT 401  
 Qy 122 tTTPValPheThrTyrValGlyAlaLeuPheAasnGlyLeuThrLeuLeuLeuAlaLe 142  
 Db 402 GTGGGTGTTCACTACGTGTGTGCTGTGTGTTAAATGGTCTGACATCTACTGATCTGGCTTT 461  
 Qy 142 uileSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTy 162  
 Db 462 GATTTCGCTGTTCACTGCTCTGTTCTGTTATTTATGAGAGACATCAGGCCCCAGATCGACCATTA 521  
 Qy 162 rLeuGlyLeuAlaAasnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 522 TTTGGGACTAGTGAAACAGACGTCAAAGATGCGATGCGTGAAGATCCCAAGCAAGATCCC 581  
 Qy 182 oGlyLeuLysArgLysAlaAsp 189  
 Db 582 TGGGCTGAGCGCAAACTGAG 603

RESULT 92  
 B1547877  
 LOCUS 603192073F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5263026 5',  
 DEFINITION mRNA sequence.

ACCESSION B1547877.1 GI:15435189  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 614)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toehiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM11663 row: b column: 19  
 High quality sequence stop: 614.

FEATURES  
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 1. 614  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5263026"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH MGC 95"  
 /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (Gcgag); Oligo-qt primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
 Pred. No.: 7,89e-92 Length: 614  
 Score: 828.00 Matches: 169  
 Percent Similarity: 98.85% Conservative: 3  
 Best Local Similarity: 97.13% Mismatches: 2  
 Query Match: 89.51% Indels: 0  
 DB: Gaps: 4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x B1547877 (1-614)

Qy 16 ValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35  
 Db 7 GTGGTGTGTGGTGGCCGCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGC 66  
 Qy 36 ValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLys 55  
 Db 67 GTAAACAGCCATACATTGCTTTGGCCCTCTCTCTGTGACCATCAGCTTTTAGGATATACAG 126  
 Qy 56 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 75  
 Db 127 GGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAA 186  
 Qy 76 SerGluValAlaIleSerGluLeuValGlnLysTyrSerAasnSerAlaLeuGlyHis 95  
 Db 187 TCTGAGTTGCTATATCTGAGGAGTTGGTTTCAGAAATACAGTAAATCTCTGCTCTTTGGTCAT 246  
 Qy 96 ValAasnSerThrIleLysGluLeuArgAlaLeuPheLeuValAspLeuValAspSer 115  
 Db 247 GTGAACCTGACAGTAAGGAACCTCTCTCTTAGTGTGATGATTTAGTTGATTTCT 306  
 Qy 116 LeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeuPheAasnGlyLeu 135  
 Db 307 CTGAGTTTGCAGTGTGTGATGTTGGTATTTACCTATGTTGGTGGCTTTGTTAAATGGTCTG 366  
 Qy 136 ThrLeuLeuLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHis 155  
 Db 367 ACACCTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCAT 426  
 Qy 156 GlnValGlnIleAspHisTyrLeuGlyLeuAlaAasnLysSerValLysAspAlaMetAla 175  
 Db 427 CAGGCACAGATAGATCATTTATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCT 486  
 Qy 176 LysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189  
 Db 487 AAATCCACAGCAAAATCCCTGATTCAGCGCAAGCTGAA 528

RESULT 93  
 CR771272

LOCUS CR771272

DEFINITION DKFZp469F2235\_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone

ACCESSION CR771272

VERSION CR771272.1 GI:52614545

KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

REFERENCE 1 (bases 1 to 644)

AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,

Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and

Wiemann, S.

TITLE Pongo pygmaeus mRNA (Poustka, A., Albert, R., Moosmayer, P., et al.)

JOURNAL Unpublished (2004)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for

ordering:

<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469F2235>

Further information about the clone and the sequencing project is



RESULT 95  
BG568630  
LOCUS  
DEFINITION 602587637F1 NIH\_MGC\_76 Homo sapiens CDNA clone IMAGE:4716393 5',  
mRNA sequence.  
ACCESSION BG568630  
VERSION BG568630.1 GI:13576283  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 755)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)  
UNPUBLISHED (1999)  
CONTACT: Robert Strauberg, Ph.D.  
Email: [rsraube@mail.nih.gov](mailto:rsraube@mail.nih.gov)  
Tissue Procurement: CLONETECH Laboratories, Inc.  
CDNA Library Preparation: CLONETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI564 row: j column: 10  
High quality sequence stop: 719.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4716393"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NIH\_MGC\_76"  
/notes="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGCGGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

## FEATURES

source

RESULT 96  
BUI16870  
LOCUS  
DEFINITION 603138816F1 CSEQCHL15 Gallus gallus CDNA clone CHEST12704 5', mRNA  
sequence.  
ACCESSION BUI16870  
VERSION BUI16870.1 GI:25324153  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 934)  
BOARDMAN, P.R., SANZ-EZQUERRO, J., OVERTON, I.M., BURT, D.W., BOSCH, E.,  
FONG, W.T., TICKLE, C., BROWN, W.R.A., WILSON, S.A. and HUBBARD, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392  
PUBMED  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).  
Location/Qualifiers  
1. 934  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST12704"  
/sex="Female"  
/tissue\_type="cerebrum"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHL15"  
/notes="Organ: brain; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
[Stratagene] vector to accommodate cDNA produced with the  
T-primed protocol (Construction of uni-directionally  
cloned cDNA libraries from messenger RNA for improved 3'  
end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
Ligate in double stranded adaptor containing BglI and  
BamHI sites [5'ggcgcggtgcagcccgatccgaaaaaag]

## ORIGIN

Alignment Scores:  
Pred. No.: 1.06e-91 Length: 755  
Score: 828.00 Matches: 178  
Percent Similarity: 95.81% Conservative: 5  
Best Local Similarity: 93.19% Mismatches: 5  
Query Match: 89.51% Indels: 4  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG568630 (1-755)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 178 GTTGTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGCGTGTGTCGCCAGC 237  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 238 CTATTCCTGCTGCTTTCAATGACAGTATTTCAGCATTTGTGACGCTACAGCTCATTTGCC 297  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 298 TTGCGCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCGTGTGTCGCCAGCTATC 357  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 358 CAGAAATCAGATGAAGGCCACCCATTGAGGCGCATCTCGGAATCTGGAATCTGGAATCTATATCT 417

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValaAsnSerThrIleLys 101  
Db 418 GAGGAGTTGGTTTTCAGAGTACAGTAATCTGCTCTGGTTCATGTGAACCTGCACGATAAG 477  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 478 GAACCTCAGGCGCTCTCTTCTAGTTGATGATTAGTTGATTCTCTGAAGATTTCAGAGTGTG 537  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 538 ATGTGGGTATTATACCTATGTTGGTCCCTGTTTAAATGCTGCACACTACTGAT-TTGGCT 596  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 597 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 656  
Qy 162 TyrIleGlyLeuAlaLeuLysSerValLysAspAla-MetAlaLysIleGlnAla--Lys 180  
Db 657 TATCTAGGACTTGCAAATAGAATGTTACAGATGCTAATGTTAAATCCAAAGCAAAAA 716  
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 717 ATCCCTGGATTGAAGCGCAAAAGTGAA 743

## RESULT 96

BUI16870

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT

DEPARTMENT

UNIVERSITY

(UMIST)

PO BOX

TEL:

FAX:

EMAIL:

LOCATION/QUALIFIERS

1. 934

/ORGANISM="Gallus gallus"

/MOL\_TYPE="mRNA"

/STRAIN="Compton Line 151"

/DB\_XREF="taxon:9031"

/CLONE="CHEST12704"

/SEX="Female"

/TISSUE\_TYPE="cerebrum"

/DEV\_STAGE="adult"

/LAB\_HOST="DH10B"

/CLONE\_LIB="CSEQCHL15"

/NOTES="Organ: brain; Vector: pBluescript II KS(+); Site 1:

EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)

[Stratagene] vector to accommodate cDNA produced with the

T-primed protocol (Construction of uni-directionally

cloned cDNA libraries from messenger RNA for improved 3'

end DNA sequencing by Glenn Fu, et al. U.S. Patent #

6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.

Ligate in double stranded adaptor containing BglI and

BamHI sites [5'ggcgcggtgcagcccgatccgaaaaaag]



[5'aattcttttttcggtccggggtgcagc]

## ORIGIN

## Alignment Scores:

Pred. No.: 1.43e-91 Length: 934  
Score: 828.00 Matches: 169  
Percent Similarity: 96.20% Conservativity: 8  
Best Local Similarity: 91.85% Mismatches: 7  
Query Match: 89.51% Indels: 1  
DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BUL16870 (1-934)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 173 GTGTGTGACCTCTTCTGCGGACACATTAAAGACAGGAGTGTGT-GGTCCAGC 231  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 232 TTGTTCTGCTGCTCTCAATTAACAGTTCAGCATCGTGAGCGTGACAGTTACATTGCC 291  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 292 TTGGCCCTGCTTCTGTGACCATCAGCTTAGGATATACAGGGAGTTATCCAGGCAATC 351  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 352 CAAAGTCCGATGAAGGCCCATCCATTTAGGGCTTACTTGAGGTCTGATGTAGTGTGTCT 411  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 412 GNAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGTTCATCATCAAGGCACAGTCAAG 471  
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 472 GAGCTGAGAGCGCTCTCTCGTTCATGACTTGGTTGATCTCTCAAGTTGTCAGTGTG 531  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
DB 532 ATGTGGGTTCACATTACGTGGTGCTGCTGTTTAAATGCTGTGACATTACTGATCTGCT 591  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 592 TTGATTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 652 TATTGGGACTAGTGAACAAGAACCTCAAGATGCGATGGCAAGATCAAGCAAGATC 711  
QY 182 ProGlyLeuLys 185  
DB 712 CCTGGGCTGAAA 723

## RESULT 97

LOCUS BG696431  
DEFINITION 602659532F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4802911 5',  
mRNA sequence.

ACCESSION BG696431  
VERSION BG696431.1 GI:13961567

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 934)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10697 Row: 0 Column: 08  
High quality sequence stop: 763.

## FEATURES

## source

Location/Qualifiers  
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/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NCI\_CGAP\_Skn3"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.76e-91 Length: 991  
Score: 826.00 Matches: 177  
Percent Similarity: 96.26% Conservativity: 3  
Best Local Similarity: 94.55% Mismatches: 5  
Query Match: 89.30% Indels: 3  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG696431 (1-991)

QY 4 AspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe 23  
DB 216 GACCTCTGTTACTCGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGCTATTC 275  
QY 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43  
DB 276 CTGCTGCTTTTCATTCAGCAGTATTCAGCATTTGTGAGCGTAAAGCTATCATTCGCTTGGCC 335  
QY 44 -LeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLy 63  
DB 336 CCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAA 395  
QY 63 sSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluG 83  
DB 396 ATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGA 455  
QY 83 uLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLe 103  
DB 456 GTAGTTTCAGAACTACAGTAATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 515  
QY 103 uArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTr 123  
DB 516 CAGGCGCTCTCTTCTTAGTATGATGATTTAGTTGATTTCTCTGAAGTTGCGATGTTGATGTG 575  
QY 123 pValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuL 143  
DB 576 GGTATTTACCTATGTTGGTGGCTTTGTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634  
QY 143 eSerLeuPheSerIleProValIleTyrGluArgHisGlnVal-GlnIleAspHisTyrL 163  
DB 635 TTCACTCTTCAGTCTCTCTGTTATTTATGAACGGCATCAGGCAACAGATAGATCATTCATC 694  
QY 163 euGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProG 183  
DB 695 TAGGACTTGCATAAAGAAATGTCAAAGATGCTATGGGTAAATCAAGCAAAAAATCCCTG 754  
QY 183 lyLeuLysArgLysAla 188  
DB 755 GATTGAAGCGCAAAAGC 771

## RESULT 98

AW230936





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Query Match: 88.92% Indels: 3
DB: 4 Gaps: 0
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QY 2 ValValAspLeuLeuTyrTrpArgAspIleValSerThrGlyValValPheGlyAlaSer 21
DB 169 GTTGTGACCTCTCTGCTGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 228
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 229 CTATTCTCTGCTCTTTCATTGACAGTATTGAGCGTAAACAGCCTACATTGCC 288
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 289 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGCTGTGATCCAGCTATC 348
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 349 CAGAATCAGATGAAGGCCACCGATTGAGGCTATCTGGAATCTGGAAGTTGCTATATCT 408
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 409 GAGGAGTTGGTTTCAAGTACAGTAATCTGCTCTTGGTCACTGTAAGTCAAGATAAG 468
QY 102 GluLeuArgArgLeuPheLeuValAsp-AspLeuValAspSerLeuLysPheAlaValLe 121
DB 469 GAACTCAGCGCGCTCTCTTCTAGTCACTGATTAGTATTCTCTGAAAGTTTGCAAGTGT 528
QY 121 uMetTrpValPheThrTyrValGlyValAlaPheAsnGlyLeuThrLeuLeuAl 141
DB 529 GATGGGGTATTACCTAGTTGGGCTTGTGTTTATGATGCTGACACTACTGATTTGGC 588
QY 141 aleuIleSerLeuPheSer-IleProValIleTyrGluArgHisGlnValGlnIleAspH 161
DB 589 TCTCATTTCACTCTTCAGCTGTTCTGTTTATTATGAACGCGCATCAGGCACAGATAGATC 648
QY 161 IeTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
DB 649 ATTATCTAAGATGCG--AATAGAATGTATAGGATGCTATGTTTAAAAATCCAAGCAAAA 706
QY 181 leProGlyLeuLysArgLysAlaAsp 189
DB 707 TCCCTGGATTGAAGCGCAAGTTGAA 732

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## RESULT 100

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AV702687 719 bp mRNA linear EST 08-OCT-2000
LOCUS AV702687 ADB Homo sapiens cDNA clone ADBBB01 5', mRNA sequence.
DEFINITION AV702687
ACCESSION AV702687
VERSION AV702687.1 GI:10719017
KEYWORDS EST.
SOURCE Homo sapiens (human)

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## ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,
Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,
Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,
Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801319(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

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## FEATURES

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Search completed: June 19, 2005, 10:16:37
Job time : 2588 secs

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XhoI"

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## ORIGIN

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Alignment Scores: 7.26e-91 Length: 719
Score: 821.00 Matches: 171
Percent Similarity: 96.67% Conservative: 3
Best Local Similarity: 95.00% Mismatches: 5
Query Match: 88.76% Indels: 1
DB: 1 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x AV702687 (1-719)
QY 11 IleValLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30
DB 1 ATTAAGAAGACTGGAGTGGTGTGGTGCCAGCCTATTCTGCTGCTTTCATTGACAGTA 60
QY 31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSer 50
DB 61 TTCAGCATTTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTCTCTGTGACCATCAGC 120
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
DB 121 TTTAGGATATACAAAGGCTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCATTC 180
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
DB 181 AGGCGATATCTGGAATCTGAAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 240
QY 91 SerAlaLeuGlyHisValAsnSerThrIleLysGlnLeuArgLeuPheLeuValAsp 110
DB 241 TCTGCTCTTGGTCACTGTAACCTGCACGATAAAGAACTCAGCGCGCTCTTCTTAGTTGAT 300
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyVala 130
DB 301 GATTTAGTTGATCTCTGAAAGTTTGACGTGTGATGGGTATTTCCTATGTTGGTGCC 360
QY 131 LeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSerIleProVal 150
DB 361 TTGTTTAATGCTCTGACACTACTGATTTTGGCTCTCTCATTTCCAGTGTTCCTGTT 420
QY 151 IleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerVal 170
DB 421 ATTTATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATAAAGAATGTT 480
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIlePro-GlyLeuLysArgLysAlaAsp 189
DB 481 AAAGATGCTATGGCTTAANATCCAGCAAAAAATCTTGGATTGAGGCCANAGCTGAA 538

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## FEATURES

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1..719
source

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 170.11 Seconds  
(without alignments)  
2678.292 Million cell updates/sec

Title: US-09-830-972-29

Perfect score: 5923

Sequence: 1 MEDLDQSLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRAE 1178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5882	99.3	1178	3	AAY71311 Human neu
2	5815	98.2	1192	4	AAU04591 Human Nog
3	5815	98.2	1192	5	ABP68600 Human pan
4	5815	98.2	1192	6	ABR59667 Human Nog
5	5815	98.2	1192	8	ADP45551 Human Nog
6	5810	98.1	1192	3	AAY56967 Human MAG
7	5810	98.1	1192	4	AAAB82349 Human Nog
8	5810	98.1	1192	5	ABG30938 Human Nog
9	5810	98.1	1192	5	ABB81078 Human neu
10	5810	98.1	1192	8	ADP67234 Human Nog
11	5810	98.1	1192	8	ADR13966 Human Nog
12	5808	98.1	1192	8	ADO08103 Human pol
13	5794	97.8	1192	7	ADK67502 Human RTN
14	5758	97.2	1192	8	ADO26400 Human tru
15	5526.5	93.3	1246	4	AAU33228 Novel hum
16	4560	77.0	983	6	ABU11573 Human MDD
17	4400	74.3	893	3	AAAY95012 Human sec
18	4296.5	72.5	1163	3	AAY71310 Rat neu
19	4296.5	72.5	1163	5	ABB81074 Rat neuro
20	4296.5	72.5	1163	8	ADO26399 Rat trunc
21	4296.5	72.5	1163	8	ADP45572 Rat NogoA
22	4294.5	72.5	1162	3	AAY71557 Rat Nogo
23	4289	72.4	1162	8	ADT89537 Mus muscu
24	4286.5	72.4	1163	3	AAY71384 Alternati
25	4277.5	72.2	1163	8	ADO08105 Mouse pol

26	3931	66.4	819	8	ADP45553	Human NiG
27	3388.5	57.2	974	3	AAY71560	Rat Nogo
28	3146.5	53.1	642	2	AAW58383	Human sec
29	3146.5	53.1	642	4	AAAB90682	Human BGI
30	2715	45.8	803	3	AAY71562	Rat Nogo
31	2593.5	43.8	798	8	ADO26414	Rat trunc
32	2529.5	42.7	737	3	AAY71386	Rat Nogo
33	2487.5	42.0	746	3	AAY71391	Rat Nogo
34	2457	41.5	736	3	AAY71398	Rat Nogo
35	2449.5	41.4	732	3	AAY71399	Rat Nogo
36	2425.5	41.0	739	8	ADO26415	Rat trunc
37	2405.5	40.6	695	3	AAY71387	Rat Nogo
38	2344.5	39.6	684	3	AAY71394	Rat Nogo
39	1948.5	32.9	552	3	AAY71388	Rat Nogo
40	1743	29.4	502	3	AAY71396	Rat Nogo
41	1634.5	27.6	475	3	AAY71389	Rat Nogo
42	1566.5	26.4	403	3	AAY71563	Rat Nogo
43	1552.5	26.2	457	3	AAY71392	Rat Nogo
44	1495.5	25.2	373	3	AAAY53624	A bone ma
45	1495.5	25.2	373	3	AAAY56969	Human MAG

## ALIGNMENTS

RESULT 1

AAAY71311  
ID AAY71311 standard; protein; 1178 AA.

XX AC

AAAY71311;

DT 02-NOV-2000 (first entry)

DE Human neurite growth inhibitor Nogo.

XX Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; menigioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.

XX OS Homo sapiens.

EH Key Location/Qualifiers

FT Misc-difference 187 /label= Unknown

FT Misc-difference 188 /label= Unknown

FT Misc-difference 189 /label= Unknown

FT Misc-difference 190 /label= Unknown

FT Misc-difference 221 /label= Unknown

FT Misc-difference 328 /label= Unknown

FT Misc-difference 477 /label= Unknown

FT Region 977..1012

FT Region 994..1174

FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

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FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

FT Region /note= "Region specifically described in claim 16"

PR 06-NOV-1998; 98US-0107446P.  
 XX (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 XX Schwab ME, Chen MS;  
 XX  
 XX WPI; 2000-400052/34.  
 DR  
 XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 XX Claim 11; Fig 13; 122pp; English.  
 XX  
 CC The present sequence is a human Nogo protein which is a potent neural  
 CC cell growth inhibitor and is free of all central nervous system (CNS)  
 CC myelin material with which it is naturally associated. The human Nogo  
 CC sequence was derived by aligning human expressed sequence tags (ESTs)  
 CC e.g. AAL58636, A3333267, AA081783, AAL67765, AA322318, AA092565, AA081525  
 CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments  
 CC displaying neurite growth inhibitory activity are used in the treatment  
 CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
 CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
 CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,  
 CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
 CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
 CC activity can be used to treat or prevent hyperproliferative or benign  
 CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
 CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
 CC production of Nogo protein to induce regeneration of neurons or to  
 CC promote structural plasticity of the CNS in disorders where neurite  
 CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers  
 XX  
 XX Sequence 1178 AA;  
 SQ

Query Match 99.3%; Score 5882; DB 3; Length 1178;  
 Best Local Similarity 99.7%; Pred. No. 9.3e-297;  
 Matches 1175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEDDQSPVLSSSDSPRPQPAFKYQVREPEDEEEDEDEDEDELEEVLERKPA 60  
 DB 1 MEDDQSPVLSSSDSPRPQPAFKYQVREPEDEEEDEDEDEDELEEVLERKPA 60  
 QY 61 AGLSAAPVPTAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQPSWDPSPVSTVPAP 120  
 DB 61 AGLSAAPVPTAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQPSWDPSPVSTVPAP 120  
 QY 121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVWTPPAPAPAPSTPAAPKRG 180  
 DB 121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVWTPPAPAPAPSTPAAPKRG 180  
 QY 181 SSGAVVXXXXKIMDLKEQPGNTISAQEDFPVLLLETAASPSLSPLSAASPKHEYLGN 240  
 DB 181 SSGAVVXXXXKIMDLKEQPGNTISAQEDFPVLLLETAASPSLSPLSAASPKHEYLGN 240  
 QY 241 LSTVLPTGTEGLQENVSSEASKEVSEKAKTLLIDRLTERSELYSEMGSSFSVSPKAESAV 300  
 DB 241 LSTVLPTGTEGLQENVSSEASKEVSEKAKTLLIDRLTERSELYSEMGSSFSVSPKAESAV 300  
 QY 301 IVANPREELIVKNDEEKLVSNNILHXQOELPTALTCLVKDEDEVVSSSEKAKDSFNKRV 360  
 DB 301 IVANPREELIVKNDEEKLVSNNILHXQOELPTALTCLVKDEDEVVSSSEKAKDSFNKRV 360  
 QY 361 AVEAMPREYADFKPERVWEVKDSKEDSDMLAAGKIESNLESKVDKCFADSLSEQTNH 420  
 DB 361 AVEAMPREYADFKPERVWEVKDSKEDSDMLAAGKIESNLESKVDKCFADSLSEQTNH 420

QY 421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDTSENXTDE 480  
 DB 421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDTSENXTDE 480  
 QY 481 KKIEBKAAQIVTEKNTSTKTNPPFFVAAQDSEDTVTTDNLTKVTEEVVANNPEGLTPDL 540  
 DB 481 KKIEBKAAQIVTEKNTSTKTNPPFFVAAQDSEDTVTTDNLTKVTEEVVANNPEGLTPDL 540  
 QY 541 VOEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSEFESEATPPSVLPDI 600  
 DB 541 VOEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSEFESEATPPSVLPDI 600  
 QY 601 VMEAPLNSAVPSAGASVTOPSSSPLEASSVNYESIKHEPENPPPPPEEAMSVSLKVSIGKE 660  
 DB 601 VMEAPLNSAVPSAGASVTOPSSSPLEASSVNYESIKHEPENPPPPPEEAMSVSLKVSIGKE 660  
 QY 661 EIKEPENINAALOETEAPYISITACDLIKETKLSAPAPDFSDYSEMAKVEQVPDHSSELV 720  
 DB 661 EIKEPENINAALOETEAPYISITACDLIKETKLSAPAPDFSDYSEMAKVEQVPDHSSELV 720  
 QY 721 EDSSPDSPPVDLFSDDSIPIVPOKQDETMVLVKSLSLTSTSFESMIETENKELKSALPPEG 780  
 DB 721 EDSSPDSPPVDLFSDDSIPIVPOKQDETMVLVKSLSLTSTSFESMIETENKELKSALPPEG 780  
 QY 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVYSNDDLFISKQAQIRE 840  
 DB 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVYSNDDLFISKQAQIRE 840  
 QY 841 TETFSDDSPIEIIIDFPFTLISKTDTSFKLAREYTDLEVSHKSEIANAPDAGSLPCTEL 900  
 DB 841 TETFSDDSPIEIIIDFPFTLISKTDTSFKLAREYTDLEVSHKSEIANAPDAGSLPCTEL 900  
 QY 901 PHDSLKNIQPKVEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVPKVLE 960  
 DB 901 PHDSLKNIQPKVEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVPKVLE 960  
 QY 961 KEAEKKLPSTDEKEDRSPSAIFSADLGTSVVDLLYWRDIKKTGVVFGASFLLLSLTVF 1020  
 DB 961 KEAEKKLPSTDEKEDRSPSAIFSADLGTSVVDLLYWRDIKKTGVVFGASFLLLSLTVF 1020  
 QY 1021 STVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVOKYSNS 1080  
 DB 1021 STVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVOKYSNS 1080  
 QY 1081 ALGHVNCITKELRRLFLVDDLVDSLKPAVLMWVFTYVYGALFNGLTLLILALISLSPVPI 1140  
 DB 1081 ALGHVNCITKELRRLFLVDDLVDSLKPAVLMWVFTYVYGALFNGLTLLILALISLSPVPI 1140  
 QY 1141 YERHOAQIDHYGLANKNVKDMAMAKIOPGLKRAE 1178  
 DB 1141 YERHOAQIDHYGLANKNVKDMAMAKIOPGLKRAE 1178  
 RESULT 2  
 AAU04591  
 ID AAU04591 standard; protein; 1192 AA.  
 XX  
 AC AAU04591;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE Human Nogo protein.  
 XX  
 KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;  
 KW cranial trauma; cerebral trauma; spinal cord injury; stroke;  
 KW demyelinating disease; multiple sclerosis; monophasia demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;  
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;  
 KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;  
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;  
 XX  
 XX Krabbe's disease.  
 XX  
 XX Homo sapiens.

XX	Key	Location/Qualifiers	Db	61	AGLSAAVPPTAPAAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDSPVSTVPAP	120
FT	Domain	1054..1119				
FT		/label= Luminal_extracellular_domain				
FT	Peptide	/note= "This sequence is specifically claimed"	Qy	121	SPLSAAAIVSPSKLPEDDEPPAPRPDPASVSPQAEVWTPPAPAPAPPTTAPAKRG	180
FT		1055..1094				
FT		/label= Pep1	Db	121	SPLSAAAIVSPSKLPEDDEPPAPRPDPASVSPQAEVWTPPAPAPAPPTTAPAKRG	180
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	181	SSGA-----VVXXXKIMDLKEQPGNTISAGQEDPSPVLETTAASPSLSP	226
FT	Peptide	1064..1088				
FT		/label= Pep2	Db	181	SSGSVDETLPALPAASEPVRSSAENMDLKEQPGNTISAGQEDPSPVLETTAASPSLSP	240
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	227	LSAASFKEHYLGNLSTVLPTEGTLQENVSPASKEVSEKAKTLIDRLDTFSELEYSEM	286
FT	Peptide	1074..1098				
FT		/label= Pep3	Db	241	LSAASFKEHYLGNLSTVLPTEGTLQENVSPASKEVSEKAKTLIDRLDTFSELEYSEM	300
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	287	GSSFSVSPKAEASAVIVANPREIIVKKNDBEELVNNILHQQOELPTALTKLVKEDSVV	346
FT	Peptide	1084..1108				
FT		/label= Pep4	Db	301	GSSFSVSPKAEASAVIVANPREIIVKKNDBEELVNNILHQQOELPTALTKLVKEDSVV	360
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	347	SSEKAKDSFNEKRVAVAPMREYADPKPFRVWVVKDSKEDSDMLAAGGKIESNLESKV	406
FT	Peptide	1095..1119				
FT		/label= Pep5	Db	361	SSEKAKDSFNEKRVAVAPMREYADPKPFRVWVVKDSKEDSDMLAAGGKIESNLESKV	420
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	407	DKKCFADSLQTNHEKDSSESNDDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
FT	Peptide		Db	421	DKKCFADSLQTNHEKDSSESNDDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
XX	WO200151520-A2.					
XX	19-JUL-2001.					
XX	12-JAN-2001; 2001WO-US001041.					
XX	12-JAN-2000; 2000US-0175707P.					
PR	26-MAY-2000; 2000US-0207366P.					
PR	29-SEP-2000; 2000US-0236378P.					
XX	(UYUA ) UNIV YALE.					
XX	Strittmatter SM;					
XX	WPI; 2001-442138/47.					
DR	N-PSDB; AAS09453.					
XX	Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders.					
XX	Example 1; Page 101-104; 109pp; English.					
PS	The sequence is the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasia demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease					
XX	Sequence 1192 AA;					
Qy	Query Match	98.2%; Score 5815; DB 4; Length 1192;				
Db	Best Local Similarity	97.2%; Pred. No. 2.8e-293;				
Qy	Matches 1160; Conservative	4; Mismatches 13; Indels 16; Gaps 3;				
Qy	1 MEDLDQSLVSSSSPPRPQAFKYQFVRPEDEDEDEDEDEDEDEDEDEDEDELEVLKPA	60				
Db	1 MEDLDQSLVSSSSPPRPQAFKYQFVRPEDEDEDEDEDEDEDEDEDEDEDELEVLKPA	60				
Qy	61 AGLSAAVPPTAPAAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDSPVSTVPAP	120				



QY 1126 LILALISLFSVPVIERHQAQIDHYLGANKVNDAMAKIQAKIPGLKRAE 1178  
 |||||  
 Db 1140 LILALISLFSVPVIERHQAQIDHYLGANKVNDAMAKIQAKIPGLKRAE 1192

## RESULT 4

ABR59667  
 ID ABR59667 standard; protein; 1192 AA.

XX ABR59667;

XX 22-JUL-2003 (first entry)

XX Human NogoA protein.

XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

XX Homo sapiens.

XX WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US0322007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYVA ) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.

XX N-PSDB; ACC81048.

XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 PT injury, e.g. spinal cord injury.

XX Disclosure; Page 131-135; 148pp; English.

CC The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 CC human Nogo receptor (Ngr) NTLRRCT domain), or residues 27-309 of P1 with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 CC axonal growth by a central nervous system (CNS) neuron. The Ngr  
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an Ngr protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention

XX Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 6; Length 1192;

Best Local Similarity 97.2%; Pred. No. 2.8e-293;

Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

QY 1 MEDLQSPFLVSSSDSPRPQPAFKYQFVREPEDEEEDEDELEBLEVLKPKA 60

Db 1 MEDLQSPFLVSSSDSPRPQPAFKYQFVREPEDEEEDEDELEBLEVLKPKA 60  
 QY 61 AGLSAAVPPTAPAGAPLMDFGNDVPPAPRGPLPAPAPVAPERQPSWDPSVSTVPAP 120  
 Db 61 AGLSAAVPPTAPAGAPLMDFGNDVPPAPRGPLPAPAPVAPERQPSWDPSVSTVPAP 120  
 QY 121 SPLSAAA VSPSKLPEDDEPPAPPPPPASVSPQAEPVWTPAPAPAPPTPAPAKRGG 180  
 Db 121 SPLSAAA VSPSKLPEDDEPPAPPPPPASVSPQAEPVWTPAPAPAPPTPAPAKRGG 180  
 QY 181 SSGA-----VVXXYKIMDLKQPGNTTISAGQEDPSSVLETAASPSLSP 226  
 Db 181 SSGVDETLFALPAASEPVITSSAENMDLKQPGNTTISAGQEDPSSVLETAASPSLSP 240  
 QY 227 LSAASFKEHYGLNLSVLTPTGTLQENVSASKEVSEKAKTLLIDRLTTFSELEYSEM 286  
 Db 241 LSAASFKEHYGLNLSVLTPTGTLQENVSASKEVSEKAKTLLIDRLTTFSELEYSEM 300  
 QY 287 GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQQELPTALTCLKVKEDEV 346  
 Db 301 GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQQELPTALTCLKVKEDEV 360  
 QY 347 SSEKAKOSFNEKRVAVAPMRREYADPKPFRVWEVKDSKEDSDMLAAGGKIESLSEKV 406  
 Db 361 SSEKAKOSFNEKRVAVAPMRREYADPKPFRVWEVKDSKEDSDMLAAGGKIESLSEKV 420  
 QY 407 DKCFCADSLQTNHEKDSSENDDTSPSTPEGIKDRSGAYITCAPFPNPAATESIATNIF 466  
 Db 421 DKCFCADSLQTNHEKDSSENDDTSPSTPEGIKDRSGAYITCAPFPNPAATESIATNIF 480  
 QY 467 PLEDDPTSENKTDKKEKKAQIVTEKNTSTKSNPFFVAAQDSEDTYVTTDNLTKVTE 526  
 Db 481 PLLGDPTSENKTDKKEKKAQIVTEKNTSTKSNPFLVAAQDSEDTYVTTDNLTKVTE 540  
 QY 527 EVVANMPGLTPDLVQACSESELNEVTGTKIAYETKMDLVQTSVMQESLPPAAQLCPSP 586  
 Db 541 EVVANMPGLTPDLVQACSESELNEVTGTKIAYETKMDLVQTSVMQESLPPAAQLCPSP 600  
 QY 587 EESATSPVLDPVMEAPLNSAVPSAGASVIOSSSPLEASSVNYESIKEHPENPPPYE 646  
 Db 601 EESATSPVLDPVMEAPLNSAVPSAGASVIOSSSPLEASSVNYESIKEHPENPPPYE 660  
 QY 647 EAMSVSL-KVSGIKKEIKPENINAALQETEPAYISIACDLIKETKLSAEPAPOFSDYSE 705  
 Db 661 EAMSVSLKVSGIKKEIKPENINAALQETEPAYISIACDLIKETKLSAEPAPOFSDYSE 720  
 QY 706 MAKVEQVPVPHSELVSSPDSEPVDFLSDDSIDPVQKQDETVMLVKESLTETSFESMI 765  
 Db 721 MAKVEQVPVPHSELVSSPDSEPVDFLSDDSIDPVQKQDETVMLVKESLTETSFESMI 780  
 QY 766 EYENKEKLSALPPGGKPYLESFKLSLQNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 825  
 Db 781 EYENKEKLSALPPGGKPYLESFKLSLQNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840  
 QY 826 SNDDLFIKSAQIRETETFSDDSPIIIDEPTLISKTDSFSLAREYTDLEVSHKSEI 885  
 Db 841 SNDDLFIKSAQIRETETFSDDSPIIIDEPTLISKTDSFSLAREYTDLEVSHKSEI 900  
 QY 886 ANAPDGAGSLPCTPDLPHDLSLKNTQPKVEEKISDFDSFKNGSATSKVLLLPDVSALGH 945  
 Db 901 ANAPDGAGSLPCTPDLPHDLSLKNTQPKVEEKISDFDSFKNGSATSKVLLLPDVSALGH 959  
 QY 946 TOABIESIVKPKVLEKAEKKLPDTEKEDRSPSAISADLGKTSVVDLLYWRDIKKTGV 1005  
 Db 960 TOABIESIVKPKVLEKAEKKLPDTEKEDRSPSAISADLGKTSVVDLLYWRDIKKTGV 1019  
 QY 1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOIKQSDGHPFRAYLES 1065  
 Db 1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOIKQSDGHPFRAYLES 1079  
 QY 1066 EVALISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGLFNGLT 1125  
 Db 1080 EVALISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGLFNGLT 1139













XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmologic; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; human; receptor.  
 XX Homo sapiens.  
 OS  
 XX US2002072493-A1.  
 XX 13-JUN-2002.  
 XX 28-JUN-2001; 2001US-00893348.  
 XX 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 PA Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI Moalem G;  
 XX WPI; 2002-607255/65.  
 DR N-PSDB; ABN86601.  
 XX  
 XX Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX  
 XX Example; Page 53-56; 93pp; English.  
 PS  
 XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-artritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polynuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the human  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen  
 XX  
 SQ Sequence 1192 AA;  
 Query Match 98.1%; Score 5810; DB 5; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 5.1e-293;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;  
 QY 1 MEDLQSPVSSSDSPRPQAFKQFVREPEDEDEDEDEDEDELEVLERKPA 60

Db 1 MEDLQSPVSSSDSPRPQAFKQFVREPEDEDEDEDEDEDELEVLERKPA 60  
 QY 61 AGLSAAPVPTAPAAAGAPLMDFGNDVPPAPRGPLPAAPVAPERQSPWDPSPVSVTPAP 120  
 Db 61 AGLSAAPVPTAPAAAGAPLMDFGNDVPPAPRGPLPAAPVAPERQSPWDPSPVSVTPAP 120  
 QY 121 SPLSAAAUSPSKLPEDDEPPAPPPPPASVSPQAEVWTPPAPAPAAPSPAPAKRKG 180  
 Db 121 SPLSAAAUSPSKLPEDDEPPAPPPPPASVSPQAEVWTPPAPAPAAPSPAPAKRKG 180  
 QY 181 SSGA-----VVXXXKIMDLKEQPGNTISAGQEDFSPVLLLETAASXPSLSP 226  
 Db 181 SSGVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFSPVLLLETAASLSP 240  
 QY 227 LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLTETSELEYSEM 286  
 Db 241 LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLTETSELEYSEM 300  
 QY 287 GSSFSVSPKASAVIVANPREIIVKNKDEEEKLVSNILHXXQOELPTALTCLKVKEDEVV 346  
 Db 301 GSSFSVSPKASAVIVANPREIIVKNKDEEEKLVSNILHXXQOELPTALTCLKVKEDEVV 360  
 QY 347 SSEKAKDSFNKRVAVEAPMREYADFKPFERVWEVKDSKEDSDMLAAGKIESNLESKV 406  
 Db 361 SSEKAKDSFNKRVAVEAPMREYADFKPFERVWEVKDSKEDSDMLAAGKIESNLESKV 420  
 QY 407 DKCFADSLQTNHEKDSSESNDDTSFPSTPGIKDRSGAYITCAPFNPAATESIATNIF 466  
 Db 421 DKCFADSLQTNHEKDSSESNDDTSFPSTPGIKDRSGAYITCAPFNPAATESIATNIF 480  
 QY 467 PLLEDPTSENXYTDEKKIEKKAQIVTEKNTSTKTSNPPFVAQDSETDVTTDNLTKVTE 526  
 Db 481 PLLGDPTSENKTYDEKKIEKKAQIVTEKNTSTKTSNPPFVAQDSETDVTTDNLTKVTE 540  
 QY 527 EYVANNPEGLTDLVQEAACESLNEVTGKIAETKMDLVQTSVEMQESLYPAAQLCPSP 586  
 Db 541 EYVANNPEGLTDLVQEAACESLNEVTGKIAETKMDLVQTSVEMQESLYPAAQLCPSP 600  
 QY 587 ESEATPPSVLPDIIVMEAPLNSAVPSAGASVITOPSSSPLEASVNVYESIKHPENPPPYE 646  
 Db 601 ESEATPPSVLPDIIVMEAPLNSAVPSAGASVITOPSSSPLEASVNVYESIKHPENPPPYE 660  
 QY 647 EAMSVSL-KVSGIKKEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 705  
 Db 661 EAMSVSLKKVSGIKKEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720  
 QY 706 MAKVEQVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPOKQDETVMLVKESLTETSPESMI 765  
 Db 721 MAKVEQVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPOKQDETVMLVKESLTETSPESMI 780  
 QY 766 EYENKEKLSALPPEGKPYLESFKLSLMDNTKOTLPDDEVSTLSKKEKIPLOMEELSTAVY 825  
 Db 781 EYENKEKLSALPPEGKPYLESFKLSLMDNTKOTLPDDEVSTLSKKEKIPLOMEELSTAVY 840  
 QY 826 SNNDLFISKEAQIRETETSDSPLEIIDEFPPLTSSKTDTSFKLAREYTDLEVSHKSEI 885  
 Db 841 SNNDLFISKEAQIRETETSDSPLEIIDEFPPLTSSKTDTSFKLAREYTDLEVSHKSEI 900  
 QY 886 ANAPDAGSLPCTELPHDLISLXNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH 945  
 Db 901 ANAPDAGSLPCTELPHDLISLXNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALJA- 959  
 QY 946 TQAEIESIVKPKVLEKEAKKLPSPDTEKEDRSPSAIFSDALGKTSVVDLLYWRDIKKTGV 1005  
 Db 960 TQAEIESIVKPKVLEKEAKKLPSPDTEKEDRSPSAIFSAELSCTSVDLLYWRDIKKTGV 1019  
 QY 1006 VFGASLFLLSLTVFSIVSVTAVIALALLSVTISFRIYKGVIOAIQKSGEGHFRAYLES 1065  
 Db 1020 VFGASLFLLSLTVFSIVSVTAVIALALLSVTISFRIYKGVIOAIQKSGEGHFRAYLES 1079  
 QY 1066 EVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDLSLKFAVLMMVFVYVGLFNGLT 1125

Db 1080 EVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDLVDLSKFAVLMMVFTYVGFALFNGLT 1139

Qy 1126 LLILALISLFSVPVYERHQAOIDHYGLGNKXNDAMAKIOAKIPGLKRAE 1178

Db 1140 LLILALISLFSVPVYERHQAOIDHYGLGNKXNDAMAKIOAKIPGLKRAE 1192

RESULT 10

ADP67234

ID ADP67234 standard; protein; 1192 AA.

XX ADP67234;

AC

XX

DT 09-SEP-2004 (first entry)

XX

DE Human Nogo-A protein.

XX

KW human; Nogo-A; neurite outgrowth inhibitor; Nogo;

KW contactin-associated protein-1; Caspr; neuroprotective; gene therapy;

KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.

XX

OS Homo sapiens.

XX

PN WO2004052389-A2.

XX

PD 24-JUN-2004.

XX

PF 05-DEC-2003; 2003WO-GB005329.

XX

PR 06-DEC-2002; 2002US-0431549P.

PR 20-JUN-2003; 2003US-0480138P.

XX

PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.

PA (FORR/) FORREST G R.

XX

PI Xiao Z;

XX

DR WPI; 2004-468705/44.

XX

PT New composition comprising Nogo and Caspr or a substance capable of

PT promoting interaction between Nogo and Caspr useful for treating injury

PT to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis,

PT epilepsy or stroke.

XX

PS Disclosure; Page 14; 202pp; English.

XX

CC The invention relates to a novel composition comprising neurite outgrowth

CC inhibitor (Nogo) and contactin-associated protein-1 (Caspr) or its

CC mimetics or a substance capable of promoting interaction between Nogo and

CC Caspr, in combination with a carrier. A composition of the invention has

CC neuroprotective activity, and may have a use in gene therapy. The

CC composition is useful for treating injury to or disease of the CNS, e.g.

CC spinal cord injury, multiple sclerosis, epilepsy or stroke. The present

CC sequence represents human Nogo-A.

XX

SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 8; Length 1192;

Best Local Similarity 97.2%; Pred. No. 5.1e-293;

Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLQSPVLVSSSDSPRPQPAFKYQVREPEDEDEDEDEDEDELEVLKCPA 60

Db 1 MEDLQSPVLVSSSDSPRPQPAFKYQVREPEDEDEDEDEDEDELEVLKCPA 60

Qy 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120

Db 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120

Qy 121 SPLSAAAVSPKLPDEDDPPAPPPPPPPASVSPOAEVWTPPPAPAPAPPSTPAAPKRG 180

Db 121 SPLSAAAVSPKLPDEDDPPAPPPPPPPASVSPOAEVWTPPPAPAPAPPSTPAAPKRG 180

Qy 181 SSGA-----VAXXXKIMDLKEQPGNTISAGQEDFPFVLETTAASPSLSP 226

Db 181 SSGVDETLPALPAASEPVISSAENMDLKEQPGNTISAGQEDFPFVLETTAASPSLSP 240

Qy 227 LSAAAFKEHEYLGNLSTVLTPTGTLQENVSEASKEVSEKAKTLLIDRLTFESELEYSRM 286

Db 241 LSAAAFKEHEYLGNLSTVLTPTGTLQENVSEASKEVSEKAKTLLIDRLTFESELEYSRM 300

Qy 287 GSSFSVSPKASAVIVANPREIIVKNKDEBEKLVNNILHXQOELPTALTTLVKDEDEV 346

Db 301 GSSFSVSPKASAVIVANPREIIVKNKDEBEKLVNNILHNQOELPTALTTLVKDEDEV 360

Qy 347 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGGKIESLESKV 406

Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGGKIESLESKV 420

Qy 407 DKCFADSLQTNHEKDSSESNDDTSPSTPEGIKORSNAVITCAPFNPAAATESIATNIF 466

Db 421 DKCFADSLQTNHEKDSSESNDDTSPSTPEGIKDRPGAVITCAPFNPAAATESIATNIF 480

Qy 467 PLLDPTSENXTDEKKIEEKAQIVTEKNTSTKSNPFVAAQDSEDTYVTDNLTKVTE 526

Db 481 PLLDPTSENXTDEKKIEEKAQIVTEKNTSTKSNPFVAAQDSEDTYVTDNLTKVTE 540

Qy 527 EVANMPGLTPDLVQEAECESLNEVTGKTIAYETKMDLVOTSEVMQBSLYPAAQLCPSF 586

Db 541 EVANMPGLTPDLVQEAECESLNEVTGKTIAYETKMDLVOTSEVMQBSLYPAAQLCPSF 600

Qy 587 ESEATSPVLPDIVMEAPLNSAVPSAGASVIQSPSSPLEASSVNYESIKEHPENPPYE 646

Db 601 ESEATSPVLPDIVMEAPLNSAVPSAGASVIQSPSSPLEASSVNYESIKEHPENPPYE 660

Qy 647 EAMSUSL-KVSGIKKEIKPENINAALOETAPYISIACDLIKETKLSAEPAPDFSDYSE 705

Db 661 EAMSUSLKVSGIKKEIKPENINAALOETAPYISIACDLIKETKLSAEPAPDFSDYSE 720

Qy 706 MAKVEQPVPHSELVEDSSPSEVDLFSDDSIPOVPOKQDETVMLVKESLTETSFESMI 765

Db 721 MAKVEQPVPHSELVEDSSPSEVDLFSDDSIPOVPOKQDETVMLVKESLTETSFESMI 780

Qy 766 EYENKEKLSALPPEGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 825

Db 781 EYENKEKLSALPPEGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840

Qy 826 SNDDLFIKSAQIARETETFSDDSPIIIDEPTLISSKTSFSLAREYTDLEVSHKSEI 885

Db 841 SNDDLFIKSAQIARETETFSDDSPIIIDEPTLISSKTSFSLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNTQPKVEEKISFSDDFSKNGSATSKVLLPPDVLSALGH 945

Db 901 ANAPDGAGSLPCTELPHDLSLKNTQPKVEEKISFSDDFSKNGSATSKVLLPPDVLSALA- 959

Qy 946 TQAEIESIVPKVLEKABKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005

Db 960 TQAEIESIVPKVLEKABKLPSTDEKEDRSPSAIFSABLSKTSVVDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIOAKQSDGHPFRAYLES 1065

Db 1020 VFGASLFLLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIOAKQSDGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDLVDLSKFAVLMMVFTYVGFALFNGLT 1125

Db 1080 EVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDLVDLSKFAVLMMVFTYVGFALFNGLT 1139

Qy 1126 LLILALISLFSVPVYERHQAOIDHYGLGNKXNDAMAKIOAKIPGLKRAE 1178

Db 1140 LLILALISLFSVPVYERHQAOIDHYGLGNKXNDAMAKIOAKIPGLKRAE 1192

RESULT 11

ADRI3966

ID ADRI3966 standard; protein; 1192 AA.

XX





XX	01-JUL-2004 (first entry)
DT	Human polypeptide #65.
XX	Human; fat cell number; fat cell size; obesity; diabetes; anorectic;
XX	antidiabetic.
KW	
KW	
XX	Homo sapiens.
OS	
XX	US2004071700-A1.
PN	
XX	15-APR-2004.
PD	
XX	09-OCT-2002; 2002US-00267502.
PF	
XX	09-OCT-2002; 2002US-00267502.
PR	
XX	(LIFE-) LIFE SCI DEV CORP.
PA	
XX	Kim J, Galant R;
PI	
XX	WPI; 2004-328526/30.
DR	
DR	N-PSDB; ADO07886.
XX	Identifying compounds that influence fat cell number or size for treating
PT	or preventing obesity or diabetes by exposing the cell to the agent and
PT	identifying fat cell number or size relative to cells not exposed to the
PT	agent.
XX	
PS	Claim 14; SEQ ID NO 429; 275pp; English.
XX	
CC	The invention relates to a method of identifying compounds that influence
CC	fat cell number or size comprising providing a cell that expresses a gene
CC	and an agent, exposing the cell to the agent and identifying fat cell
CC	number or size relative to cells not exposed to the agent. The method
CC	also comprises providing an expression vector and an agent, exposing the
CC	vector to the agent, detecting a change in expression of the gene
CC	relative to expression of the gene in an expression vector not exposed to
CC	the agent, treating a subject with the agent and identifying fat cell
CC	number or size in the subject. The agent comprises an antisense
CC	oligonucleotide. The subject comprises a mammal, preferably a human. The
CC	method also comprises providing a polypeptide and an agent, exposing the
CC	polypeptide to the agent, detecting binding of the agent to the
CC	polypeptide or a change in an activity of the polypeptide, treating a
CC	subject with the agent and identifying fat cell number or size in the
CC	subject. The agent comprises an antibody. A method of regulating fat cell
CC	number or size comprises providing a subject containing fat cells and an
CC	agent that changes the expression of a gene, and treating the subject
CC	with the agent under conditions so that fat cell size or number in the
CC	subject is altered. The method is useful for identifying compounds that
CC	influence fat cell number or size, for preparing a composition for
CC	treating or preventing obesity or diabetes. This sequence represents a
CC	human polypeptide used in the scope of the invention.
XX	
XX	Sequence 1192 AA;
XX	
XX	Query Match 98.1%; Score 5808; DB 8; Length 1192;
XX	Best Local Similarity 97.1%; Pred. No. 6.5e-293;
XX	Matches 1158; Conservative 5; Mismatches 14; Indels 16; Gaps 3
Qy	1 MEDLDGSLVSSSDSPRRPQAFKQFVREDEDEEEDEDEDEDEDELEVLERKPA 60
Db	1 MEDLDGSLVSSSDSPRRPQAFKQFVREDEDEEEDEDEDEDEDELEVLERKPA 60
Qy	61 AGLSAAPVPTAAGAPLMDGNDVFPVAPRGPLPAAPVAPRQSPWDPSPVSSVTVPAP 120
Db	61 AGLSAAPVPTAAGAPLMDGNDVFPVAPRGPLPAAPVAPRQSPWDPSPVSSVTVPAP 120
Qy	121 SPLSAAAVSPSKLPEDDDEPPAPPPPPPPASVSQAEVPVWTPPPAPAAPSTPAAPKRRG 180
Db	121 SPLSAAAVSPSKLPEDDDEPPAPPPPPPPASVSQAEVPVWTPPPAPAAPSTPAAPKRRG 180





PI	Skerra A, Fiedler M;	
XX	WPI; 2004-376159/35.	
XX		
PT	New isolated truncated Nogo-A polypeptide that corresponds to a truncated	
PT	form of the Nogo-A protein, useful for identifying a compound having	
PT	detectable affinity to a Nogo-A protein.	
XX		
PS	Claim 1; Fig 6B; 80pp; English.	
XX		
CC	The present invention relates to an isolated truncated Nogo-A polypeptide	
CC	that corresponds to a truncated form of the Nogo-A protein from the rat	
CC	and from the human. The truncated polypeptide is useful for identifying a	
CC	compound having detectable affinity to a Nogo-A protein. The present	
CC	sequence is a Nogo-A polypeptide of the invention.	
XX		
XX	Sequence 1192 AA;	
SQ		
	Query Match 97.2%; Score 5758; DB 8; Length 1192;	
	Best Local Similarity 96.2%; Pred. No. 2.6e-290;	
	Matches 1148; Conservative 11; Mismatches 18; Indels 16; Gaps 3;	
Qy	1 MEDLDQSLVSSDPPRPQAFKQFVREDEDEDEDEDEDEDEDEDEDEDELEVLKPA 60	
Db	1 MEDLDQSLVSSDPPRPQAFKQFVREDEDEDEDEDEDEDEDEDEDEDELEVLKPA 60	
Qy	61 AGLSAAPVPTAPAGAPLMDGNDVFPAPRGPLPAAPPVAPERQSPVSTVPAP 120	
Db	61 AGLSAAPVPTAPAGAPLMDGNEFVFPAPRGPLPAAPPVAPERQSPVSTVPAP 120	
Qy	121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTWTPAPAPAPPSTPAAPKRG 180	
Db	121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTWTPAPAPAPPSTPAAPKRG 180	
Qy	181 SSGA-----VWXXXKIMDLKQPGNTISAGQEDFPVLTAAKSPSLSP 226	
Db	181 SSGVDETLFALPAASEPVIRSSAENMELKQPGNTISAGQEDFPVLTAAKSPSLSP 240	
Qy	227 LSASFKEHYLGNLSTVLTGTLQENVSSASKEVSEKATLIDRLTFSELEYSEM 286	
Db	241 LSASFKEHYLENLSTVLTGTLQENVSSASKEVSEKATLIDRLTFSELEYSEM 300	
Qy	287 GSSFSVSPKASAVIVANPREIIVKNKDEBEKLVNNILHQQBELPTALTKLKEDEVV 346	
Db	301 GSSFSVSPKASAVIVANPREIIVKNKDEBEKLVNNILHQQBELPTALTKLKEDEVV 360	
Qy	347 SSEKAKDSFNKRVAVAPMREEVADPKPFRVVEVKDSKEDSDMLAAGGKIESNLSKV 406	
Db	361 SSEKAKDSFNKRVAVAPMREEVADPKPFRVVEVKDSKEDSDMLAAGGKIESNLSKV 420	
Qy	407 DKKCFADSLQTNHEKDSSESSNDTSFPTPEGIKDRSGAVITCAPFNPAATESIATNIF 466	
Db	421 DKKCFADSLQTNHEKDSSESSNDTSFPTPEGIKDRSGAVITCAPFNPAATESIATNIF 480	
Qy	467 PLLDEDPTSENKTDKKEIEKKAQIVTEKNTSTKTSNPPFVAAQSDSETDYVTTDLTKVTE 526	
Db	481 PLLGDPTSENKTDKKEIEKKAQIVTEKNTSTKTSNPPFVAAQSDSETDYVTTDLTKVTE 540	
Qy	527 EVVANMPGLTPDLVQEAACESLNEVTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 586	
Db	541 EVVANMPGLTPDLVQEAACESLNEVTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 600	
Qy	587 EESATSPSPVLPDIWMEAPLNSAVPSAGASVIOQSSSPLEASSVNYESIKHEPNPPPYE 646	
Db	601 EESATSPSPVLPDIWMEAPLNSAVPSAGASVIOQSSSPLEASSVNYESIKHEPNPPPYE 660	
Qy	647 EAMSVSL-KVSGIKKEEIKPENINAAQETAPYISACDLIKETKLSAEPAPDFSQYSE 705	
Db	661 EAMSVSLKVSGIKKEEIKPENINAAQETAPYISACDLIKETKLSAEPAPDFSQYSE 720	
Qy	706 MAKVEQVPVDSHSELVEDSSSPSEVPDLFSDDSIPDPVQKQDETVMVKESLETSPFESMI 765	
Db	721 MAKVEQVPVDSHSELVEDSSSPSEVPDLFSDDSIPDPVQKQDETVMVKESLETSPFESMI 780	

Qy	766 EYENKEKLSALPPRGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 825	
Db	781 EYQKEKLSALPPRGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 840	
Qy	826 SNDDLFIKSAQIRETETFSDDSPSIEIIDEPPTLISSKTDSPSKLAREYTTDLEVSHKSEI 885	
Db	841 SNDDLFIKSAQIRETETFSDDSPSIEIIDEPPTLISSKTDSPSKLAREYTTDLEVSHKSEI 900	
Qy	886 ANAPDAGSLPCTELPHDLSLKNIQPKVEEKISFSDSPKNGSATSQVLLLPDVSALCH 945	
Db	901 AQAPDAGSLPCTELPHDLSLKNIQPKVEEKISFSDSPKNGSATSQVLLLPDVSALCH 959	
Qy	946 TOAIESIVKPKVLEKAEKLPDTEKEDRSPSAIPSDADLGKTSVVDLLYWRDIKKTGV 1005	
Db	960 TOAIESIVKPKVLEKAEKLPDTEKEDRSPSAIPSDADLGKTSVVDLLYWRDIKKTGV 1019	
Qy	1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1065	
Db	1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1079	
Qy	1066 EVAISEBELVQKYSNSALGHVNVCTIKELRRLFLVDDLVDSLKPAVLMMVFTYVVGALFNGLT 1125	
Db	1080 EVAISEBELVQKYSNSALGHVNVCTIKELRRLFLVDDLVDSLKPAVLMMVFTYVVGALFNGLT 1139	
Qy	1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1178	
Db	1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1192	
RESULT 15		
AAU33228		
ID	AAU33228 standard; protein; 1246 AA.	
XX	AC AAU33228;	
DT	18-DEC-2001 (first entry)	
XX	DE Novel human secreted protein #3719.	
XX	Human; vaccination; gene therapy; nutritional supplement;	
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;	
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.	
XX	OS Homo sapiens.	
XX	PN WO200179449-A2.	
XX	PD 25-OCT-2001.	
XX	PP 16-APR-2001; 2001WO-US008656.	
XX	PR 18-APR-2000; 2000US-00552929.	
PR	26-JAN-2001; 2001US-00770160.	
XX	(HYSE-) HYSEQ INC.	
XX	Tang YT, Liu C, Drmanac RT;	
XX	WPI; 2001-611725/70.	
XX	Nucleic acids encoding a range of human polypeptides, useful in genetic	
PT	vaccination, testing and therapy.	
XX	PS Claim 20; Page 737; 765pp; English.	
XX	The invention relates to novel human secreted polypeptides. The	
CC	polypeptides and antibodies to the polypeptides are useful for	
CC	determining the presence of or predisposition to a disease associated	
CC	with altered levels of polypeptide. The polypeptides are also useful for	
CC	identifying agents (agonists and antagonists) that bind to them. Cells	
CC	expressing the proteins are useful for identifying a therapeutic agent	
CC	for use in treatment of a pathology related to aberrant expression or	



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 44.4839 seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSLVSSDSPRPQ.....VKDAMAKIQKIPGLKRAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	931	15.7	199	2	US-08-700-607-1
2	931	15.7	201	4	US-09-949-016-9124
3	787.5	13.3	776	2	US-08-700-607-5
4	787.5	13.3	776	4	US-09-949-016-6998
5	727.5	12.3	439	4	US-09-949-016-9180
6	705	11.9	356	2	US-08-700-607-6
7	688	11.6	208	2	US-08-700-607-7
8	671	11.3	267	2	US-08-700-607-8
9	638	10.8	129	4	US-09-513-999C-5000
10	627.5	10.6	192	4	US-09-949-016-8859
11	541.5	9.1	168	4	US-09-149-476-563
12	522.5	8.8	219	4	US-09-270-767-45132
13	514	8.7	588	4	US-09-949-016-7290
14	513	8.7	241	2	US-08-700-607-3
15	347	5.9	68	4	US-09-513-999C-6304
16	344.5	5.8	75	4	US-09-621-976-4600
17	344.5	5.8	75	4	US-09-621-976-4601
18	316	5.3	8991	4	US-08-714-741-32
19	299	5.0	324	4	US-09-538-092-1246
20	296.5	5.0	2468	4	US-09-976-594-726
21	296.5	5.0	2468	4	US-09-538-092-1135
22	296.5	5.0	2522	4	US-09-949-016-10237
23	286	4.8	2753	4	US-09-949-016-7659
24	286	4.8	2753	4	US-09-949-016-7660
25	285	4.8	92	4	US-09-149-476-411
26	276.5	4.7	1786	3	US-08-973-462-8
27	267.5	4.5	1601	4	US-09-345-473E-40

28	265	4.5	1596	4	US-08-978-277A-4	Sequence 4, Appli
29	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
30	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
31	261	4.4	4377	4	US-09-949-016-6978	Sequence 6978, Ap
32	258	4.4	3913	4	US-09-949-016-10933	Sequence 10933, A
33	257.5	4.3	1781	4	US-09-961-403-13	Sequence 13, Appl
34	256	4.3	1780	1	US-08-769-309A-5	Sequence 5, Appli
35	256	4.3	1780	3	US-08-994-570-5	Sequence 5, Appli
36	252	4.3	114	4	US-09-513-999C-7861	Sequence 7861, Ap
37	249.5	4.2	2079	4	US-09-949-016-8301	Sequence 8301, Ap
38	240	4.1	1878	4	US-09-949-016-8902	Sequence 8902, Ap
39	240	4.1	1878	4	US-09-949-016-8903	Sequence 8903, Ap
40	238	4.0	1346	2	US-08-635-121-2	Sequence 2, Appli
41	238	4.0	1346	4	US-08-978-277A-2	Sequence 2, Appli
42	237.5	4.0	688	3	US-09-141-047-8	Sequence 8, Appli
43	237.5	4.0	1270	4	US-07-757-022B-44	Sequence 44, Appl
44	237.5	4.0	1311	4	US-07-757-022B-42	Sequence 42, Appl
45	237.5	4.0	1313	4	US-07-757-022B-142	Sequence 142, Appl

ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA: US/08/700,607  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus  
US-08-700-607-1

Query Match 15.7%; Score 931; DB 2; Length 199;  
Best Local Similarity 99.0%; Pred No. 1e-49;  
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 988 KTSVVDLLYMRDKTKTGVVFGASLFLLSLTVFSIVSVYATIALALLSVTISFRIYKGV 1047

Db 9 KDKVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAIYIALLSVTISFRIYKGI 68  
QY 1048 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 1107  
Db 69 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 128  
QY 1108 AVLMMVFTYVYVGFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 1167  
Db 129 AVLMMVFTYVYVGFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 188  
QY 1168 AKIPGLKRAE 1178  
Db 189 AKIPGLKRAE 199

## RESULT 2

US-09-949-016-9124  
; Sequence 9124, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9124  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9124

Query Match 15.7%; Score 931; DB 4; Length 201;

Best Local Similarity 99.0%; Pred. No. 1e-49; Indels 0; Gaps 0;  
Matches 189; Conservative 0; Mismatches 2;

QY 988 KTSVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAIYIALLSVTISFRIYKGI 1047  
Db 11 KDKVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAIYIALLSVTISFRIYKGI 70  
QY 1048 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 1107  
Db 71 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 130  
QY 1108 AVLMMVFTYVYVGFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 1167  
Db 131 AVLMMVFTYVYVGFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 190  
QY 1168 AKIPGLKRAE 1178  
Db 191 AKIPGLKRAE 201

## RESULT 3

US-08-700-607-5  
; Sequence 5, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 776 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307307  
US-08-700-607-5

Query Match 13.3%; Score 787.5; DB 2; Length 776;

Best Local Similarity 31.9%; Pred. No. 4.5e-40; Indels 207; Gaps 25;  
Matches 229; Conservative 91; Mismatches 190;

QY 588 ESEATPSVLPDI--VMEAPLNSA-----VFSAGASVIQPSSSPLE---ASSVNY----- 632  
Db 141 EELGTGPSLPDPVPGIESRGLFSSDGIEMTFAESTEVNKKILADPLDQMAEAYKIDIT 200  
QY 633 --BSIKHEPENPPYEEA-----MSVLSKVGIGKEIKPENINAAAL-----QET 675  
Db 201 RPEEVKHQHPHELEDKDLDFKNKDTSIKPEGVREPK-PAPVEGKIHKHLLSEST 259  
QY 676 EAPYISIAIDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722  
Db 260 PAPYID--DLSEQRRAPIITPVKITLITEPSVE-----TTQKTPKQDICKL 309  
QY 723 SSPDSEFVDFLS---DDS-----IPDVPOKQ-----DETVMLVKESLTSTSF 761  
Db 310 PSPDTVTPTVSEPDSPGSIPTPPSSGTEPSAASQSGKGSISEDELITAIKEA----- 363  
QY 762 ESMIEYENKEKLSALPPEGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMEELS 821  
Db 364 -KGLSYETAENRPVQGLADRP-----EYKARSGPTTIPSPDLDEA 403  
QY 822 TAVYSNDLDFISKEAQIRETETFSDDSSPIEIDFP-----TLISSKTDGFS----- 868  
Db 404 SNAESGD-----SEIELVSEDPMAAEDALPSGVVFGVGHVGGPPSP 444  
QY 869 -----KLAREYTDLEVSHKGEIANAPDAGSLPCTELPHDLSLKNIPKVEEKISFSD 921  
Db 445 ASPSIQYSILREAREAEALDSIELIIESCDASSAS-----EESPKREQDSPMPKPSALD 496  
QY 922 DF-----SKNGSATSKVLL-----LPPDVVSALGHTQAIESIVKP 956  
Db 497 AIREETGVRAERAPRRRGLAPGSGFLDYFSTEPQGPPELPPGDGAL-----EPETMPLP 551  
QY 957 KVLEKEAEKKLPDSTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001  
Db 552 -----RKPEEDSSSNQSPAATKGPGLPGAPPPPLLF---LNKQKAILLYWRDIK 599



Db 257 YRDIKQGTGIVFGSFLLLFSLTQFVSVVAYLALAAALSATISFRIYKSVQAVQKTD 316  
 QY 1056 GHPFRAYLSEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLSLKFAVLMWVFT 1115  
 Db 317 GHPFKAYLEITLSQEQIKYTDCLQFYVNSTLXELRRLFLVQDLVDSLKFAVLMWLT 376  
 QY 1116 YVGALENGTLILALISLFSVPVIYERHQAQIDHYLGLANKVNDAMAKIOAKIPGLKR 1175  
 Db 377 YVGALENGTLILMAYVSMFTLPPVYVKEHQADQYGLVTRTHINAVVAKIOAKIPGAKR 436  
 QY 1176 KAE 1178  
 Db 437 HAE 439

RESULT 6  
 US-08-700-607-6  
 ; Sequence 6, Application US/08700607  
 ; Patent No. 5858708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Goli, Surya K.  
 ; APPLICANT: Hillman, Jennifer L.  
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: Filed Herewith  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0114 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 356 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 307309  
 ; US-08-700-607-6

Query Match 11.9%; Score 705; DB 2; Length 356;  
 Best Local Similarity 42.8%; Pred. No. 1.7e-35;  
 Matches 168; Conservative 55; Mismatches 86; Indels 85; Gaps 11;  
 QY 803 EVSTLSKKEKIPLOMEELSTAVYNSDDLFSKSAQIRTEFTSDSSPIBIDEFPPLISS 862  
 Db 30 QYSLREERAEALDSLI---IESCDASSASESPKRE---QDSPMK-----PSALDA 77  
 QY 863 KTDSPSKLAREYTDLEVSHKSEIANPDGAGSL---PCTELPHDLSLKNIQPKVEKISF 919  
 Db 78 -----IREETGVRAEERAPRRGLBPGSLDYPSTE-----PQGPPE----- 115

QY 920 SDDPSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPS 979  
 Db 116 -----LPPGDGAL-----EPETMLP-----RKPEEDSSSSNQSPA 145  
 QY 980 A-----IFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVS 1024  
 Db 146 ATKPGCPGPGAPPPLF---LNKQKAIDLLYWRDIKGTGIVFGSFLLLFSLTQPSVVS 202  
 QY 1025 VTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSEVAISELVQKYSNSALGH 1084  
 Db 203 VVAYLALAAALSATISFRIYKSVLQAVQKTDGHPFKAYLEITLSQEQIKYTDCLQFY 262  
 QY 1085 VNCTIKELRRLFLVDDLSLKFAVLMWVFTYVGALENGTLILALISLFSVPVIYERH 1144  
 Db 263 VNSTLXELRRLFLVQDLVDSLKFAVLMWLTYYVGALENGTLILMAVSMFTLPPVYVVKH 322  
 QY 1145 QAQIDHYLGLANKVNDAMAKIOAKIPGLKRKAE 1178  
 Db 323 QAQIDQYLGVLVTRTHINAVVAKIOAKIPGAKRHAE 356

RESULT 7  
 US-08-700-607-7  
 ; Sequence 7, Application US/08700607  
 ; Patent No. 5858708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Goli, Surya K.  
 ; APPLICANT: Hillman, Jennifer L.  
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/700,607  
 ; FILING DATE: Filed Herewith  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0114 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 208 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 307311  
 ; US-08-700-607-7

Query Match 11.6%; Score 688; DB 2; Length 208;  
 Best Local Similarity 67.5%; Pred. No. 8.9e-35;  
 Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;  
 QY 988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1047  
 Db 18 KQQAIDLLYWRDIKGTGIVFGSFLLLFSLTQFVSVVAYLALAAALSATISFRIYKSVL 77

Db	129	AVLWELLFVVGALFNGLTLLLMVVUSMFTLPVTVVKHQAVDQVGLGLVRTHINTVVAKIQ	188
Qy	1168	AKIPGLK	1174
Db	189	AKIPGAR	195

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RESULT 9
US-09-513-999C-5000
; Sequence 5000, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5000
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 106
; OTHER INFORMATION: Xaa=Glu or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 107
; OTHER INFORMATION: Xaa=Lys or Thr
US-09-513-999C-5000

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Query Match      10.8%; Score 638; DB 4; Length 129;
Best Local Similarity 98.4%; Pred. No. 5.3e-32;
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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Db      1 MAKVEQVPVPHSELVEDSSPDSEVDLFSDDSIDPVQKQDETVMLVKESLTETSFESMI 60

Qy      766 EYENKEKLSALPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOQMEELSTAVY 825
Db      61 EYENKEKLSALPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOQMEELSTAVY 120

Qy      826 SNDDLFSFK 834
Db      121 SNDDLFSFK 129

RESULT 10
US-09-949-016-8859
; Sequence 8859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USBS THERE
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match          10.6%; Score 627.5; DB 4; Length 192;
Best Local Similarity 61.1%; Pred. No. 4.1e-31;
Matches 116; Conserved 38; Mismatches 35; Indels 1; Gaps 1;

QY 990 SVVDLLYWDIKKGVVGCASLFLLLSLTVFSVSVTAIALALLSVTISFRYKGVQIA 1049
Db 3 SVHDLIFWDRVKTGTFVGTTLMLLSLAFAFVSIVSVYLIALLSVTSFRYKSVIQIA 62
QY 1050 IOKSDSGHPFRAYLSEVAISELQKYSNSALGHVNCITKELRRFLVDDLDVDSLKFVAV 1109
Db 63 VQKSEGHFPFKAYLDVDTLSSEAFHNYNMMVHNRALKLIIRLFVDELVDLSLKLAV 122
QY 1110 LMWVFTYVGALENGLLTLLIALISLFSVPVYERHQADHYHGLANKNVKDMAKIQAK 1169
Db 123 FWMWLYVGAVENTLLILAEILLFSPVTVYEKTKTQIDHYVVGVIARDQTKSIVEKIQAK 182
QY 1170 IPGL-KRAE 1178
Db 183 LPGIAKKAE 192

RESULT 11
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
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; EARLIER APPLICATION NUMBER: 60/047,618
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; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
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; EARLIER APPLICATION NUMBER: 60/047,584
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; EARLIER APPLICATION NUMBER: 60/047,500
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; EARLIER APPLICATION NUMBER: 60/047,492
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; EARLIER APPLICATION NUMBER: 60/047,598
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; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
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; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
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; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
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; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
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; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
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APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 7290  
LENGTH: 588  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7290

Query Match 8.7%; Score 514; DB 4; Length 588;  
Best Local Similarity 28.2%; Pred. No. 1.9e-23;  
Matches 169; Conservative 81; Mismatches 186; Indels 164; Gaps 18;

QY 676 EAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPD-SEPVDL-F 733  
DB 56 EAP-----STASSTPDSTEGNDDSDFRELTAREFSEDEB--ETTSQDMGTPRELTF 107  
QY 734 S-----DSDIPDQKODETVMVKESITETSFESMIYENKELKLSALPPSG 780  
DB 108 SYIAFGVGVGGRRDRTARRPQGRSVSEPRDQHPQPSLGDLSIESLSQSPFGR 167  
QY 781 GKPYLESFKLSLNDTDTLLPDVSTLSKKEKIPQMEBELSTAVYGNDDLFISKEAQIRE 840  
DB 168 GDP-----DTAPPSE-----RPLEDLRLDLHLG-----WVARGTSGSE 201  
QY 841 TETFSOSSPIEIDEPPTLISSKTSDFSKLARYTDLEVSHKSEIANAPDAGSLPCTEL 900  
DB 202 DSSTSSSTPLE--DEEP-----QPNRLETGEAGE-----EL 231  
QY 901 PHDLKLNKIQPKVEEKI-----SFSDDFSKNGSATSKVLLLPDVSALGHT 946  
DB 232 --DLRLAQAQSPSEVITLQSPGSGTPQAGTSPSRSDNSGCPREPLLEEEKQWGL 289  
QY 947 QAE-----IESIVKPKVLEKEAE-----KKLP----- 968  
DB 290 EREPVRGQCLDSTDQLEFTEVPEPLLTAMEWLKTSLLAVYKTVPIELSPPLWTAIGWV 349  
QY 969 -----SDTEKEDRSFSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL 1011  
DB 350 QRGFTPTPTVPLRVLLKWAQSPSSGVPFSLSLGADMG--SKVADLLYWKDRTSGVWFTGLM 408  
QY 1012 FLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIAQOKSDEGHPFRAYLSEVAISE 1071  
DB 409 VSLCLLHFSIVSVAHALLLCGTSISLRVYKRVLOAVHVGDCANFPQAYLDVDTLTR 468  
QY 1072 ELVQKYSNLSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMWVFTYVVGALFNGTLTLLAL 1131  
DB 469 EQTERLSHQITSRVWSAATQLRHFFLVEDLVDSKLALLFYILTFVGAIFNGTLTLLIGV 528  
QY 1132 ISLFSVPVYIYERHQAQIDHYGLANKNVKDMAKIOAKIPGL 1178  
DB 529 IGLFTPLLYRHOQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGALASAAAASVSGSKAKAE 588

RESULT 14  
US-08-700-607-3  
Sequence 3, Application US/08700607  
Patent No. 5858708  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Au-Young, Janice  
APPLICANT: Goli, Surya K.

APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: THP1NOB01  
CLONE: 31870  
US-08-700-607-3

Query Match 8.7%; Score 513; DB 2; Length 241;  
Best Local Similarity 47.7%; Pred. No. 6.1e-24;  
Matches 102; Conservative 37; Mismatches 55; Indels 20; Gaps 1;

QY 963 AEKKLPSDTEKEDRSFSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 1022  
DB 20 AEPAPGGGGGCGPCALGTCKSCSSCAVHDLIXRDKTKTGFVGTTLMLLSLAASFV 79  
QY 1023 VSVTAYIALALLSVTISPRIYKGVIAQOKSDEGHPFRAYLSEVAISELSEVQKYSNLSAL 1082  
DB 80 ISVSVYLLALLSVTISPRIYKSVIAQVQKSEGHPPFKAYLDVDTLSSEAFHNYNMAAM 139  
QY 1083 GHVNCITIKELRRLFLVDDLVDSLKFAVLMWVFTYVVGALFNGTLTLLILALISLFSVPVIYE 1142  
DB 140 VHINRAKLIIIRFLVEDLVDSKLAVFMWLMTYVGVAVFNGITLLILABELLIXSVPIVYX 199  
QY 1143 RHQAQIDHYGLANKNVKDMAKIOAKIPGLKKR 1176  
DB 200 KY-----KVPSKTPWNRQK 213

RESULT 15  
US-09-513-999C-6304  
Sequence 6304, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 6304  
 ; LENGTH: 68  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-513-999C-6304

Query Match 5.9%; Score 347; DB 4; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDLQSPVSSSDSPRPQPAFKYQVREPEDEDEDEDEDEDELEVLKPA 60  
 |||||  
 Db 1 MEDLQSPVSSSDSPRPQPAFKYQVREPEDEDEDEDEDELEVLKPA 60  
 |||||

QY 61 AGLSAAPV 68  
 |||||  
 Db 61 AGLSAAPV 68

Search completed: June 16, 2005, 12:33:39  
 Job time : 45.4839 secs

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1	5815	98.2	1192	9	US-09-758-140-6	Sequence 6, Appli
2	5815	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
3	5815	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
4	5810	98.1	1192	9	US-09-789-386-2	Sequence 2, Appli
5	5810	98.1	1192	9	US-09-893-348-23	Sequence 23, Appl
6	5810	98.1	1192	15	US-10-267-502-429	Sequence 429, App
7	5810	98.1	1192	16	US-10-327-213-9	Sequence 9, Appli
8	5810	98.1	1192	16	US-10-466-258-9	Sequence 9, Appli
9	5810	98.1	1192	16	US-10-810-653-23	Sequence 23, Appl
10	5794	97.8	1192	15	US-10-408-967-7	Sequence 7, Appli
11	4296.5	72.5	1163	9	US-09-893-348-18	Sequence 18, Appl



587	Qy	EESATSPVL	PDIVMEAPLN	SVPSAGASV	IQSSSPLEASSV	VNYESI	IKHEPEN	PPPYE	646																																																	
601	Db	EESATSPVL	PDIVMEAPLN	SVPSAGASV	IQSSSPLEASSV	VNYESI	IKHEPEN	PPPYE	660																																																	
647	Qy	EAMSVSI	-KVS	GKIEEK	KEPENNAAL	QET	EAPYIS	IACDLIKET	KLASAP	DFSDYSE	705																																															
661	Db	EAMSVSI	-KVS	GKIEEK	KEPENNAAL	QET	EAPYIS	IACDLIKET	KLASAP	DFSDYSE	720																																															
706	Qy	MAKVEQ	VPVPHSEL	VEDSS	PDSE	PVDL	FSDDS	IPDVP	QKQDET	VMLVKES	LIT	TSPESMI	765																																													
721	Db	MAKVEQ	VPVPHSEL	VEDSS	PDSE	PVDL	FSDDS	IPDVP	QKQDET	VMLVKES	LIT	TSPESMI	780																																													
766	Qy	EYENKE	KL	SAL	PE	GGKPYLES	FKLS	LDNT	KOTLL	PD	EVSTLS	SKKEKI	PI	LOMBEL	STAVY	825																																										
781	Db	EYENKE	KL	SAL	PE	GGKPYLES	FKLS	LDNT	KOTLL	PD	EVSTLS	SKKEKI	PI	LOMBEL	STAVY	840																																										
826	Qy	SNDDL	FL	ISK	EAQ	IRET	ET	FS	DSS	PIEL	IID	EF	PTL	ISS	KTDS	FS	KLAREY	TD	LEVSHKSEI	885																																						
841	Db	SNDDL	FL	ISK	EAQ	IRET	ET	FS	DSS	PIEL	IID	EF	PTL	ISS	KTDS	FS	KLAREY	TD	LEVSHKSEI	900																																						
886	Qy	ANAPD	GAGSL	P	CTEL	PHDLS	L	KN	IQ	KV	BEKI	S	FS	DD	FS	KNGS	ATS	KV	LL	PD	V	SALGH	945																																			
901	Db	ANAPD	GAGSL	P	CTEL	PHDLS	L	KN	IQ	KV	BEKI	S	FS	DD	FS	KNGS	ATS	KV	LL	PD	V	SALGH	959																																			
946	Qy	TOA	BES	I	V	KP	KVL	E	K	E	A	E	K	L	P	S	D	T	E	K	E	D	R	S	P	A	I	S	F	S	A	D	L	G	K	T	S	V	V	D	L	L	Y	W	R	D	I	K	T	G	V	1005						
960	Db	TOA	BES	I	V	KP	KVL	E	K	E	A	E	K	L	P	S	D	T	E	K	E	D	R	S	P	A	I	S	F	S	A	D	L	G	K	T	S	V	V	D	L	L	Y	W	R	D	I	K	T	G	V	1019						
1006	Qy	VFGAS	L	L	I	S	L	S	T	V	F	S	V	T	A	I	A	L	L	S	V	T	I	S	F	R	I	Y	K	G	V	I	O	A	I	O	K	S	D	E	G	H	P	P	R	A	Y	L	E	S	1065							
1020	Db	VFGAS	L	L	I	S	L	S	T	V	F	S	V	T	A	I	A	L	L	S	V	T	I	S	F	R	I	Y	K	G	V	I	O	A	I	O	K	S	D	E	G	H	P	P	R	A	Y	L	E	S	1079							
1066	Qy	EVA	I	S	E	L	V	O	K	S	N	S	A	L	G	H	V	N	C	T	I	K	E	L	R	R	L	F	L	V	D	D	L	V	D	L	S	L	K	F	A	V	L	M	M	V	T	T	V	G	A	L	F	N	G	L	T	1125
1080	Db	EVA	I	S	E	L	V	O	K	S	N	S	A	L	G	H	V	N	C	T	I	K	E	L	R	R	L	F	L	V	D	D	L	V	D	L	S	L	K	F	A	V	L	M	M	V	T	T	V	G	A	L	F	N	G	L	T	1139
1126	Qy	L	L	I	A	L	I	S	L	S	P	V	P	I	Y	E	R	H	O	A	D	I	H	I	G	L	A	N	K	N	V	O	A	M	A	K	I	O	A	I	P	G	L	K	E	K	A	E	1178									
1140	Db	L	L	I	A	L	I	S	L	S	P	V	P	I	Y	E	R	H	O	A	D	I	H	I	G	L	A	N	K	N	V	O	A	M	A	K	I	O	A	I	P	G	L	K	E	K	A	E	1192									

### RESULT 3

US-10-060-036-71  
; Sequence 71, Application US/10060036

; Publication No. US20  
; GENERAL INFORMATION:

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; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuchu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INFECTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0

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Query Match	98.2%	Score 5815;	DB 14;	Length 1192;
Best Local Similarity	97.2%;	Fred.No. 3.4e-361;		
Matches 1160; Conservative	4;	Mismatches 13;	Indels 16;	Gaps 3;
Qy	1	MEDLDQSPVLYSSDSDPPRPOPAFYQVRPEDEEEEEEEEDDEDLFELEVLKPKA	60	
Dd	1	MEDLDQSPVLYSSDSDPPRPOPAFYQVRPEDEEEEEEEEDDEDLFELEVLKPKA	60	

Qy 1126 LLILALISIFSVPIYERHQAIIDHYLGIANKNVKDAMAKIQAKIPGLKRKAE 1178  
1140 LLILALISIFSVPIYERHQAIIDHYLGIANKNVKDAMAKIQAKIPGLKRKAE 1192



Best Local Similarity 97.2%; Pred. No. 5,9e-261; Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;									
Qy	1	MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDEDELEEVLERKPA	60						
Db	1	MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDEDELEEVLERKPA	60						
Qy	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP	120						
Db	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP	120						
Qy	121	SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG	180						
Db	121	SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG	180						
Qy	181	SSGA-----VVXXXKIMDLKEQPGNTISAGQEDFPSVLETAASPSLSP	226						
Db	181	SSGSVDETLFPALPAASEPVIRSAENMDLKEQPGNTISAGQEDFPSVLETAASPSLSP	240						
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM	286						
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM	300						
Qy	287	GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV	346						
Db	301	GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV	360						
Qy	347	SSEKAKDSFNKRVAVEAPMREYADFKPFERVWEVKDSKEDSMDLAAGGKIESLKV	406						
Db	361	SSEKAKDSFNKRVAVEAPMREYADFKPFERVWEVKDSKEDSMDLAAGGKIESLKV	420						
Qy	407	DKKCFADSLQTNHEKDSSESSNDTSPSTPGIKORSGAYITCAPFNPAAATESIATNIF	466						
Db	421	DKKCFADSLQTNHEKDSSESSNDTSPSTPGIKORSGAYITCAPFNPAAATESIATNIF	480						
Qy	467	PLLEDPTSENXTDEKKIEKKAQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE	526						
Db	481	PLLGDPSTENKTDKIEKKAQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE	540						
Qy	527	EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSF	586						
Db	541	EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSF	600						
Qy	587	EBSEATPSPVLPDIIVMEAPLNSAVPSAGASVLOPSSPLEASVNYESI KHEPENPPYE	646						
Db	601	EBSEATPSPVLPDIIVMEAPLNSAVPSAGASVLOPSSPLEASVNYESI KHEPENPPYE	660						
Qy	647	EMSVSL-KVSGIKBEIKPENINAALQTEAPYISACDLIKETKLSAEPAPDFS DYSE	705						
Db	661	EMSVSLKKVSGIKBEIKPENINAALQTEAPYISACDLIKETKLSAEPAPDFS DYSE	720						
Qy	706	MAKVEQVPDHSSELVEDSPDVLPSDDSIPOVPQKQDETVMVLESLETFSFEMI	765						
Db	721	MAKVEQVPDHSSELVEDSPDVLPSDDSIPOVPQKQDETVMVLESLETFSFEMI	780						
Qy	766	EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY	825						
Db	781	EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY	840						
Qy	826	SNDDLFIKGAQIRETETFSDSPIEIIDEFPPLISSKTDGFSKLAREYTDLEVSHKSEI	885						
Db	841	SNDDLFIKGAQIRETETFSDSPIEIIDEFPPLISSKTDGFSKLAREYTDLEVSHKSEI	900						
Qy	886	ANAPGAGSLPCTELPHDLNLKNIQPVKEEKISFSDDFSNGKSATSKVLLIIPDVVSALGH	945						
Db	901	ANAPGAGSLPCTELPHDLNLKNIQPVKEEKISFSDDFSNGKSATSKVLLIIPDVVSALA-	959						
Qy	946	TOAETESIVKPVLEKEKELPSDTEKEDRSPSAIFSA DLGKTSVVDLLIYWRDIIKKTGV	1005						
Db	960	TOAETESIVKPVLEKEKELPSDTEKEDRSPSAIFSAELSKTSVVDLLIYWRDIIKKTGV	1019						
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRAYLES	1065						

Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRAYLES	1079						
Qy	1066	EVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMMWFTYYGALPNGLT	1125						
Db	1080	EVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMMWFTYYGALPNGLT	1139						
Qy	1126	LILIALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAKIPGLKRAE	1178						
Db	1140	LILIALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAKIPGLKRAE	1192						
RESULT 6									
US-10-267-502-429									
; Sequence 429, Application US/10267502									
; Publication No. US20040071700A1									
; GENERAL INFORMATION:									
; APPLICANT: Kim, Jaeseob									
; APPLICANT: Galant, Ron									
; TITLE OF INVENTION: Obesity Linked Genes									
; FILE REFERENCE: LSD-07416									
; CURRENT APPLICATION NUMBER: US/10/267,502									
; CURRENT FILING DATE: 2003-01-27									
; NUMBER OF SEQ ID NOS: 439									
; SOFTWARE: Patent in version 3.2									
; SEQ ID NO 429									
; LENGTH: 1192									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-267-502-429									
Query Match 98.1%; Score 5810; DB 15; Length 1192;									
Best Local Similarity 97.2%; Pred. No. 5,9e-261;									
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;									
Qy	1	MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEEVLERKPA	60						
Db	1	MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEEVLERKPA	60						
Qy	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP	120						
Db	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP	120						
Qy	121	SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG	180						
Db	121	SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG	180						
Qy	181	SSGA-----VVXXXKIMDLKEQPGNTISAGQEDFPSVLETAASPSLSP	226						
Db	181	SSGSVDETLFPALPAASEPVIRSAENMDLKEQPGNTISAGQEDFPSVLETAASPSLSP	240						
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM	286						
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM	300						
Qy	287	GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV	346						
Db	301	GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV	360						
Qy	347	SSEKAKDSFNKRVAVEAPMREYADFKPFERVWEVKDSKEDSMDLAAGGKIESLKV	406						
Db	361	SSEKAKDSFNKRVAVEAPMREYADFKPFERVWEVKDSKEDSMDLAAGGKIESLKV	420						
Qy	407	DKKCFADSLQTNHEKDSSESSNDTSPSTPGIKORSGAYITCAPFNPAAATESIATNIF	466						
Db	421	DKKCFADSLQTNHEKDSSESSNDTSPSTPGIKORSGAYITCAPFNPAAATESIATNIF	480						
Qy	467	PLLEDPTSENXTDEKKIEKKAQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE	526						
Db	481	PLLGDPSTENKTDKIEKKAQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE	540						
Qy	527	EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSF	586						
Db	541	EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSF	600						



RESULT 8  
US-10-466-258-9  
; Sequence 9, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; PRIORITY FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-466-258-9  
Query Match 98.1%; Score 5810; DB 16; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 5.9e-261;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;  
Qy 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Db 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Qy 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQSPWDPSPVSTVPAP 120  
Db 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQSPWDPSPVSTVPAP 120  
Qy 121 SPLSAAAVSPSKLPEDDPPRPPPPPPASVSPQAEVPTWTPAPAPAPPSTPAAPKRG 180  
Db 121 SPLSAAVSPSKLPEDDPPRPPPPPPASVSPQAEVPTWTPAPAPAPPSTPAAPKRG 180  
Qy 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFSPVLETAAXPSLSP 226  
Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFSPVLETAAXPSLSP 240  
Qy 227 LSAAFKHEHYGNLSTVLPTEGTLOENVSEASKEVSEKAKTLIDRLTTFSELEYSEM 286  
Db 241 LSAAFKHEHYGNLSTVLPTEGTLOENVSEASKEVSEKAKTLIDRLTTFSELEYSEM 300  
Qy 287 GSSFSVSPKASAVIVANPREIIVKNKDEEKLVSNNILHXQQLPTALTKLVKEDVV 346  
Db 301 GSSFSVSPKASAVIVANPREIIVKNKDEEKLVSNNILHNQQLPTALTKLVKEDVV 360  
Qy 347 SSEKAKDSFNEKRVAVAEAPMREEVADFKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 406  
Db 361 SSEKAKDSFNEKRVAVAEAPMREEVADFKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 420  
Qy 407 DKCFADSLQTNHEKDSSENNDDTSPTSTPEGIKDRSGAVITCAPFNPAATESIATNIF 466  
Db 421 DKCFADSLQTNHEKDSSENNDDTSPTSTPEGIKDRSGAVITCAPFNPAATESIATNIF 480  
Qy 467 PLLDPTSENKTDKKEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTTDNLTKYTE 526  
Db 481 PLLDPTSENKTDKKEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTTDNLTKYTE 540  
Qy 527 EVVANMPGLTPDLVQACESELNEVTGKTIAYETKMDLVQTVSEVMQESLYPAAQLCPSP 586  
Db 541 EVVANMPGLTPDLVQACESELNEVTGKTIAYETKMDLVQTVSEVMQESLYPAAQLCPSP 600  
Qy 587 ESEATPSPVLPDIWMEAPLNSAVPSAGASVIQPSSSPLEASSNYESIKHEPNPPPYE 646  
Db 601 ESEATPSPVLPDIWMEAPLNSAVPSAGASVIQPSSSPLEASSNYESIKHEPNPPPYE 660  
Qy 647 EAMSVSL-KVSGIKKEIKPENINAAOETAPYISIACDLIKTKLSAEPAPDFSDYSE 705  
Db 661 EAMSVSLKKVSGIKKEIKPENINAAOETAPYISIACDLIKTKLSAEPAPDFSDYSE 720  
Qy 706 MAKVEQPVDPHSELVEDSSPDSEPVDLFSDDSIPDPVQKQDETVMVKESLTETSFESMI 765

Db 721 MAKVEQPVDPHSELVEDSSPDSEPVDLFSDDSIPDPVQKQDETVMVKESLTETSFESMI 780  
Qy 766 EYENKEKLSALPPGGKPYLESFKLSLNTKOTLLPDEVSTLSKKEKIPLOWEELSTAVY 825  
Db 781 EYENKEKLSALPPGGKPYLESFKLSLNTKOTLLPDEVSTLSKKEKIPLOWEELSTAVY 840  
Qy 826 SNDDLFTSKAQIRETETFSOSSPIIIDEPTLISSKTDSFSLKAREYTDLEVSHKSEI 885  
Db 841 SNDDLFTSKAQIRETETFSOSSPIIIDEPTLISSKTDSFSLKAREYTDLEVSHKSEI 900  
Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSXNGSATSFKVLLPPDPVSALGH 945  
Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSXNGSATSFKVLLPPDPVSALA- 959  
Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIIKKTGV 1005  
Db 960 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIIKKTGV 1019  
Qy 1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKDEGHPFRAYLES 1065  
Db 1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKDEGHPFRAYLES 1079  
Qy 1066 EVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLVDLSKFAVLMVFTYVVGALFNGLT 1125  
Db 1080 EVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLVDLSKFAVLMVFTYVVGALFNGLT 1139  
Qy 1126 LLIILALISLFSVPVIYERHQAOIDHYGLANKNVKDMAKIOAKIPGLKRKAE 1178  
Db 1140 LLIILALISLFSVPVIYERHQAOIDHYGLANKNVKDMAKIOAKIPGLKRKAE 1192

RESULT 9

US-10-810-653-23  
; Sequence 23, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONOGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-810-653-23

Query Match 98.1%; Score 5810; DB 16; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 5.9e-261;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;  
Qy 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Db 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Qy 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQSPWDPSPVSTVPAP 120

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Db 61 AGLSAAPVTAPAAAGAPLMDFGNDFFVPPAPRGPLPAAPVAPERQSPWDPSPVSVSTVPAP 120
QY 121 SPLSAAAVSPKLPEDDEPPARPPPPPPASVSPQAEPPVMTTAPAPAAAPSTPAPAKRRG 180
Db 121 SPLSAAAVSPKLPEDDEPPARPPPPPPASVSPQAEPPVMTTAPAPAAAPSTPAPAKRRG 180
QY 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPFVSVLLETAASXPSLSP 226
Db 181 SSGSVDETLPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPFVSVLLETAASLPSLSP 240
QY 227 LSAAASFKHEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRDLTETSELEYSEM 286
Db 241 LSAAASFKHEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRDLTETSELEYSEM 300
QY 287 GGSFVSFSPKASAVIVANPREEIIIVKNKDEEEKLVSNLILHXQQLPTALTALTKLVKEDEVV 346
Db 301 GGSFVSFSPKASAVIVANPREEIIIVKNKDEEEKLVSNLILHXQQLPTALTALTKLVKEDEVV 360
QY 347 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKTESNLESKV 406
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKTESNLESKV 420
QY 407 DKKCFADSLQTNHKEKSSNDTSPSTPEGIDKRSWAYITCAPNPAATESIATNIF 466
Db 421 DKKCFADSLQTNHKEKSSNDTSPSTPEGIDKRPAGAYITCAPNPAATESIATNIF 480
QY 467 PLLDEPTSENKTDKKEIEBKAKIIVTEKNTSTKTSNPPFFVAAQDSSTDVTTDNLTKVTE 526
Db 481 PLLGDPSTSENKTDKKEIEBKAKIIVTEKNTSTKTSNPPFLVAAQDSSTDVTTDNLTKVTE 540
QY 527 EVVANNPEGLTPDLVQEAACESLNEVTGKIAVETKMDLVQTSVMQESLYPAAQICPSF 586
Db 541 EVVANNPEGLTPDLVQEAACESLNEVTGKIAVETKMDLVQTSVMQESLYPAAQICPSF 600
QY 587 ESEATPSPVLPIVMEAPLNSAVPSAGASVIOQSSPLEASVNYESI KHEPENPPYE 646
Db 601 ESEATPSPVLPIVMEAPLNSAVPSAGASVIOQSSPLEASVNYESI KHEPENPPYE 660
QY 647 EAMSVSL-KVSGIKBEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 705
Db 661 EAMSVSLKKVSGIKBEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 706 MAKVEQVPDHSSELVSDSPDVPDLFSDDSIPDPVQKQDETVMVLVKSLSLTETSPESMI 765
Db 721 MAKVEQVPDHSSELVSDSPDVPDLFSDDSIPDPVQKQDETVMVLVKSLSLTETSPESMI 780
QY 766 EYENKEKLSALPPEGKPYLESFKLSIDNTKOTLLPDEVSTLSKKEKIPLOMEELESTAVY 825
Db 781 EYENKEKLSALPPEGKPYLESFKLSIDNTKOTLLPDEVSTLSKKEKIPLOMEELESTAVY 840
QY 826 SNDDLFTSKEAQIRETETTFSDSPIEIIIDFPPTLISSKTDSFSKLAREYTDLEVSXKSEI 885
Db 841 SNDDLFTSKEAQIRETETTFSDSPIEIIIDFPPTLISSKTDSFSKLAREYTDLEVSXKSEI 900
QY 886 ANAPDGAGSLPCTELPHDLSLKNIQKVEBKISFSDDFKNGSATSXVLLPPDPVSALGH 945
Db 901 ANAPDGAGSLPCTELPHDLSLKNIQKVEBKISFSDDFKNGSATSXVLLPPDPVSALGA- 959
QY 946 TQAEIESIVKPKVLEKAEKLPDTEKEDRSPSAIFSDALGKTSVVVDLLYWRDIKKTGV 1005
Db 960 TQAEIESIVKPKVLEKAEKLPDTEKEDRSPSAIFSAELSKTSVVVDLLYWRDIKKTGV 1019
QY 1006 VFASLFLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1065
Db 1020 VFASLFLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1079
QY 1066 EVAISELVQKYSNLSALCHVNCIIEKLRLLFLVDDDLVDSLKPAVLMWVFTYVICALNGLT 1125
Db 1080 EVAISELVQKYSNLSALCHVNCIIEKLRLLFLVDDDLVDSLKPAVLMWVFTYVICALNGLT 1139
QY 1126 LLILALISLFSVPVIERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1192
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Db 1140 LLILALISLFSVPVIERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1192
RESULT 10
US-10-408-967-7
; Sequence 7, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-7
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Query Match 97.8%; Score 5794; DB 15; Length 1192;
Best Local Similarity 97.0%; Pred No. 3.2e-260;
Matches 1157; Conservative 4; Mismatches 16; Indels 16; Gaps 3;
QY 1 MEDLDQSPLVSSSDSPRPQAPAKYQFVREPEDEDEDEDEDEDEDEDEDEDEDEDELEVLERKPA 60
Db 1 MEDLDQSPLVSSSDSPRPQAPAKYQFVREPEDEDEDEDEDEDEDEDEDEDEDELEVLERKPA 60
QY 61 AGLSAAPVTAPAAAGAPLMDFGNDFFVPPAPRGPLPAAPVAPERQSPWDPSPVSVSTVPAP 120
Db 61 AGLSAAPVTAPAAAGAPLMDFGNDFFVPPAPRGPLPAAPVAPERQSPWDPSPVSVSTVPAP 120
QY 121 SPLSAAAVSPKLPEDDEPPARPPPPPPASVSPQAEPPVMTTAPAPAAAPSTPAPAKRRG 180
Db 121 SPLSAAAVSPKLPEDDEPPARPPPPPPASVSPQAEPPVMTTAPAPAAAPSTPAPAKRRG 180
QY 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPFVSVLLETAASXPSLSP 226
Db 181 SSGSVDETLPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPFVSVLLETAASLPSLSP 240
QY 227 LSAAASFKHEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRDLTETSELEYSEM 286
Db 241 LSAAASFKHEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRDLTETSELEYSEM 300
QY 287 GGSFVSFSPKASAVIVANPREEIIIVKNKDEEEKLVSNLILHXQQLPTALTALTKLVKEDEVV 346
Db 301 GGSFVSFSPKASAVIVANPREEIIIVKNKDEEEKLVSNLILHXQQLPTALTALTKLVKEDEVV 360
QY 347 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKTESNLESKV 406
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKTESNLESKV 420
QY 407 DKKCFADSLQTNHKEKSSNDTSPSTPEGIDKRSWAYITCAPNPAATESIATNIF 466
Db 421 DKKCFADSLQTNHKEKSSNDTSPSTPEGIDKRPAGAYITCAPNPAATESIATNIF 480
QY 467 PLLDEPTSENKTDKKEIEBKAKIIVTEKNTSTKTSNPPFFVAAQDSSTDVTTDNLTKVTE 526
Db 481 PLLGDPSTSENKTDKKEIEBKAKIIVTEKNTSTKTSNPPFLVAAQDSSTDVTTDNLTKVTE 540
QY 527 EVVANNPEGLTPDLVQEAACESLNEVTGKIAVETKMDLVQTSVMQESLYPAAQICPSF 586
Db 541 EVVANNPEGLTPDLVQEAACESLNEVTGKIAVETKMDLVQTSVMQESLYPAAQICPSF 600
QY 587 ESEATPSPVLPIVMEAPLNSAVPSAGASVIOQSSPLEASVNYESI KHEPENPPYE 646
Db 601 ESEATPSPVLPIVMEAPLNSAVPSAGASVIOQSSPLEASVNYESI KHEPENPPYE 660
QY 647 EAMSVSL-KVSGIKBEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 705
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Db 517 TEAVATMEGLTPDLVQACBSLNEATGKIAVETKVDLVOTSBIAQESYPTAQLCP 576
Qy 585 SPEESEATSPVLPDIWMEAPLNSAVPSAGASYIQSSSPLEA--SSVNYESIKHEPENPP 643
Db 577 SPEEAEATSPVLPDIWMEAPLNSLPGTASVAQSPASPLEVPSPVSDGKLEPENPP 636
Qy 644 PYEAMSVLKVSGIKKEIKBPENINAALQETAPYISACDLIKETKLSABPADPDSY 703
Db 637 PYEAMSVALKTSKDEKKEIKESFNAAAQEAAPYISACDLIKETKLSABPADPDSY 696
Qy 704 SEMAKVEQVPDHSSELVEDSSPDSEVDLPSDSDIPDPQKODETVMVKESITETSPES 763
Db 697 SEIAKPEKSVDPHCELVDDSSPESEVDLPSDSDIPDPQKODETVMVKESITETSPES 755
Qy 764 MIEYENKELKLSALPPGEGKPYLESFKLSLNDKDTLLPDEVSTLSKKEKIPLOMBELSTA 823
Db 756 VTQHKHERLSASPOEVGKPYLESFQPNLHITKDA--ASNEIPTLTCKETISLQMEEFNTA 814
Qy 824 VYSNDLFLSKAQIRRETTFSDSSPIEIIDBPPTLISKTSFSKLAREYTDLEVSHKS 883
Db 815 IYSNDLFLSKKEDKMKESSETFSDSSPIEIIDBPPTFVSAKDDSD---PKEYTDLEVSNS 870
Qy 884 ETANAPDGAGSLPCTELPHDLISLKNIOKPVKEKISFSDDFSKNGSATSQVLLLPDVSAL 943
Db 871 ETANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSVSKVPILLPNVSAL 928
Qy 944 GHTQAEIESIVKPKVLEKEAEKLPDTEKEDRSPSAIFSDADLGKTSVVDLLYWRDIKKT 1003
Db 929 -ESQIEMGNIVKPKVLTKEAEKLPDTEKEDRSLTAVLSAELNKTSSVVDLLYWRDIKKT 987
Qy 1004 GVYFGASLFLLSLTVFSIVSTAYTIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYL 1063
Db 988 GVYFGASLFLLSLTVFSIVSTAYTIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYL 1047
Qy 1064 ESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLMVFTYVGVALFNG 1123
Db 1048 ESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLMVFTYVGVALFNG 1107
Qy 1124 LTLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAIKIPGLKRAE 1178
Db 1108 LTLILALISLFSIPVYIERHQAQIDHYGLANKSVKDMAKIOAIKIPGLKRAE 1162

RESULT 15
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 431
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431

Query Match 72.2%; Score 4277.5; DB 15; Length 1163;
Best Local Similarity 73.8%; Pred. No. 6e-190;
Matches 883; Conservative 108; Mismatches 154; Indels 51; Gaps 19;

Qy 1 MEDLDOSPLVSS--DSPPRPQAFKQFVREDEDEDEDEDEDEDEDEDEDEDELEVLERKP 59
Db 1 MEDIDQSSLVSSADSPPPPPAFKQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLERKP 60
Qy 60 AAGLSAAPPVTPAAGAPLMDFNDFVPPAPRGPLPAAPPVAPEROPSPDPSVSTVPA 119
Db 61 AAGLSAVPVP--PAA-APLLDSSDSVPPAPRGPLPAAPPVAPEROPSPWERSPAAS--A 114
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Qy 120 PSPLSAAAVSPSKLDEDEPPARPPPPASVSPQAEPPVWTPPAPAPAPPPSTPAAPKRR 179
Db 115 PSLPAAAVLPSKLPDEDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163
Qy 180 GSSG-----AVVXXXKIMDKLEOPGNTISAGOEDPSPVLLETAASPSLUS 225
Db 164 GSGSVDETLFALPAASEPVPISSAEKIMDKLEOPGNTVSSGOEDPSPVLFETAASPSLUS 223
Qy 226 PLASAAAFKEHEYGLNLSTVLPTEGLQENVSEASKEVSEKAKTLLTIDRLDTFSELEYSE 285
Db 224 PLSTVSFKEHGYGLNL SAVASTEGTIEETLNEASRELPERATNPFWNRESAFLVLEYSE 283
Qy 286 MGSSFSVSPKASAVIVANPREIIIVKNKDBEKLVSNNILHXQELPTALTKLVKEDV 345
Db 284 MGSSFNFGSPKGSAMLVENTKEEVIVRSKDKED-LVCSAALHNPOESPATLTKVVKEDGV 342
Qy 346 VSSEKAKDSFNEKRVAVAPMEEEYADFKPFRVMEVKDSKEDS--DMLAAGGKIESNLSES 404
Db 343 MSPEKTMDFINEMKMSVAVPVEEYADFKPFPQAEVXDYEGSRDVLAA----RANMES 398
Qy 405 KVDKCFADSLFQTNHEKDSSESSNDTSPSPTEGIKDRSGAYITCAPENPAATSIATN 464
Db 399 KVDKCFEDSLQKSHGKDSERNENASFPSPPELVKDGSRAYITCDSFT--SATESTAN 457
Qy 465 IPPLEDPTSENKTDKKEIKKIAQIVTEKNTSTKSNPFFVAAODSETDYVTTNLTKV 524
Db 458 IPPVLEDHTSENKTDKKEIKKIAQIITEK--TSPKTSNPFLVAIHDSADYVTTNLTSLV 516
Qy 525 TEEVANNMEGLTPDLVQACBSLNEATGKIAVETKVDLVOTSEVWOESLYPAQALCP 584
Db 517 TEAVATMEGLTPDLVQACBSLNEATGKIAVETKVDLVOTSEVWOESLYPAQALCP 576
Qy 585 SPEESEATSPVLPDIWMEAPLNSAVPSAGASYIQSSSPLEA--SSVNYESIKHEPENPP 643
Db 577 SPEEAEATSPVLPDIWMEAPLNSLPGTASVAQSPASPLEVPSPVSDGKLEPENPP 636
Qy 644 PYEAMSVLKVSGIKKEIKBPENINAALQETAPYISACDLIKETKLSABPADPDSY 703
Db 637 PYEAMSVALKTSKDEKKEIKESFNAAAQEAAPYISACDLIKETKLSABPADPDSY 696
Qy 704 SEMAKVEQVPDHSSELVEDSSPDSEVDLPSDSDIPDPQKODETVMVKESITETSPES 763
Db 697 SEIAKPEKSVDPHCELVDDSSPESEVDLPSDSDIPDPQKODETVMVKESITETSPES 755
Qy 764 MIEYENKELKLSALPPGEGKPYLESFKLSLNDKDTLLPDEVSTLSKKEKIPLOMBELSTA 823
Db 756 VTQHKHERLSASPOEVGKPYLESFQPNLHITKDA--ASNEIPTLTCKETISLQMEEFNTA 814
Qy 824 VYSNDLFLSKAQIRRETTFSDSSPIEIIDBPPTLISKTSFSKLAREYTDLEVSHKS 883
Db 815 IYSNDLFLSKKEDKMKESSETFSDSSPIEIIDBPPTFVSAKDDSD---PKEYTDLEVSNS 870
Qy 884 ETANAPDGAGSLPCTELPHDLISLKNIOKPVKEKISFSDDFSKNGSATSQVLLLPDVSAL 943
Db 871 ETANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSVSKVPILLPNVSAL 928
Qy 944 GHTQAEIESIVKPKVLEKEAEKLPDTEKEDRSPSAIFSDADLGKTSVVDLLYWRDIKKT 1003
Db 929 -ESQIEMGNIVKPKVLTKEAEKLPDTEKEDRSLTAVLSAELNKTSSVVDLLYWRDIKKT 987
Qy 1004 GVYFGASLFLLSLTVFSIVSTAYTIALALLSVTISFRIYKGVIOAIQKSDGHPFRAY 1062
Db 988 GVYFGASLFLLSLTVFSIVSTAYTIALALLSVTISFRIYKGVIOAIQKSDGHPFRAY 1047
Qy 1063 LESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLMVFTYVGVALF 1122
Db 1048 LESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLMVFTYVGVALF 1107
Qy 1123 LTLILALISLFSVPVYIERHQAQIDHYGLANKNVKDMAKIOAIKIPGLKRAE 1178
Db 1108 LTLILALISLFSIPVYIERHQAQIDHYGLANKSVKDMAKIOAIKIPGLKRAE 1163
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Search completed: June 16, 2005, 13:04:04  
Job time : 158.811 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 35.4224 Seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSLVSSDSPRPQ.....VKDAMAKIQAKIPGLKRAE 1178.

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	787.5	13.3	776	2 A46583	neuroendocrine-spe
2	688	11.6	208	2 I60904	neuroendocrine-spe
3	671	11.3	267	2 A60021	tropomyosin-relate
4	528	8.9	2484	2 T26216	hypothetical prote
5	519.5	8.8	2607	2 T26215	hypothetical prote
6	340.5	5.7	222	2 T26213	hypothetical prote
7	331	5.6	7962	2 I38346	elastic titin - hu
8	325.5	5.5	5327	2 T13564	microtubule-associ
9	324.5	5.5	865	2 A47282	calcium-binding pr
10	320.5	5.4	873	2 A47283	calphotin - fruit
11	299.5	5.1	3488	2 T34418	hypothetical prote
12	299	5.0	3924	2 S37431	ankyrin 2, neuroa
13	290.5	4.9	1274	2 T16251	hypothetical prote
14	289	4.9	2364	2 A65577	microtubule-associ
15	289	4.9	2464	1 QRMSP1	microtubule-associ
16	287.5	4.9	971	2 T19431	hypothetical prote
17	285.5	4.8	1621	2 A82255	hypothetical prote
18	278	4.7	1948	2 S00485	gene 11-1 protein
19	274	4.6	3507	2 T34513	hypothetical prote
20	272.5	4.6	1829	2 T24583	hypothetical prote
21	272.5	4.6	2361	2 T25752	hypothetical prote
22	271	4.6	2187	2 T30826	nascent polypeptid
23	270	4.6	1230	2 T22458	hypothetical prote
24	267.5	4.5	1851	2 T19964	hypothetical prote
25	263.5	4.4	2409	1 A60979	versican precursor
26	262.5	4.4	6642	2 T29757	protein UNC-89 - C
27	261	4.4	1558	2 B71603	RESA-H3 antigen PF
28	260.5	4.4	3381	2 T42389	versican precursor
29	259.5	4.4	1828	2 A40115	microtubule-associ

30	258	4.4	1616	2 G64242	cytadherence-acces
31	257.5	4.3	5170	2 T15348	hypothetical prote
32	256	4.3	990	2 I51618	nucleolar phosphop
33	256	4.3	1634	2 T26517	hypothetical prote
34	255.5	4.3	1684	2 JW0057	gravin - human
35	253	4.3	1189	2 S56852	hypothetical prote
36	252.5	4.3	1224	2 T14007	microtubule-associ
37	252	4.3	4377	2 A55575	ankyrin 3, long sp
38	250.5	4.2	1824	1 ORHUMT	microtubule-associ
39	250.5	4.2	1830	2 A37981	microtubule-associ
40	248	4.2	1825	2 S13507	microtubule-associ
41	248	4.2	1890	2 T04556	hypothetical prote
42	248	4.2	3421	1 WZBE86	367K tegument prot
43	246	4.2	1110	2 I51116	NF-180 - sea lampr
44	244.5	4.1	1029	2 T30351	mucin-like protein
45	243	4.1	1320	2 JC5630	TCOF1 protein - mo

ALIGNMENTS

RESULT 1

A46583  
neuroendocrine-specific protein, splice form A - human  
N:Contains: neuroendocrine-specific protein, splice form B  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C:Accession: A46583; I60903  
R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V  
J. Biol. Chem. 268, 13439-13447, 1993  
A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe  
A:Reference number: A46583; MUID:93293865; PMID:7685762  
A:Accession: A46583  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-776 <ROE1>  
A:Cross-references: UNIPROT:Q16799; GB:L10333; NID:G307306; PIDN:AAA59950.1; PID:G307307  
A:Accession: I60903  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 421-776 <ROE2>  
A:Cross-references: GB:L10334; NID:G307308; PIDN:AAA59951.1; PID:G307309  
C:Genetics:  
A:Gene: GDB:RTN1; NSP  
A:Cross-references: GDB:203968; OMIM:600865  
A:Map position: 14q21-14q22

Query Match	13.3%;	Score	787.5;	DB 2;	Length	776;
Best Local Similarity	31.9%;	Pred. No.	7.4e-25;			
Matches	229;	Conservative	91;	Mismatches	190;	Indels 207; Gaps 25;
Qy	588	ESEATPSPVLDDI--VMEAPLNSA-----	--VPSAGASVIQSSSPLE---ASSVNY----	632		
Db	141	EELTGPGLSPDVGIESRGLFSDSGSIEMTPASTEVNKLADLPDQMAEAYKIDIT	200			
Qy	633	--ESIKHEPNPPVEEA-----	--NSVLKVGSIKEIKEPENINAA-----OBT	675		
Db	201	RPEVKGQEQHPLEKDLDFKNKDTDISIKPGVREPK-PAPVEGKIHKHLLERST	259			
Qy	676	EAPYISACDL-----	IKETKLSAEPAPDFSDYSEMAKVSPQVPDHSVELD	722		
Db	260	FAPVID--DLSEQRAPQITTPVKITLTIEPSVE-----	TTTQKTPKQDKCLK	309		
Qy	723	SSPSPSEVDLFS---DDS-----	IPDVQKQ-----DETVMVKESLTETSF	761		
Db	310	PSPDTVTVTVSEPEDPSGSIPTPSSGTEPSAAESQSGSISEDLITAKA-----	363			
Qy	762	ESMTEYENKEKLSALPPEGKPYLESFKLSLNDTKDTLLPDDEVSTLSKKEIKIPQMBSLS	821			
Db	364	-KGLSYETAENPRPVQLADRP-----	EVKARSQPTIPSPLDHEA	403		
Qy	822	TAVYSNDDLFLFSKQAIRETETFTSDSSPIEIDFPF-----	TLISKTSQFS-----	868		

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Db 404 SBAESGD-----SEIELVSEDPMAAEDALPSGYVSGHVGPPSP 444
QY 869 -----KLAREYTDLEVSHKSEIANAPDCAGSLPCTELPHDLISLKNIOPKVEEKISFSD 921
Db 445 ASPSIQYSILREERAELSELIESCDASSAS-----EESPKREQDSPMKPSALD 496
QY 922 DF-----SKNGSATSKVLL-----LPPDVSALGHTQAEISIVKP 956
Db 497 AIREETGVRAERAPRRGLAEPGSLDYPTSPQPGPELPPGDGAL-----EPETPMLP 551
QY 957 KVLKEAEKKLPDSTEKEDEKSPSA-----IFGADLGKTSVDVLLYWRDIK 1001
Db 552 -----RKEEDSSSQSPARTKGPGLPGAPPPPLF---LNKQKADLLYWRDIK 599
QY 1002 KTVGVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGEGHPPRA 1061
Db 600 QTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDGEGHPPKA 659
QY 1062 YLESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDVLSLKPFAVLMMWFTYVYGALP 1121
Db 660 YLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVDVLSLKPFAVLMMWLLTYVYGALP 719
QY 1122 NGTLTLLALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1178
Db 720 NGTLTLLMAVSMFTLPVYVYKHQAQIDQYGLVLRTHINAVAKIOAKIPGAKRAE 776

RESULT 2
160904
neuroendocrine-specific protein C - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I60904
R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V
A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe
A;Reference number: A46583; MUID:93293865; PMID:7685762
A;Accession: I60904
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PID:AAA59952.1; PID:g307311
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203969; OMIM:600865
A;Map position: 14q21-14q22

Query Match 11.6%; Score 688; DB 2; Length 208;
Best Local Similarity 67.5%; Pred. No. 1.4e-21;
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

QY 988 KTSVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1047
Db 18 KQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVL 77
QY 1048 QAIQKSDGEGHPPRAYLESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDVLSLKP 1107
Db 78 QAVQKTDGEGHPPKAYLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVDVLSLKP 137
QY 1108 AVLMMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIO 1167
Db 138 AVLMMWLLTYVYGALFNGLTLLMAVSMFTLPVYVYKHQAQIDQYGLVLRTHINAVAKIO 197
QY 1168 AKIPGLKRAE 1178
Db 198 AKIPGAKRAE 208

RESULT 3
A60021
tropomyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
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C;Accession: A60021
R;Wiczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021
A;Molecule type: mRNA
A;Residues: 1-267 <WIE>
A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Query Match 11.3%; Score 671; DB 2; Length 267;
Best Local Similarity 66.3%; Pred. No. 9.4e-21;
Matches 124; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

QY 988 KTSVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1047
Db 9 KQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVL 68
QY 1048 QAIQKSDGEGHPPRAYLESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDVLSLKP 1107
Db 69 QAVQKTDGEGHPPKAYLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVDVLSLKP 128
QY 1108 AVLMMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIO 1167
Db 129 AVLMMWLLTYVYGALFNGLTLLMAVSMFTLPVYVYKHQAQIDQYGLVLRTHINAVAKIO 188
QY 1168 AKIPGLK 1174
Db 189 AKIPGAR 195

RESULT 4
T26216
hypothetical protein W06A7.3c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26216
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26216
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2484 <WIL>
A;Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CRSP:W
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3c
A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 8.9%; Score 528; DB 2; Length 2484;
Best Local Similarity 20.9%; Pred. No. 1.3e-13;
Matches 277; Conservative 186; Mismatches 461; Indels 402; Gaps 54;

QY 1 MEDLOSPLVSSDSPPRPQPAFKYQFVREPDDEE-----BE 38
Db 1397 LEKVEVQP--DLSONSPAPHKIIDLHF-NIPKDHEDYGNIDYVPFGTSESEESQKADGNQE 1453
QY 39 ESEED-----EDEDLELEVLERKPA-----AGLSAAP----- 67
Db 1454 NOEEEDVVAELNPHPIRQWRDEVDVLSQLSKLSLVAEVCITVDVADVNEQDEESTLKIL 1513
QY 68 --VPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPPVAP--ERQPSW----- 108
Db 1514 KVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVWIIADAVKEVSEMEVV 1569
QY 109 -----DPSPVSSSTVPAPSPLSAAAVSPSKLP-EDDEFPARPPPPPPASVSPQAEPVW 159
Db 1570 TESEISEMAPQVSESTCTPIPEPL-----ADLKLPLVEDDEKTEPEPEVPVPGQVERIPIE 1624
QY 160 TPPAPA-PAAPPSTPAAPKRRGSSGAVVXXKKIMDLKQEPGNTISAGQEDFPSVL--LE 216
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Db      1625  VEQAPTIPQRPAP-----: : : : :
Qy      217  TAASXPSLSA-----ASPEHEYLGNLSTVLPTGTLQENVSEASKEVSEKATLL 270
Db      1652  DSKSRVAPLNIKGRVTSQOQKELVESLERPL-TIITOQKPEKPTEDIG--ALGPL 1708
Qy      271  IDRLDTESELEYSEMGSSFSVSPKAESAVIVANPREEIIIVKNDEEKLVENNIIHLHQ 330
Db      1709  SPNTLAEEVEVPMQMOS-----VHSPQE-----KQEEIALSEII----- 1745
Qy      331  ELPTALTCLKVDEVVSSKAKDSNEKRVAVEAPMRBEYADFK---PFRVWVEKDSKE 387
Db      1746  BEFOAMKEVEKPE-SAPEKNESLEAPEI-INEPIRRVLVETKIMGPGKSLNEDND 1803
Qy      388  D-SDMLAAGGKIESNKVDKCCADSLQTNHKKDESS---NDTSPSTPEGIKD 442
Db      1804  DQSECLDSIGDUS---ERTIQR--FNTSIDDPSIRDSFSSISSFGDRQKFRTAENIRQ 1858
Qy      443  RSGAYITCAPFNPAATESIATNIFLLEDPTSENKTDEKKIEKKAQIVTEKNTSTKTSN 502
Db      1859  -----DLLPFQSSVSQVLRSSPNP-----SQQLVTN----- 1885
Qy      503  PFFVAQOSETVYTDNLTKVTEEVVANMPGLTDLVQEAESSELNEVTGKIAYETK 562
Db      1886  -----LSMDSPSD--LSPNAPPVGFENTAQFLEKLOE-DRPSAEGSIDSSGPEKVDHE-- 1936
Qy      563  MDLVQTSVMQESLSYPAALQCPSESEATPSVLPDIMEAPLNSAVPSAGASVIOQSS 622
Db      1937  -----GLDEFAAPP-----VHDPMQKSVFSGSLGSDDMKPGS 1967
Qy      623  SP-----LEASSVNYESIKEPENPPPYEEAMSVLSKVGIKEIKEPENIN-----AAL 672
Db      1968  QDDGVFIERNEAN-----EATLKKQKMSHHNDVIEKNYFNDAIPTAAL 2013
Qy      673  QETAPYISACDLIKETKLSABAPDFSDYSEMA-----KVEQVPDPHSEL 719
Db      2014  --LESPIAEARKLVQDAVESA-----SEYKQAVDSGEIGRELLDNVEQKIEQVKEP 2065
Qy      720  VEDSDPEVDLFDSDSIDPVQKQDETVMVLKESLTETSPESIMEVENKEKLSALPE 779
Db      2066  IVDSL--HKAYDGVGDFVHETVPNAVDFVRAEKQLPESPVPKEI-----TPE 2113
Qy      780  GGPYLEFKLSLMDTKTL--LPDEVSTLSKKEKIPLOMEELSTAVYSNDDLFISKAQ 837
Db      2114  -----PLVDIHTVDKVDENVNFLREPTP-PFETDDVAPLSDDKPQFGNQTP 2161
Qy      838  IRETTFSDSPSIEIIDFPPTLISSKTSDFSKLAREYTDLVSHKSEIANAPDGAAGSLPC 897
Db      2162  BEDETTFRKGLPTIPEEVEKAAAQNDLD---DFDPLVTSNTGAAGAAVGAAGAAA-- 2215
Qy      898  TELPHDLSLKNQPKVEEKISFSDDFSNGSATSKVILLPPDVSLGHQTAQIESIVKPK 957
Db      2216  -----VESITTEEM-----FGH--QKFVTPRPP 2237
Qy      958  VLEKAEKKLPDTEKEDRSPSAIFSADIG-----KT-- 989
Db      2238  T-----PPKDISDEVDKSTV---NLGSPSHSHSPSSPHSHILKHGDAWIDFKTVP 2286
Qy      990  -SVDDLKYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIFRIYKGVQ 1048
Db      2287  PCVLVDIYWRDAKSAIVLSALLVFLVLAQYPLTVTVTYSLLALGAAAGFRVPEKVEA 2346
Qy      1049  AIQKDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDLVDLSKFA 1108
Db      2347  QIKKTDSEHPFSEIILALILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 1168
Qy      1109  VLMVFTYVYGALFNGLTLLIALLISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 1168
Db      2407  LVNLSLTIWASFSGFTAILGLIGVFSVPKVBESNQEAIDPHLATISGHKLNQVNIIDE 2466
Qy      1169  KIPGLK 1174

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Db      2467  KLPLRL 2472
RESULT 5
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26215
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; EMBL:Z78066; PIDN:CA01522.2; GSPDB:GN00023; CESP:W06A7
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match      8.8%; Score 519.5; DB 2; Length 2607;
Best Local Similarity 20.4%; Pred. No. 3e-13;
Matches 292; Conservative 175; Mismatches 474; Indels 491; Gaps 55;
Qy      1 MEDLDQSPLVSSSDSPRPQAPFKVQVREPEDEE-----EE 38
Db      1397 LEKVEVQ--DLSONSPAPHKIIDLHF-NIPKDHEDYDGYVVPFGTSESSESKADGNQ 1453
Qy      39 EEEED-----EEDLEELVLRKPA-----AGLSAAP----- 67
Db      1454 NQEEEDVVAELNFIPIRQWRDEDVISLQSLKSLVAEVCITDVSADNEQDEESTLKIL 1513
Qy      68 -VPTAPAGAPLMDFGNDFVPPAPRGLPAAPVAP--ERQPSW----- 108
Db      1514 KVPSEPSLLE--LDFTND--PKVIHVPILMEPATMYLEEMVEWIIADAVKEVSEMEVV 1569
Qy      109 -----DPFSVSTVPAPSPLSAAVSPSKLP-EDDEPPARPPPPPPASVPOAEPW 159
Db      1570 TESIEMAPQVSESTCPIPEPL-----ADLKLPEVEDKTPPEPPEVVPVGGQOEIRIIP 1624
Qy      160 TTPAPA-PAAPSTP-----AAPKRRGSGAVVXXXKKIMDKLKEQPGNTISAGQE-- 208
Db      1625 VEQAPTIPQRPAPKSELKPAKPLDSDKS-----RVRFAPLNILKGRVTSQOQKEL 1678
Qy      209 ----DFPSVLLETAASXP-----SLSPLSAASFKHEHY--LGNLSTVLPTGTLQEN 254
Db      1679 VESLERPLTII-TQKPEKPTEDIGALSPLSPNTLASVEEVPMMDQSVPHSPQEKQEE 1737
Qy      255 VSEASKEVSEKATLLIDRLDTESELEYSEMGSSFSVSPKAESAVIVANPREEIIIVK-- 312
Db      1738 I-EALSEIIEPQAM-----KEVEKPVESAPEKDNESLEAPEIINEPIRRLVETK 1787
Qy      313 -----NKDEEKLVSNNILHXQOELPTALTCLKVDEDEVVSSSEKAKDSFNEKRVAVEA 364
Db      1788 IMGPKSLNEDNDSDGSECLDSIGDL-----SERTIQRFN--TSIDD 1829
Qy      365 P--MREEYADPKPFRVWVEKDSKED--SDMLAAGGKIESNKVDKCCADSLQTNH 420
Db      1830 PSIRRDSPSSISSFGDRQKFRTAENIRQDILLPQSSVSQVLRSSPNP--SQQLVTNL 1886
Qy      421 EKDESNDTSPSTPEGI-----KDRSGA--YITCAPFNPAATESIATNIF 466
Db      1887 SMDSPS---DLSPNAPPVGFENTAQFLEKLOEDRPSAEGSIDSSGPEKVDHEGFAA 1943
Qy      467 PLLSDPTSEN-----XTDEKK-----IEEKKAQIVTEKNTSTKTSNPPFFVAQDS 511
Db      1944 PPVHDPMQKSVFSGSLGSDDMKPGSQDQDGFVIERNEANEATLKKQKMSHHNDVIEKNY 2003
Qy      512 ETDVYTTDNLTKVTEEVVANMPGLTDLVQEAESSELNEV-TGTKIAYE----TKMDLV 566

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Db 2004 FNDNAPT---AALLSPFAEEARKLVQDAVESASEYKKQAVDSGDGEIGRELLDNVEQKIE 2060
QY 567 QTSEVWQESLYPAQICPSESEATPSVLPDIVMEAPINSVPSGAGASVIOQSSPLE 626
Db 2061 QVKEPIVDSLHKAYDGVGFVH-ETVPNAV-DDFVREAE-----2097
QY 627 ASSVNTYESIKHPENPPPYEAMSVSLKVGIGKEEIKPENINAALQETAPYISTACDL 686
Db 2098 -----KOLPESVVP-----EKIETPE-----PLVDIHDIV 2122
QY 687 IK-----ETKLSAEPAPDFSDYSEMAKVQVPDHSSELVEDSDSPDSEPVLDLSDSDIPDV 741
Db 2123 DKVHDEVDFNLREPTTPE-----TDDVAPLSDDKPQGNQI-----2160
QY 742 PQQDSTVMLVKSLEPTTFESMIEYENKEKLSALPPEGKPYLESFKLSLONTKDTLLP 801
Db 2161 -PEDETTTDRKGPLT-----EKAAAAQNND-----IP 2177
QY 802 DEVSTLSKKEKIPLOMEELSTAVYSNDDLFIISKEAQIRETETPDSDSPIEIIDEPFTLIS 861
Db 2178 EEV-----EKAAAAQNND-----LODFDPLVT 2199
QY 862 SKT-----DSFSKLAR-----EYTDLEVSHKSEIANAPD 890
Db 2200 SNTGAAGFAAGVAAAVESITEEMFGHQKFETVPRPTPKDISDEDVK-PSTVNLGFS 2258
QY 891 GAGSLPCTELPHD-----LSLKNTPKPVEEKIS-----FSDDFS 924
Db 2259 HHSHSPSS--PHHSILKHGHDWIDFKTVPPCAQNAPFSGEIMFLLAFFVYLSCFASRFS 2316
QY 925 KNGSATSKVLL-----PPDVSALG-----944
Db 2317 KSLPLLDNLSSLVVLVYLSLIHVKHKKRFRMNEEQATMSKLGAVGRGLYALIAFVNI 2376
QY 945 --HTQAEIESIVKPKVLEKEAEKLPSTDEKEDRSAPSAIFSADLGKTSVVDLLYWRDIKK 1002
Db 2377 VLEVGNLVALVGVAVSAHEAYLTKS-----SGVLRKKEVLDVIYWRDACK 2423
QY 1003 TGVVFGASIFLLLSLTVFSIVSVYAYIALALSVTISFRIYKGVIOAQIKSDGEGHFRAY 1062
Db 2424 SAIVLSLALLVPLAKYPLLTVTYSLIALGAAAGFRVKKVEAQIKKTDSEHPFSEI 2483
QY 1063 LSEVAISELVQKYSNLSALGHVNCVTKELRLFLVDDLDVLSLKEAVLMMVFTVGCALN 1122
Db 2484 LAQDLTLPQKHQAQADVFEHATCIANKLKLVFVESPLESIKFGVLWLSLTIASWFS 2543
QY 1123 GLTLILALISLFSVPVIVYERHQAQIDHYGLANKNVKQAMAKIQAKIPGLK 1174
Db 2544 GFTLAILGLLVFSVPKVNYESNQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

RESULT 6
T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26213
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-222 <WIL>
A:Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CA801523.1; GSPDB:GN00023; CBSP:W0
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CBSP:W06A7.3b
A:Map position: 5
A:Introns: 27/1; 77/2; 201/2

Query Match 5.7%; Score 340.5; DB 2; Length 222;
Best Local Similarity 32.4%; Pred. No. 1.9e-07;
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Matches 66; Conservative 52; Mismatches 83; Indels 3; Gaps 2;
QY 972 EKEDRSPSAIFGADL-GKTSVVDLLYWRDIKKTGTVFGASLFLLLSLTVFSIVSVTAYTA 1030
Db 9 KKYKQPTWVPATDPFGK--ILDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTIVVYSL 66
QY 1031 LALLSVTISFRIYKGVIOAQIKSDGEGHFRAYLSEVAISELVQKYSNLSALGHVNCVTK 1090
Db 67 LIALGAAAGFRVKKVEAQIKKTDSEHPFSEIQAQDLTPQKHQAQADVFEHATCIAN 126
QY 1091 ELRLFLVDDLDVLSLKFVLMVFTVVGALFNGLTLILALISLFSVPVIVYERHQAQIDH 1150
Db 127 KLKLVFVESPLESIKFGVLWLSLTIASWFSFTLAILGLLVGFSVPKVNYESNQEAIDP 186
QY 1151 YGLANKNVKQAMAKIQAKIPGLK 1174
Db 187 HLATISGHLKNVQNIIDEKLPFLR 210

RESULT 7
I38346
elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38346
R:Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: Giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: I38346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7962 <RES>
A:Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q31

Query Match 5.6%; Score 331; DB 2; Length 7962;
Best Local Similarity 20.0%; Pred. No. 6.3e-05;
Matches 235; Conservative 144; Mismatches 404; Indels 392; Gaps 48;
QY 32 EDEEEEEEEDEDEDELE--VLERK--PAAGLSAPV-----PTAPA 73
Db 6176 EBEREEEEAEVTEYEVMEEPPEYVVEEKLIISKVREAPAEVTERQSKIVLKEKIPA 6235
QY 74 AGAPLMDFGNDVFPAPGRPLPAAP-PVAPERQPSWDPSVSVSTVPAPSPLSAAAVSPSK 132
Db 6236 K-----IESPPPAKVPAPKIVPEKK-----VPAPVP-KKEKVPVPPK 6272
QY 133 LPEDDEPPA---RPPP-----PPPASVS-----POAEPVWTPPAPAPAPPS-TPAA 175
Db 6273 VPPEPKVPPEKKVPKVPKMEPLPAKVTEKHMQITQEEKVLAVYTKKEAPKARVPEE 6332
QY 176 PKRRGSSGAVVXXXKIMDLK---EQPGNTISAGQEDF---PSVLLETAASXPS-LSPL 227
Db 6333 PKR-----AVPEEKVLKPKREEPKPAKVTEFRKVVVKEEKVSIAPKREPQIKEV 6385
QY 228 SAASFKHEHYLGNLTVLPTGTLQEN-VSEASKVESEKAKTLLIDRLDTFSESELYSEM 286
Db 6386 TIMEEKERAY-----TLEEEAVSVQREEEYEEV-----EYDYKEFEYEPTEE 6429
QY 287 GSGFS-----VSPKAESAVIV--ANPREI 309
Db 6430 YDQYEEYERERYVEEHEEYITEPEKPIPVKVPPEEPVPTPKPAKVLKKAAPVPEEK 6489
QY 310 IV-----KNKDEEEKLVSNLILHXQQLPTALTKLVKDEWVSEKAKDSFNEKRVAVEAP 365
Db 6490 FVPIPKLAPPPPKVPEEPKVPFEKIHISITK--REKQVTEPAKVPKPKRVVAEEK 6547
QY 366 MREEYADPKPFRVWVEVKSDSDMLAAGGKIESNLESKVDKCKCFADSLQTNHKKOSE 425
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Db      2206 TESVIPPKADKSPKEVLQVPMSTETIREDAQPMKPSQAESRRSIAESIKASSPRDE 2265
QY      1001 KKTGVVFGASLFLLLSLTVFSIVSVTAYTALALLSVTISFRIVKVGIVQAIQKSDGHPFR 1060
Db      2266 KSP-----LASEKASRPGSV-----AESIKYDLDKPQIIXDDKSTE-HSRR 2305
QY      1061 AYLESEVAI--SEELVOKYNSALGH 1084
Db      2306 ESLEDKSAVTSEKSVSRPLSVASDH 2330

RESULT 9
A47282
Calcium-binding protein calphotin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47282
R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993
A;Title: Calphotin: a Drosophila photoreceptor cell calcium-binding protein.
A;Reference number: A47282; MUID:93165729; PMID:8094559
A;Accession: A47282
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-865 <MAR>
A;Cross-references: UNIPROT:Q02910; GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032
A;Experimental source: photoreceptor cells
A;Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBI:124956)
C;Genetics:
A;Gene: FlyBase:Cpn
A;Cross-references: FlyBase:FBgn010218
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: calcium binding

Query Match      5.5%; Score 324.5; DB 2; Length 865;
Best Local Similarity 22.3%; Pred. NO. 5.6e-06;
Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;

QY      59 PAAGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPLPAAAPPVAPVAPQSPQWDFSPVSTVP 118
Db      9 PVSAPVAPV--TPSAVAPVQVVSAPAAVAPAPAAPIATVFPVAPPPTLASVQPAV--TIP 65
QY      119 APSPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVPVWTPAP-----APAAPP--ST 172
Db      66 APAPIAASVTP---VASVAPPVVAAPTTPAA--SPVSTPVVAQIPVAVSAPVAPVVAAT 121
QY      173 PAAPKRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAF 232
Db      122 PTPVQIPVAAPIAT-----PPVAASA-----PT-----PAAVTPVISPVIAS-- 160
QY      233 KEHEYLGNLSTVLPTGTLQENVSASEKSEKAKTLLIDRLDTEFSELEYSEMGSSFSV 292
Db      161 -----PPVVPANTT-----VPVAPVAAVPAAPVVPVAPVAP-----AV 194
QY      293 SPKASAVIVAN-----PREIIVKKNDBEEKLVSNILHXQOELTALTATKLKVEDEVVS 347
Db      195 APAV--APVVAETPAPPVVAEIPVAT-----IPECVAPLIPEVSVVA 234
QY      348 SEKAKDSFNEKRVAVEAPMEEEVADPKPFERVWEVKDSKEDSDMLAAGGKIESNLESKYD 407
Db      235 T-----KPLAAAEPPVVVAPPATET-----FVVAPAAASPHVSVAPAVETVAVPVS 280
QY      408 KCFADSLQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIPP 467
Db      281 -----ASTEPPV---AAATLTATPETAL----- 301
QY      468 LLEDPTSENXTDKKIEEKAQIVTEKNTSTKTSNPFVFAAQOSETDYVTDTMLTKVTEE 527
Db      302 -----APVVAESQ-----VAA-----NTVVATTP 320
QY      528 VVANMPGLTPDLVQEAECSELNEVTGTKIAYETKMDLVQTSVMQESLYPA----- 579
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Db      321 TPAPRPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371
QY      580 -AQLCPSESEATSPVLDPDIVMEAPLNSAVPSAGASVIQSPSSPLEASSVNYESIKHE 638
Db      372 PATLAVTDPDVTASAVPELPVPIAPSPVSAVAETPVDLAPPVLPVPAAPVPAVVAEET 431
QY      639 PENPPPYEEMSV-SLKVSGIKKEEIKPENINAAIQETAPYISTACDLIKETKLSAEP 697
Db      432 PETPAPASAPVTIAALDIPVAVPIAAPSADAPAEAPAAPIVSTPPTTASVPETTPAPA 491
QY      698 P-----DFSYSSEMAKVEQVPVDHSEL-----VEDSSPDSBPVDLFSDDSI--DVPOK 744
Db      492 AVPTPEIDVSLSE-AAETPVAPPVEVTEVAVADVAPPEAAADLIIEPVPEPAPIPDL 550
QY      745 ODETVMVKESITETSFESMIEYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEV 804
Db      551 LEQTTSPVAVEAAESTSSPIE-----TSLPPNEAVASPEVAVAPITAPEPIPEPEP 603
QY      805 STLSKKEKIPLO-----MEELSTAVVSNDDLFISKEAQIRETETFSDDSSPIELIDEPPTLI 860
Db      604 SLATTEPIPVAPVVIQEAADV-----EVPVTETST---SIP-ETTVEPPEAV 649
QY      861 SSKTDSFSKLAREYTDLEV-SHKSEIANAPDCAGSLPCTELP-----HDLSL 906
Db      650 AEKV-----LDPAITEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701
QY      907 KNIQPKVEEKISFDDFSKNGSATSKVLL-----LP-----PDVSALG----- 944
Db      702 PVIDPPVQGEIAVA-EIPETDTKPAEIVQEQTIPTEAPVPEVSKYAEVISEAPAAAEVP 760
QY      945 -----HTQAEISIVKPVLEKAEKKLSDTEKEDRSAPSAISADLGTSTVDLLY 996
Db      761 ITAGDNPDNTSGVIGSEW-PTIAEKPVVEEVTSEIPEQSSSPSD--SVPVAK--ITPLL- 814
QY      997 WRDIKKTGV 1005
Db      815 -RDLQTTDV 822

RESULT 10
A47283
calphotin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A47283
R;Ballinger, D.G.; Xue, N.; Harshman, K.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993
A;Title: A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and
A;Reference number: A47283; MUID:93165730; PMID:8434015
A;Contents: photoreceptor cells
A;Accession: A47283
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-873 <BAL>
A;Cross-references: UNIPROT:Q02910; GB:L05080; NID:g157071; PIDN:AAA28420.1; PID:g15707
A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBI:124959)
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match      5.4%; Score 320.5; DB 2; Length 873;
Best Local Similarity 22.5%; Pred. NO. 8.2e-06;
Matches 235; Conservative 122; Mismatches 367; Indels 321; Gaps 50;

QY      59 PAAGLSAAPV-PTAPAAAGAPLMDFGNDVFPAPRGPLPAA-----PVAPERQPSW-DPSP 112
Db      9 PVSAPVAAAPVTPSAVAPVQVVSAPAAVAVAPVAPAPAAPTAVTPVAP--PPTLASVQP 66
QY      113 VSTVTPAPSPLSAAAVSPSKLPEDDEPPARPPPPPSVSPQAEVPVWTPP-----A 163
Db      67 ATTVTPAPAPIAASVAP---VASVAPPVVAAPTTPA-----ASPSTPFPVAPVAPVAV 118
QY      164 PAPAAPP-----STPAAPKRRGSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLET-- 217
Db      119 SAPVAPPVAAATPTPVAP-----IPVAAPIVATPPVAAASAPT 154
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Db 823 AKTPVKRPDPSPKKAAPAKPSTKTADAPPVSVKPEFVSKPKE---PSPKKAEPNSP 876

RESULT 14  
A56577  
microtubule-associated protein MAP 1B - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: A56577  
R:Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.  
Eur. J. Cell Biol. 57, 66-74, 1992  
A:Title: Identification of two distinct microtubule binding domains on recombinant rat M  
A:Reference number: A56577; MUID:92347374; PMID:1639092  
A:Accession: A56577  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2364 <ZAU>  
A:Cross-references: UNIPROT:P15205; GB:X60550  
A:Experimental source: brain  
A:Note: nucleotide sequence not given; conceptual translation not complete  
C:Superfamily: microtubule-associated protein MAP1B

Query Match 4.9%; Score 289; DB 2: Length 2364;  
Best Local Similarity 20.3%; Pred. No. 0.00061;  
Matches 275; Conservative 158; Mismatches 462; Indels 422; Gaps 61;

QY 30 EPEDEEEEEEDEDEDELEELVLERKPAAGLSAAPTAPAAAPLMDGFNDVPPA 89  
DB 909 EAEQSEEEGEEEDKAEDAREEDHEPDKTEADYVMAVVDKAAEAGVTEQY--DFL--- 963  
QY 90 PRGFLPAAPP--VAPERQSWDPSPVSVTPAPSPLSAAAVSPSKLPEDDEPPARPPPP 147  
DB 964 ---GTPAKQGVQSPSREPA--SSIHDETLPGGSEATA-----SDEENREDQPEEF 1011  
QY 148 PASVSVQAEVPTTPAPAPAPSTPAAPKRGSSGAVVXXXXKINDLKEQPGNTLSAQ 207  
DB 1012 TATSGVQTQSTIEISSEPTMDMESTP-----RDVMTDETNEETESPQ 1055  
QY 208 E-----DFPSVLLETAAEXP---SLSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENV 255  
DB 1056 EFWNITKYESSLYQOEYKPVVASFNGLSGSKTDATDGRDYNASASTISPPSSMEEDXF 1115  
QY 256 SEAS-----KEVSEK-----AKTLIDRLDTE 277  
DB 1116 SKSALRDAYRPEETDVTKTGAELDKVSDERLSPAKSPSLSPSPSPPIETPLGERSV-N 1174  
QY 278 FS-----ELEYSEMGSFSS-VSPKASAVI---VANPRE---ETIIVKNK----- 314  
DB 1175 FSLTPNEIKASAGEATAVVSPGVQAVVEHCASPEEKTELVVSPSQSVTGSAGHTPPY 1234  
QY 315 ----DDEEKLVSNLHXXQQLPTALTKLKVEDEVVSSE--KAKDSFNKRVAAVEAPMRE 368  
DB 1235 QSPTDEKSHLPTVETNAQAVP-----VSFEFTEAKDE-NER--SSISPMDE 1279  
QY 369 EYADF-KPERWE-----VKDSKEP---SDMLAAGKIESNLESKYDKKCFADSL 415  
DB 1280 PVPDSESPIEKVLSPRLSPPLIGESAYEDFLSADDKALGRSESPFEGKNGQGFSD-- 1337  
QY 416 EQTNHEKDSSESSNDDTFSPSTPGIKDRSGAVITCAPENP--AATESIATNIFPLED- 471  
DB 1338 -----KESPVLS-DLISDLVDQKQEKRGAFIPIKEDFSPEKKASDAEIMSSQSALALDE 1390  
QY 472 -----PTSXNKTDKIEEKKAQIVTEKNTSTXTSNPFFVAAQDSEDTYVTTDNLTK 523  
DB 1391 RLKGGDSPQVDVSVQFGSPKEDTKMSISBGTVDKSAATVDBGAEPT---YHMEGVAS 1447  
QY 524 VTEEVA--NMPGLGFLDVLQVACESRLNEVTCTKATAYTKMDLVQTSVMQRS-IYPAA 580  
DB 1448 VSTASVATSSFPPEPTDD--VSPSLHAEVGSPHSTVEDDLSLSVSVVQPTPTTFQETEMSPK 1506  
QY 581 QLCF-----SFESEATPSPVLPDVIWMEAPLNSAV-----P 611

Db 1507 EECPRPMISPPDFSPKTAKSRTPVQDHRSEOSSMSIERGQSPESHLAMDPSRQSDHP 1566

QY 612 SAGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----ERAMSVS-LKVSQ 657

Db 1567 TVGAGMLHITENGPTEDVSPSDIQDSSLSHKIPPTPEPSYTDNDLSLISVSQVEASP 1626

QY 658 IKKEIKPENINAAQETE-----APVISTACDLIKE---TKLSAEP----- 696

Db 1627 STSSAHTPSQIASPLQEDTLSDVVPDRMSLYASLASEKQVSGLEGKLSPKSDISPLTPR 1686

QY 697 -----APDFSYSEMAK-----VEQVPDRHSELVEDS----- 723

Db 1687 ESSPYSPGFSDSTGAKESTAAYQTSSPPIDAAAAPYGFSSMLFDTMQHHLALSRD 1746

QY 724 -----SPDSEPDVLFSDD---SIPDVP---OKQD 746

Db 1747 LTTSSVEKONGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYYEKT 1806

QY 747 ETVMLE-----VKESLTETSFESMIYENKEKLSALPPGGKPYLESFKLSLONTXD 797

Db 1807 RTIKGSPDSGYSETIEKTKTPEDGGYSCETETKTRTPEGGYSY-----EISEK 1858

QY 798 TLLPDEVSS--TLSKKEKIPLOMEELSTAVYSNDD-----LFTSKEA 836

Db 1859 TTRTEVSGYTYEKTETRSRRLDDISNGYDDTDEGGHTLGCYSYVETTEKITSFPFSES 1918

QY 837 QIRETETFSDDSP-----IEIIDFPPTLISKTOSFSKLAREYT-----DL 877

Db 1919 YSVETTTKTRSPDTSAYCYETMEKITKTPQASTSYETSDRCYTPERKSPSEARQDVLD 1978

QY 878 -----EVSH-KSETANA---PDG-----AGSLPCTELPHDLSLKNIQP-----KV 913

Db 1979 CLVSVCEFPKHPKTEILSPSPFINPFWFAGEPTESEERPLTQSGGAPPSPSGKQGRQC 2038

QY 914 EKIKSFSDDFKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLKEAEKK-LPSD-- 970

Db 2039 DETPPTSVSESAPSQTSDSV---PPETE-----ECPSTADANLSDSESETIPTDKT 2088

QY 971 -----TKEDRSPS-----AIFSA DLGKTSVVDLLVYRDDIKKTG 1004

Db 2089 VTYKMDPPAPMQDRSPSPRHPDVMVDPEALAIQNILGALKKDLKEKAKTKKPG 2145

RESULT 15  
QRMSP1  
microtubule-associated protein MAP1B - mouse  
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protei  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S07549; S44387; A33645  
R:Noble, M.; Lewis, S.A.; Cowan, N.J.  
J. Cell Biol. 109, 3367-3376, 1989  
A:Title: The microtubule binding domain of microtubule-associated protein MAP1B contain  
A:Reference number: A33645; MUID:90094539; PMID:2480963  
A:Accession: S07549  
A:Molecule type: mRNA  
A:Residues: 1-2464 <NOB>  
A:Cross-references: UNIPROT:P14873; EMBL:X51396; NID:952999; PIDN:CAA35761.1; PID:953000  
R:Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.  
Arch. Biochem. Biophys. 310, 428-432, 1994  
A:Title: Binding of heat-shock protein 70 (hsp70) to tubulin.  
A:Reference number: S44387; MUID:94234720; PMID:8179328  
A:Accession: S44387  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 653-663, 'IC' <SAN>  
C:Superfamily: microtubule-associated protein MAP1B  
C:Keywords: microtubule binding; phosphoprotein; tandem repeat  
F:589-786/Domain: microtubule binding #status experimental <MB>  
R:K-E/D-X)  
F:1861-2064/Region: 17-residue repeats  
F:91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: p

F:147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (cd  
F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match		4.9%; Score 289; DB 1; Length 2464;
Best Local Similarity		19.8%; Pred. No. 0.00064;
Matches 262; Conservative 148; Mismatches 474; Indels 442; Gaps 55;		
QY	32	EEEEEEEEDEDEDL-EELEVLERKPAAGLSAAPTAPAAAGAPLMDFGNDFVPPAP 90
DB	1009	EAEQSEEEGEEDKAEDAREEGVEPKTEAEDYVMAVADKAAEAGVTEQYGY----- 1061
QY	91	RGLPLAAPV-APERQSWDPGVSTVPAPGLSAAVSPKLPBDDPPAPPPPPA 149
DB	1062	LCTSAKQPGIOGSPREPA--SSIHDETLPGSESEATA-----SDEENREDQPEEFTA 1112
QY	150	SVSPQAEPTVTPAPAPAPPTPAAPKRRGSGAVVXXXXKIMDLKEQPGNTISAGQED 209
DB	1113	TSGYQSTTIEISSEPTMDXETP-----RDVMSDETNEETSPSOEF 1156
QY	210	FPSVLLETAASPSISPLSAASFK-----EHEYLGNLSTVLPTTEGTLQENVSE 257
DB	1157	VNITKYESSLYSOEYKPAVASFNGLSEGSTDATDCKYNASASTISPPSSWEEDKFSK 1216
QY	258	AS-----KEYSEK-----AKTLIDRLDTEFS 279
DB	1217	SALRDAYCSEKELKASABLDIKDVSDERLSPAKSPSLSPSPSPTEKTPLGERSV-NFS 1275
QY	280	---ELEYSEMSSFSVSPKASAVI---VANPRE---EIIIVNK----- 314
DB	1276	LTPNEIKVSAEGEARSVPGVTQAVVEHCASPEKTLLEVSPSQSVTGSAGHTYYQSP 1335
QY	315	-DEEEKLVSNNTLHXQQLPTALTKLKVEDEVVSSEKAKDSFNEKRVAVAEAPMEYADF 373
DB	1336	TDEKSSHLPTVESENAQAVPVSF-----EFSEAKOE-NER--ASLSPMDEFPDS 1382
QY	374	K-PFERVME-----VKDSKEDSDMLAAGKIEGNLESKVDKCFADSLQETNHEKDS 425
DB	1383	ESPVEKVLSPRLSPPLGSESPYEDFLSADSKVLR-----RSESPFE 1425
QY	426	SSNDTSPSTPEGIKDRSGAVITCAPNPATATESIATNIPFLLEDPTSENKT----- 478
DB	1426	GKNGKQGPDRSPVSD-----LTSTGLYQDKQBEKSTGFIPKEDFGPEKTSVETMS 1480
QY	479	-----DEKKI-----EKKAQIVTEKNTSTKTSNPPFFVAAQDSETD 514
DB	1481	SQSALALDERKLGSDVSPQIDVSGFGKEDTKMSISEGTVSDKATP--VDEGVAEDT 1538
QY	515	YTTNLTNLTKEVTEVVA--NMPEGLTPDLVQACESELNEVTGKIAETKMDLVQTSVM 572
DB	1539	YSHMEGVASVTASVATSGFPPEPTDD-VPSLHAEVGSHPSTEVDDLSVSVVQTPTF 1597
QY	573	QSS-LYPAAQLCP-----SFESEATPSVLPDIVMEAPLNSAV-- 610
DB	1598	QETEMSPSKKECPRMSPSPDFSPKTAKRTPVQDHRSEOSMSIEFGQSPSEHSFAMD 1657
QY	611	-----PSGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EAM 649
DB	1658	FSRQSPDHPTLGASVLHITENGTEVDYSPCDIQDSSLSHKIPPTPEEPSYQDNLDSELI 1717
QY	650	SVS-LKVSGIKKEIKPENINAAQETE-----APYISACDLIKE---TKLSAE 695
DB	1718	SVSQVEASPSTSAHTPSQIASPLQEDTLSDVPPPREMSLYASLASEKVQSLGEKLSPK 1777
QY	696	P-----APDFSDYSEMAK-----VEQVPDPHSELVEDS- 723
DB	1778	SDISPLTPRESSPLSPGFSOSTSAKETAHAHQASSPPIDAATAEPYGRSGMLFDTM 1837
QY	724	-----SPDSEPVDLFSD-----DS 737
DB	1838	QHHLALNRDLTSSVEKDSGGKTPGDFNYAYOKPENAAAGSPDEEDYDYESQEKTIIRTHDV 1897
QY	738	IPDVPOKQDETVM-----VKESLTFESMIYENKELKLSALPPGEGKPYLESF 788

Search completed: June 16, 2005, 13:32:00  
Job time : 44.4224 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 159.813 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-29

Perfect score: 5923

Sequence: 1 MEDLDQSLVSSDSPRPQ.....VKDAMAKIQKIPGLKRAE 1178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5815	98.2	1192	1 RTN4 HUMAN	Q9nc33 homo sapien
2	4851	81.9	986	2 Q8IUA4	Q8Iua4 homo sapien
3	4296.5	72.5	1163	1 RTN4 RAT	Q9jkl1 rattus norv
4	4289	72.4	1162	2 Q8BGM9	Q8Bgm9 mus musculu
5	4277.5	72.2	1163	2 Q8K3G8	Q8K3g8 mus musculu
6	3658.5	61.8	1046	2 Q8BGR7	Q8Bgr7 mus musculu
7	2580.5	43.6	720	2 Q7TNB7	Q7tnb7 mus musculu
8	2527	42.7	639	2 Q8K290	Q8K290 mus musculu
9	2233	37.7	578	2 Q8OW95	Q8ow95 mus musculu
10	1735	29.3	658	2 Q6RSS8	Q6rss8 gallus gall
11	1534.5	25.9	1055	2 Q6JRV1	Q6jrv1 xenopus lae
12	1531	25.8	392	2 Q96B16	Q96b16 homo sapien
13	1518.5	25.6	1044	2 Q6JRV0	Q6jrv0 xenopus lae
14	1517.5	25.6	1043	2 Q6JRV0	Q6jrv0 xenopus lae
15	1510	25.5	1024	2 Q6JRV2	Q6jrv2 xenopus lae
16	1508.5	25.5	1032	2 Q6JRV7	Q6jrv7 xenopus lae
17	1492	25.2	1013	2 Q6JRV9	Q6jrv9 xenopus lae
18	1331.5	22.5	343	2 Q6IPN0	Q6ipn0 homo sapien
19	1201.5	20.3	375	2 Q8BHF5	Q8bhf5 mus musculu
20	1163	19.6	356	2 Q8BH78	Q8bh78 mus musculu
21	1152.5	19.5	357	2 Q8K3G7	Q8k3g7 mus musculu
22	992	16.7	250	2 Q8IG16	Q8igl6 sus scrofa
23	931	15.7	199	2 Q7YRW9	Q7yrw9 bos taurus
24	927	15.7	199	2 Q6IM70	Q6im70 sus scrofa
25	922	15.6	199	2 Q7PCJ7	Q7pcj7 macaca fasc
26	919	15.5	187	2 Q6IG15	Q6igl5 sus scrofa
27	915	15.4	199	1 RTN4 MOUSE	Q9p972 mus musculu
28	887	15.0	199	2 Q7T224	Q7t224 gallus gall
29	867	14.6	179	2 Q9GM33	Q9gm33 macaca fasc
30	804.5	13.6	315	2 Q6IFY4	Q6ify4 xenopus tro
31	792	13.4	311	2 Q6JRV3	Q6jrv3 xenopus lae

32 791 13.4 330 2 Q6JRV4 Q6jrv4 xenopus lae  
33 791 13.4 777 1 RTN1 RAT Q64548 rattus norv  
34 790 13.3 193 2 Q6IFY5 Q6ify5 xenopus tro  
35 788.5 13.3 760 2 Q90638 Q90638 gallus gall  
36 787.5 13.3 776 1 RTN1 HUMAN Q16799 homo sapien  
37 787 13.3 1013 2 Q6T930 Q6t930 homo sapien  
38 783 13.2 323 2 Q6JRW1 Q6jrw1 xenopus lae  
39 781 13.2 199 2 Q6PB23 Q6pb23 xenopus lae  
40 779 13.2 780 2 Q8K4S4 Q8k4s4 mus musculu  
41 778 13.1 193 2 Q6JRV6 Q6jrv6 xenopus lae  
42 778 13.1 780 2 Q8K0T0 Q8k0t0 mus musculu  
43 776.5 13.1 316 2 Q6JRW2 Q6jrw2 xenopus lae  
44 774.5 13.1 304 2 Q6JRW0 Q6jrw0 xenopus lae  
45 755.5 12.8 214 2 Q7T222 Q7t222 carassius a

#### ALIGNMENTS

RESULT 1  
RTN4\_HUMAN  
ID RTN4\_HUMAN STANDARD; PRT: 1192 AA  
AC Q9NC33; Q94962; Q9BXG5; Q9H212; Q9H313; Q9U042; Q9Y293; Q9Y2Y7;  
AC Q9Y5U6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).  
GN Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
RA Michalovich D., Simmons D.L., Walsh F.S.; "  
RT "Inhibitor of neurite outgrowth in humans."  
RL Nature 403:383-384(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX TISSUE=Brain;  
RC MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;  
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
RT endoplasmic reticulum and reduces their anti-apoptotic activity."  
RL Oncogene 19:5736-5746(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
RT 2p14-->2p13 by radiation hybrid mapping";  
RL Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RX Jin W.-L., Ju G.;  
RA "Developmentally-regulated alternative splicing in a novel Nogo-A";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RC TISSUE=Brain; (ISOFORM 3).  
RP TISSUE=Placenta;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
RA Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RC TISSUE=Brain; (ISOFORM 3).  
RP GU J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
RA Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
RT growth.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RC TISSUE=Brain; (ISOFORM 1).  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 5:355-364 (1998).  
RN [10]  
RC TISSUE=Brain; (ISOFORMS 2 AND 3).  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Tomihata S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [11]  
RC TISSUE=Brain; (ISOFORM 3).  
RX MEDLINE=2049367; PubMed=11042152; DOI=10.1101/gr.140200;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells.";  
RL Genome Res. 10:1546-1560 (2000).  
RN [12]  
RC TISSUE=Brain; (ISOFORM 1/4).  
RP MAO Y.M., Xie Y., Zheng Z.H.;  
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RC TISSUE=Testis; (ISOFORM 1).  
RP SHU J.H., Zhou Z.M., Li J.M.;  
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RC TOPOLOGY.

RC TISSUE=Brain;  
RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;  
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
RT "Identification of the Nogo inhibitor of axon regeneration as a  
RT Reticulon protein.";  
RL Nature 403:439-444 (2000).  
RN [15]  
RC TISSUE=Brain;  
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;  
RA Fournier A.E., GrandPre T., Strittmatter S.M.;  
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
RT regeneration.";  
RL Nature 409:341-346 (2001).  
RN [16]  
RC TISSUE=Brain;  
RX MEDLINE=2188956; PubMed=11891768; DOI=10.1002/jnr.10134;  
RA Ng C.E.L., Tang B.L.;  
RT "Nogins and the Nogo-66 receptor: factors inhibiting CNS neuron  
RT regeneration.";  
RL J. Neurosci. Res. 67:559-565 (2002).  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults.  
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xL and Bcl-2.  
CC This is likely consecutive to their change in subcellular  
CC location, from the mitochondria to the endoplasmic reticulum,  
CC after binding and sequestration.  
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
CC through 2 putative transmembrane domains.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;  
CC IsoId=QNQC3-1; Sequence=Displayed;  
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;  
CC IsoId=QNQC3-2; Sequence=VSP\_005655;  
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;  
CC IsoId=QNQC3-3; Sequence=VSP\_005652, VSP\_005653;  
CC Name=4;  
CC IsoId=QNQC3-4; Sequence=VSP\_005654;  
CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
CC widely expressed excepted for the liver. Isoform 3 is expressed in  
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
CC specific.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -!- CAUTION: Ref.11 sequence differs from that shown due to  
CC frameshifts in positions 1149 and 1156.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AJ251383; CAB99248.1; -  
CC EMBL; AJ251384; CAB99249.1; -  
CC EMBL; AJ251385; CAB99250.1; -  
CC EMBL; AB040462; BAB18927.1; -  
CC EMBL; AB040463; BAB18928.1; -  
CC EMBL; AF148537; AAG12176.1; -  
CC EMBL; AF148538; AAG12177.1; -  
CC EMBL; AF087901; AAG12205.1; -  
CC EMBL; AF320999; AAG40878.1; -  
CC EMBL; AF132047; AAD31021.1; -  
CC EMBL; AF132048; AAD31022.1; -  
CC EMBL; AB015639; BAA83712.1; -  
CC EMBL; AF077050; AAD27783.1; -  
CC EMBL; AF177332; AAG17976.1; -  
CC EMBL; AB020693; BAA74909.2; ALT\_INIT.





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Db 121 NDEEBKLVNNILNHNQQLPTRLTKLVKDEDEVSEKAKDSFKNEKRVAVVEAPMRREYAD 180
Qy 373 KXPFRVWEVKDSKSDMLAAGKIESLNSKVDKCCFADSLSEQTNHKKDSSESSNDSTS 432
Db 181 KXPFRVWEVKDSKSDMLAAGKIESLNSKVDKCCFADSLSEQTNHKKDSSESSNDSTS 240
Qy 433 FSTPREGIKDRSGAYITCAPFPNPAATESIATNIFPILLGDPSTSENKTKDEKKIEKKAQIVT 492
Db 241 FSTPREGIKDRSGAYITCAPFPNPAATESIATNIFPILLGDPSTSENKTKDEKKIEKKAQIVT 300
Qy 493 EKNTSTKTSNPPRVAQDSEDTVTTDNLTKTVEEVVANNPEGLTLDLQVQECESSELSNEV 552
Db 301 EKNTSTKTSNPPRVAQDSEDTVTTDNLTKTVEEVVANNPEGLTLDLQVQECESSELSNEV 360
Qy 553 TGTKIAYETKMDLVQTSVQWQESLYPAAQLCPSEFESEATPPSPVLPDIVWEAPLNSAVPS 612
Db 361 TGTKIAYETKMDLVQTSVQWQESLYPAAQLCPSEFESEATPPSPVLPDIVWEAPLNSAVPS 420
Qy 613 AGASVTPQSSPLEASVNYESIKHEPENPPPPYEEAMSVSL-KVSGIKKEEIKPENINAA 671
Db 421 AGASVTPQSSPLEASVNYESIKHEPENPPPPYEEAMSVSLKKVSGIKKEEIKPENINAA 480
Qy 672 LQETEPAPYISACDLIKETKLSAEPAPDFSDYSEMAKVQPPVDHSELVEDSDSPSEPDV 731
Db 481 LQETEPAPYISACDLIKETKLSAEPAPDFSDYSEMAKVQPPVDHSELVEDSDSPSEPDV 540
Qy 732 LFSDDSIIPVPOKQDETVMVKESLTETSFESMIEYENKEKLSALPPEGKPYLESFKLS 791
Db 541 LFSDDSIIPVPOKQDETVMVKESLTETSFESMIEYENKEKLSALPPEGKPYLESFKLS 600
Qy 792 LONTKDTLLPDEVSTLSKKEKIPLOMBELSTAVYSNDDLFIKSAQIRKETETFSDDSPTE 851
Db 601 LONTKDTLLPDEVSTLSKKEKIPLOMBELSTAVYSNDDLFIKSAQIRKETETFSDDSPTE 660
Qy 852 IIDEFPTLLSSKTDSPSKLAREYTDLEVSHKSIANAPDAGSLPCTELPHDLSLKNIO 911
Db 661 IIDEFPTLLSSKTDSPSKLAREYTDLEVSHKSIANAPDAGSLPCTELPHDLSLKNIO 720
Qy 912 KVEEKISFDDFSKNGSATS KVL LPPDPVSALGHTQAEIESIVKPKVLEKEAKKLPSDT 971
Db 721 KVEEKISFDDFSKNGSATS KVL LPPDPVSALA-TQAEIESIVKPKVLEKEAKKLPSDT 779
Qy 972 EKEDRSPSAIFSADLKTSTVDLLYWRDIKKTGVWFGASLFLLLSLTSTVSI SVTAYIAL 1031
Db 780 EKEDRSPSAIFSADLKTSTVDLLYWRDIKKTGVWFGASLFLLLSLTSTVSI SVTAYIAL 839
Qy 1032 ALLSVTISFRIYKGVITQAIQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNCITKE 1091
Db 840 ALLSVTISFRIYKGVITQAIQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNCITKE 899
Qy 1092 LRLFLVDDLVDLSLKFVLMWFTYVYGALFNGLTLLALISLFSVPVIYERHQAIQIDHY 1151
Db 900 LRLFLVDDLVDLSLKFVLMWFTYVYGALFNGLTLLALISLFSVPVIYERHQAIQIDHY 959
Qy 1152 LGLANKNVKDMAKIOAKIPGLKRKAE 1178
Db 960 LGLANKNVKDMAKIOAKIPGLKRKAE 986
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RESULT 3  
RTM4\_RAT

```
ID RTM4_RAT STANDARD; PRT: 1163 AA.
AC Q9JKL1; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)
DE (Glut4 vesicle 20 kDa protein).
GN Names=Rtn4; Synonyms=Nogo;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:
a new member of the reticulon family.";
RL Biochim. Biophys. Acta 1450:68-76(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
Spillmann A.A., Christ F., Schwab M.E.;
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1.";
RL Nature 403:434-439(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
RX STRAIN=Wistar Kyoto; TISSUE=vascular smooth muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in rat: one of two
minor splice variants.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
RA GrandPre T., Li S., Strittmatter S.M.;
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL Nature 417:547-551(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
block the regeneration of the nervous central system in adults (By
similarity).
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
membrane of the endoplasmic reticulum through 2 putative
transmembrane domains (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=Nogo-A, NI-220-250;
CC IsoId=Q9JKL1-1; Sequence=Displayed;
CC Name=2; Synonyms=Nogo-B, Foccen-M1;
CC IsoId=Q9JKL1-2; Sequence=VSP_005658;
CC Name=3; Synonyms=Nogo-C, VP20;
CC IsoId=Q9JKL1-3; Sequence=VSP_005656, VSP_005657;
CC Name=4; Synonyms=Foccen-M2;
CC IsoId=Q9JKL1-4; Sequence=VSP_005659;
CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
present in dorsal root ganglion, sciatic nerve and PC12 cells
after longer exposure. Isoforms 2 and 3 are detected in kidney,
cartilage, skin, lung and spleen. Isoform 3 is expressed at high
level in skeletal muscle. In adult animals isoform 1 is expressed
mainly in the nervous system.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; AF051335; AA01564.1; -
CC EMBL; AJ242961; CAB71027.1; -
CC EMBL; AJ242962; CAB71028.1; -
CC EMBL; AJ242963; CAB71029.1; -
CC EMBL; AF132045; AAD31019.1; -
CC EMBL; AF132046; AAD31020.1; -
CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
CC GO; GO:0005635; C:nuclear membrane; ISS.
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DR GO: 0005515; F: protein binding; ISS.  
 DR GO: 0019987; P: negative regulation of anti-apoptosis; ISS.  
 DR GO: 0030517; P: negative regulation of axon extension; ISS.  
 DR InterPro: IPR003388; Reticulon.  
 DR Pfam: PF02453; Reticulon; 1.  
 DR PROSITE: PS00845; RETICULON; 1.  
 KW Alternative splicing; Direct protein sequencing;  
 Endoplasmic reticulum; Transmembrane.  
 FT DOMAIN 1 989 Cytoplasmic (Potential).  
 FT TRANSMEM 990 1010 Potential.  
 FT DOMAIN 1011 1104 Lumenal (Potential).  
 FT TRANSMEM 1105 1125 Potential.  
 FT DOMAIN 1126 1163 Cytoplasmic (Potential).  
 FT DOMAIN 976 1163 Reticulon.  
 FT DOMAIN 33 46 Poly-Glu.  
 FT DOMAIN 73 76 Poly-Ala.  
 FT TRANSMEM 140 145 Poly-Pro.  
 FT VARSPPLIC 1 964 Missing (in isoform 3).  
 FT FTID=VSP 005656.  
 FT AVLSAELSKTS -> MDGQKXHWKDK (in isoform 3).  
 FT VARSPPLIC 965 975  
 FT FTID=VSP 005657.  
 FT Missing (in isoform 2).  
 FT VARSPPLIC 173 975  
 FT FTID=VSP 005658.  
 FT Missing (in isoform 4).  
 FT VARSPPLIC 192 975  
 FT FTID=VSP 005659.  
 FT CONFLICT 1130 1131 Missing (in Ref. 3: AAD31020).  
 FT SEQUENCE 1163 AA; 126386 MW; 8CB894809894F086 CRC64;  
 SQ  
 Query Match 72.5%; Score 4296.5; DB 1; Length 1163;  
 Best Local Similarity 74.0%; Pred. No. 1.4e-146;  
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;  
 QY 1 MEDLDQSLVSS-DSPPROPAPKIQVREPEDEE-BEEEEDEDEDEDELEEVLERK 58  
 DB 1 MEDLDQSLVSS-DSPPROPAPKIQVREPEDEE-BEEEEDEDEDEDELEEVLERK 60  
 QY 59 PAAGLSAAPTAPAAAGPLMDGNDVFPAPRGLPAAPVAPRQSPMDPSPVSSVTP 118  
 DB 61 PAAGLSAAPTAPAAAGPLMDGNDVFPAPRGLPAAPVAPRQSPMDPSPVSSVTP 115  
 QY 119 APSPLSAAVSPKLPEDDEPPAPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 178  
 DB 116 APSPLSAAVSPKLPEDDEPPAPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 166  
 QY 179 RGSAG-AA 224  
 DB 167 RGSAGVDETLFALPAASEPVPSPSAEKTMDLMEQGNVSSGQEDFPVLLTAALPSL 226  
 QY 225 SPLSAASPKHEYLGNLSVLTPTGTLQENVSEASKEVSEKAKTLLIDRLTFESELYS 284  
 DB 227 SPLTSVSPKEHYGNLSVSSSGTITETNEASKELPERATNPFVNRDLAEFSELYS 286  
 QY 285 EMGSFVSFSPKAEASAVIVANPREIIVKNKDEEKLVSNNILHXQQLPTALTKLKVEDE 344  
 DB 287 EMGSFVSFSPKAEASAVIVANPREIIVKNKDEEKLVSNNILHXQQLPTALTKLKVEDE 340  
 QY 345 VVSSEKAKDSFNEKRAVAEAPREYADPKPFRVWEVDSKEDS-DMLAGGKIESNLE 403  
 DB 341 VVSSEKAKDSFNEKRAVAEAPREYADPKPFRVWEVDSKEDS-DMLAGGKIESNLE 396  
 QY 404 SKVDKCPADSLQTNHSEKSSNDTSFPSTPEGIKDRSGAVITCAPFNPAAATESIAT 463  
 DB 397 SKVDKCPADSLQTNHSEKSSNDTSFPSTPEGIKDRSGAVITCAPFNPAAATESIAT 455  
 QY 464 NIFPLEDPTSENKTDKIEKKAQIVTERKNTSTKTSNPFVAAQSDSETDYVTDMLTK 523  
 DB 456 NTFPLEDHTSENKTDKIEKKAQIIITEK-TSPKTSNPFVAAQSDSETDYVTDMLTK 514  
 QY 524 VTEEVVAMPGLTPDLVQEAACESELNEVTGKTAIYETKMDLVQSEVMQESLTPAQLC 583  
 DB 515 VTEEVVAMPGLTPDLVQEAACESELNEVTGKTAIYETKMDLVQSEVMQESLTPAQLC 574

584 PSFESEATPSVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESSIKHEPNP 642  
 DB PSFESEATPSVLPDIVMEAPLNSAVPSAGASVIQPSVSPLEAPPVSYDSIKLEPNP 634  
 QY 643 PPYEAMSVSLKSGIKKEIKPENINAAQETAPYISIAACDLIKETKLSAEPAPDPSD 702  
 DB 635 PPYEAMSVSLKSGIKKEIKPENINAAQETAPYISIAACDLIKETKLSAEPAPDPSD 694  
 QY 703 YSEMAKVEOPVPHSELVDESSPDSEPDVLPSPDSIPDVPOKQDETVMVLESLETETPE 762  
 DB 695 YSEMAKVEOPVPHSELVDESSPDSEPDVLPSPDSIPDVPOKQDETVMVLESLETETPE 753  
 QY 763 SMIEYENKEKLSALPPGPGPYLESFKLSLNTKDTLLPDRVSTLSKKEKIPLOWEELST 822  
 DB 754 TVAQHK-EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPLTITKKEKISLQWEEFNT 811  
 QY 823 AVYNDLDFISKEAQIRRETETTFSSPIIIDEPTTILISSKTSDFSKLAREYTDLEVSHK 882  
 DB 812 AVYNDLDFISKEAQIRRETETTFSSPIIIDEPTTILISSKTSDFSKLAREYTDLEVSHK 870  
 QY 883 SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISPSDDSKNGSATSCKVLLPPDVSA 942  
 DB 871 SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISPSDDSKNGSATSCKVLLPPDVSA 928  
 QY 943 LGHTQABIESIVKPKVLEKAEKELPSDEKEDSPSAIFSGADLGKTSVVDLLYWRDIKK 1002  
 DB 929 L-EPQTEMGSIKSKSLTKEAEKLPSTDEKEDSLSAVLSAELSKTSVVDLLYWRDIKK 987  
 QY 1003 TGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKVIQAIQKSDGHPFRAY 1062  
 DB 988 TGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKVIQAIQKSDGHPFRAY 1047  
 QY 1063 LESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMVFTVYGALFN 1122  
 DB 1048 LESEVAISELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMVFTVYGALFN 1107  
 QY 1123 GLTLLIALLSLFSPVPIYERHQAIQIDHYLGANKNVKDMAKIQAQIPGLKRAE 1178  
 DB 1108 GLTLLIALLSLFSPVPIYERHQAIQIDHYLGANKNVKDMAKIQAQIPGLKRAE 1163

RESULT 4  
 Q8BGM9 PRELIMINARY; PRT; 1162 AA.  
 AC Q8BGM9  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RTN4.  
 GN Name=Rtn4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
 RA Oertle T., Huber C., van der Putten H., Schwab M.B.;  
 RT "Genomic structure and functional characterisation of the promoters of  
 human and mouse nogo/rtn4";  
 RL J. Mol. Biol. 325:299-323(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RX Van der Putten H.;  
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SVCJ7;  
 RX Van der Putten H., Mir A.;  
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AY102284; AAM73506.1; -.

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DR EMBL; AY102286; AAM73511.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR001388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1162 AA; 126612 MW; 855697FBEE11781F CRC64;

Query Match 72.4%; Score 4289; DB 2; Length 1162;
Best Local Similarity 73.9%; Pred. No. 2.6e-148;
Matches 883; Conservative 109; Mismatches 153; Indels 50; Gaps 18;

QY 1 MEDDQSLVSSS-DSPRRQPAPKQYQVREPEDEDEDEDEDEDEDEDEDEDEDELEVLKRP 59
DB 1 MEDIDQSLVSSSADSPRRQPAPKQYQVTEPEDEDEDEDEDEDEDEDEDEDELEVLKRP 60
QY 60 AAGLSAAPVPTAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQPSWDPSVSTVPA 119
DB 61 AAGLSAAPVP--PAA-APLLDFSSDVPPAPRGPLPAAPPTAPERQPSWERSPAAS--A 114
QY 120 PSLSAASVPSKLPDEDEPPARPPPPASVSPQAEVPMTPPAPAPAAPSTPAAPKR 179
DB 115 PSLPAPAAVLPKLPDEDEPPAR--PPAPAGASPLAE-----PAAPSTPAAPKR 163
QY 180 GSSG-----AVVXXXKIMDLKEQPGNTISAGQEDFPFVSLLETAASKPSLS 225
DB 164 GSGVDETLFPALPAASEPVISSAEKIMDLKEQPGNTVSSQGEDFPFVLFETAASLP 223
QY 226 PLSAASPKHEHYLGNLSTVLPTEGTLQENVSASKEVSEKAKTLIIDRLDTFSELEYSE 285
DB 224 PLSTVSKHEHYLGNLSTVASTEGTITLNEASRELPERATNPFVNRSAEFSVLEYSE 283
QY 286 MGSSFSVSKAEGAVIANPREIIIVKNKDEEKLVSNNLHKQQLPTALTCLKVKEDV 345
DB 284 MGSSFNKSGKESAMLVETKKEVIVRSKDKEP-LVCSAALHNQPSPATLTKVKEDGV 342
QY 346 VSEKAKDSFNEKRVAVEAPMBREYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLS 404
DB 343 MSPEKTMDFINEMKMSVWAPREYADFKPFQAEWVKDTYEGSRDVLAA----RANMES 398
QY 405 KVDKCFADSLQTNHEKDESSNDTSPSPTEGIDKRSYAYITCAPNPAATESIATN 464
DB 399 KVDKCFEDSLEQGHGKDESRNENASPPRTPELVKDGSRAYITCDSPS-SATESAAN 457
QY 465 IFFLLDPTSENKTDSEKKEKKAQIVTEKNTSTKSNPFFVAAQDSEYVTTDNLTKV 524
DB 458 IFFVLDEHSENKTDSEKKEKKAQIITEK-TSPKTSNPFVLAHDSADYVTTDNLTKV 516
QY 525 TEVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCP 584
DB 517 TEAVATMPEGLTPDLVQACESELNEATGKIAYETKVDLVQTSIAIQESIVPTAQLCP 576
QY 585 SPEESATSPVLPDVMAPLNSAVPSAGASVQPSSSPLAE-SSVNTYESIKHEPNPP 643
DB 577 SPEEATSPVLPDVMAPLNSLPPSTGASVAQPSAPLEVPSVSDGGLKEPNPP 636
QY 644 PYEAMSVSLKVSIGIKKEIKEPENINAALQETAPYISACDLIKETKLSAEPAPDFS 703
DB 637 PYEAMSVALKTSDSKEIKEPESFNAAQAEAPYISACDLIKETKLSSTEPSFSNY 696
QY 704 SEMAKVEQVPHSELVSDSPSEVDLFSDDSIIPVQKQDETVMVKESLTETSPFS 763
DB 697 SEIAKPEKSVPHCELVDSSPESEVDLFSDDSIPEVPTQEEAVMLKESLTVS-ET 755
QY 764 MIEYENKEKLSALPPGGKPYLESFKLSLDNTKOTLLPDEVSTLSKEKIPLOMEELSTA 823
DB 756 VTQHKHKEKLSAQSGVKPYLESFQPNLHITKDA--ASNEIPTLTCKETISLOMEEFNTA 814
QY 824 VYSNDLFLSKAQIRETETFSOSSPIEIIIDFPPTLISKTDSPSKLAEREYTDLEVSHKS 883
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Db 492 SVAQPSASPLEVPSVSYDGKIKLEPENPPPYEAMSVALKTSKKEIKPEPSFNAQAQ 551  
 QY 675 TRAPYSIACDLIKETKLSAEPADPSDYSEMAKVEQVPVDPHSELVEDSPSEPVDLFS 734  
 Db 552 AEAPYSIACDLIKETKLSPEPSPSYSEIAKFEKSPVDPHCELVDSPSEPVDLFS 611  
 QY 735 DSIIPVQKQDETVMVKESLTETSFESMIEYENKEKLSALPPEGKBYLSEFKLSLON 794  
 Db 612 DSIPEVPQTQBEAVMLMKESLTVS-ETVQHKHKEKLSAQFQVGPYLSFQNLHI 670  
 QY 795 TKDTLLPDSVSTLSKKEKIPLOMEELSTAVYNDLDFISKEAQIRETETFSFSSPIEID 854  
 Db 671 TKDA-ASNEIPLTKETLSLQMEENTAIYNDLDSKEDKMESETFSSSPIEID 729  
 QY 855 EPTLISSTKDSFKSLAREYTDLEVSHKSEIANAPDAGSLPCTELPHDLSLKNIQPKYE 914  
 Db 730 EPTFTVSAKDDSS---PKEYTDLVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE 785  
 QY 915 EKISFDDSKSGSATSKVLLLPDYSALGHTQAEISIVKPKLEKAEKLPSTDEKE 974  
 Db 786 AHV--SDFSKRSRSVKVPLLPNVSAL-ESQIEMGNIVKPKVLTKEAEKLPSTDEKE 842  
 QY 975 DRSPSAIFSADLCKTSWDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALL 1034  
 Db 843 DRSLTAVLSRELKNTSVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALL 902  
 QY 1035 SVTISPRIYKGVIAQIOKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITKELRR 1094  
 Db 903 SVTISPRIYKGVIAQIOKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITKELRR 962  
 QY 1095 LFLVDDLVSLSKFAVLMVFTYVYVGLFNGLTLLILALISLFSVPVIYERHQIDHYLGL 1154  
 Db 963 LFLVDDLVSLSKFAVLMVFTYVYVGLFNGLTLLILALISLFSVPVIYERHQIDHYLGL 1022  
 QY 1155 ANKNVADAMAKIOAKIPGLKRAE 1178  
 Db 1023 ANKNVADAMAKIOAKIPGLKRAE 1046  
 RESULT 7  
 Q7TNB7 PRELIMINARY; PRT; 720 AA.  
 AC Q7TNB7  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.P., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 KW EMBL; BC056373; AAH56373.1; -.  
 DR Hypothetical protein.  
 SQ SEQUENCE 720 AA; 77435 MW; 80AB78728F16EAB2 CRC64;  
 Query Match 43.6%; Score 2580.5; DB 2; Length 720;  
 Best Local Similarity 70.8%; Pred. No. 2.4e-86;  
 Matches 527; Conservative 69; Mismatches 107; Indels 41; Gaps 13;  
 QY 1 MEDLQDSPLVSSS-DSPRPQPAFKYQFVREPEDEDEDEDEDEDEDEDELEVLKRP 59  
 Db 1 MEDIQDSILVSSADSPPRPAPFKYQFVTEPEDEDEDEDEDEDEDELEVLKRP 60  
 QY 60 AAGLSAAPVPTAPAGAPLMDFGNDVPPAPRGPLPAPAPPVAPERQPSWDPSFVSTVPA 119  
 Db 61 AAGLSAAPVP--PAA-APLLDFSDSVPPAPRGPLPAPAPPVAPERQPSWERSPAAS--A 114  
 QY 120 RPSLSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTTPAPAPAPAPPTPAAPKPR 179  
 Db 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAPAPTTPAPKPR 163  
 QY 180 GSGSG-----AVVXXXKIMDLKBPQNTISAGQEDFPFVLLETAASXPSLS 225  
 Db 164 GSGSVDETLFALPAASEPVPISSAEKIMDLKBPQNTVSSGQEDFPFVLLETAASXPSLS 223  
 QY 226 PLASAASFHEHYGLNLSVLPTEGTLQENVSASKEVSEKAKTLILDRDLTFSESELYSE 285  
 Db 224 PLSTVSFKHGHLGNLSAVASTEGTIEETLNASRELPERATNPFVNRESAEFSVLEYSE 283  
 QY 286 MGSSFSVSPKABSAVIVPREEIIIVKNKDEKLVSNNILHXQQLPTALTKLVKEDSV 345  
 Db 284 MGSSFNKPGKESAMLVENTKEEVIIVRSKDED-IVCSAALNHPQESPATLTKLVKEDGV 342  
 QY 346 VSSEKAKDSFNKRVAVAPMREYADFKPFERVWEVSKDESDS-DMLAAGGKIESNLDS 404  
 Db 343 MSPKMTMDIFENMKSVVAVPREEYADFKPFQAEVVKDTYEGSRDLVLA---RANMDS 398  
 QY 405 KVDKCFADSLBOTNHEKDSSESSNDTSPSTPTEGIKORSGAYITCAPNPAATESIATN 464  
 Db 399 KYDKKCFEDSLQKGGHGDSESRNENASFPPTPELVKDGSRAYITCDSFS-SATESTAN 457  
 QY 465 IFPLLEDPTSENKTDKKEIEKKAQIVTEKNTSTKTSNPPFFVAAQDSEDDYVTTNLTKV 524  
 Db 458 IFPVLEDHTSENKTDKKEIEKKAQIVTEK-TSPKTSNPPFLVAIHDSEADYVTTNLSKV 516  
 QY 525 TEEVVANMPEGLTPDLVQACESELSNVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCP 584  
 Db 517 TEAVVATMPEGLTPDLVQACESELSNVTGTKIAYETKMDLVQTSSEIYPTAQLCP 576  
 QY 585 SFESEATPSVLPDIMEAPLNSAVPSGASVIOFSSSPLAE-SSVNYVESIKHBPENDP 643  
 Db 577 SFESEATPSVLPDIMEAPLNSLTPSGASVIOFSSSPLAE-SSVNYVESIKHBPENPP 636  
 QY 644 PYEEAMSVSLKVGSKIKEEIKPENINAAQLETPYIETACDLIKETKLSAEPAPDFSDY 703  
 Db 637 PYEEAMSVSLKVGSKIKEEIKPENINAAQLETPYIETACDLIKETKLSAEPAPDFSDY 696  
 QY 704 SEMAKVEQVPDPHSELVEDSSPDS 727  
 Db 697 SEIAKFEKSPVDPHCELVDSSPES 720  
 RESULT 8  
 Q8K290 PRELIMINARY; PRT; 639 AA.  
 AC Q8K290;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)



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DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
GN Rtn4 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032192; AAH32192.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 42.7%; Score 2527; DB 2; Length 639;
Best Local Similarity 79.5%; Pred. No. 1.8e-84;
Matches 515; Conservative 57; Mismatches 66; Indels 10; Gaps 6;

QY 532 MPEGLTPDLVQACSELNEVTGTXIAYETKMDLVQTSSEVQESLYPAAQLCPSPPESEA 591
DB 1 MPEGLTPDLVQACSELNEATGTXIAYETKVDLVQTSSEATQESLYPTAQLCPSPPESEA 60
QY 592 TPSPVLPDIMEAPLNSAVPSAGASVIOQSSSPLA-SVVNYESIKHEPENPPPYEAMS 650
DB 61 TPSPVLPDIMEAPLNSLPTSGASVQASPLEVPSVSDGKLEPENPPPYEAMS 120
QY 651 VSLKVGKKEETKEPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVE 710
DB 121 VALKTSDAKEEIKEPESFNAAQEAEPYISACDLIKETKLSAEPESFNYSIAKFE 180
QY 711 QVPDPHSELVEDSPDSEPVDFSDSIQVPOKQDETVMVKESLTSTSPESMEYENK 770
DB 181 KSPDPHCELVDDSSPESEPVDFSDSIQVPOQTEAEAVLMKESLTVS-ETVTOHKKH 239
QY 771 EKLSALPPEGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVYNSDDL 830
DB 240 ERLSASPQEVGPKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDLL 298
QY 831 FLSKAQIRETFTFSDSPPIEIIIDFPPTLISKKTDSFKSLAREYTDLEVSHKSEIANAPD 890
DB 299 LSSKEDKMKESFTFSDSPPIEIIIDFPPTFVSAKDDSDS----PREYTDLEVSNKSEIANVQS 354

Query Match 37.7%; Score 2233; DB 2; Length 578;
Best Local Similarity 78.4%; Pred. No. 8.3e-74;
Matches 460; Conservative 52; Mismatches 65; Indels 10; Gaps 6;

QY 593 PSPVLPDIMEAPLNSAVPSAGASVIOQSSSPLA-SVVNYESIKHEPENPPPYEAMSV 651
DB 1 PSPVLPDIMEAPLNSLPTSGASVQASPLEVPSVSDGKLEPENPPPYEAMSV 60
QY 652 SLKVGKKEETKEPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQ 711
DB 61 ALKTSDAKEEIKEPESFNAAQEAEPYISACDLIKETKLSAEPSPGFSNYSEIAKFEK 120
QY 712 PVPDHPSELVEDSPDSEPVDFSDSIQVPOKQDETVMVKESLTSTSPESMEYENK 771
DB 121 SVDPHCELVDDSSPESEPVDFSDSIQVPOQTEAEAVLMKESLTVS-ETVTOHKKH 179
QY 772 KLSALPPEGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVYNSDDL 831
DB 180 RLSASPQEVGPKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDLL 238
QY 832 ISKAQIRETFTFSDSPPIEIIIDFPPTLISKKTDSFKSLAREYTDLEVSHKSEIANAPD 891
DB 239 SSKEDKMKESFTFSDSPPIEIIIDFPPTFVSAKDDSDS----PREYTDLEVSNKSEIANVQS 294
QY 892 AGSLPCTELPHDLKLNQPKVBEKISFSDDFSKNGSATSKVLLPDPVVSALGHTQABIE 951
DB 295 ANSLPCTELPHDLKLNQPKVBEKISFSDDFSKNGSATSKVLLPDPVVSAL-ESQIEMG 351

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QY 952 SIVKPKVLKEAEKKLPSTDEKEDRSPSAIFSAADLGTISVOLLWYRDIKKTKGVVFGASL 1011
Db 352 NIVKPKVLKEAEKKLPSTDEKEDRSLSAVLSAELNKTISVOLLWYRDIKKTKGVVFGASL 411
QY 1012 FULLISITVSIVSVTAYIALALLSVTISPRIYKGVIOAQKSDGHPFRAYLESEVAISE 1071
Db 412 FULLISITVSIVSVTAYIALALLSVTISPRIYKGVIOAQKSDGHPFRAYLESEVAISE 471
QY 1072 ELVQKYSNLSALGHVNTICKELRRLFLVDDLDVSLKFAVLMWVFTYVYGALFNGLTLLILAL 1131
Db 472 ELVQKYSNLSALGHVNTICKELRRLFLVDDLDVSLKFAVLMWVFTYVYGALFNGLTLLILAL 531
QY 1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQKIPGLKRKAE 1178
Db 532 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQKIPGLKRKAE 578

RESULT 10
Q6RSS8 PRELIMINARY; PRT; 658 AA.
AC Q6RSS8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Neutrite outgrowth inhibitor NOGO-A (Fragment).
GN Names=NOGO;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON TER
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;

Query Match 29.3%; Score 1735; DB 2; Length 658;
Best Local Similarity 58.0%; Pred. No. 1.3e-55;
Matches 388; Conservative 83; Mismatches 164; Indels 34; Gaps 15;

QY 533 PEGLTDLVQVACESELNEVTGKIAYETMDLVQTSVWQESLYPAAQLCFSESEAT 592
Db 1 PEGLTDLVQVACESEMHDACTKLAYETKIDLVQTSVQVETLKPVTQLCFSESEAA 60
QY 593 PSPVLPIVWEAPLNSAVPSAGASVLPQSSPLE--ASSVNYESIKHEPENPPPYEAMS 650
Db 61 PSPVLPIVWEAPLSSGTAGAEASTVQLETSQGTFTVTAENVKAEKPLVQEAVN 120
QY 651 VSL-KVSGIKEET--KEPENINAAQTEAPYISIACDLIKETKLSAEPA-PDFSDYSE 705
Db 121 MPLTQAEAKEELTLKKADESTSPEDLETPIYISIACDLIKETKVSGESASPLTDYST 180
QY 706 MAKVE---QVPDHSLELVDSPPDSEPVLPFSDDSIPDPVQKQDETVMVLKESLTETSE 762
Db 181 TPITEHLSQDVSEHKEAEKLSQFGKCDLFSRQVMPDFPGKESEDQTLI---LNGKSVE 237
QY 763 SMIEYENKEKLSALPPEGKPKYLESPKSLDNTK-DTLLPDE--VSTLKKKELPLQWEE 819
Db 238 NIETDEQERLVDSLAATGKPYLESQDELDSKIVTQPSPTPAKIAKAEKIPLOWEE 297
QY 820 LSTAVYNSDDLFTSKAEQIRETETFSDDSPPIETIDFPPTLISKTDTSFKLAREYTDLEV 879
Db 298 LNALAYST-DVSVAMEPKPGDSKGLSPSPSVSVEDDFVMLVDPKTG--TEFVAEVTDTRET 354
QY 880 SHKSE---TAN-APDGAGSLPCTELPHDLSLKNIQKVEKISFSDDFSKNGSATSK--- 932

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Db 355 VHKNESKDISNBIRDEKESQAPLTELPCDLSVRNVKTEDD---AHALKSKSQADREVP 411
QY 933 ---VLLLPDPSALGHQTAETESIVKPKVLEKAEKKLPSTDEKEDRSPSAIFSAADLGT 989
Db 412 EVSMVSLPATGTSPTSSTEKEIVSVCKPEAFKEAERGAASAKEKE--KPTAVFSKLVNS 469
QY 990 SVVDLLYWRDIKKTGVWFGASLFLLLSLTFSIVSVTAYIALALLSVTISPRIYKGVIOA 1049
Db 470 SVVDLLYWRDIKKTGVWFGASLFLLLSLTFSIVSVTAYIALALLSVTISPRIYKGVIOA 529
QY 1050 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTICKELRRLFLVDDLDVSLKFAV 1109
Db 530 IQKSDGHPFRAYLESDVAVSEELIQKYSVVVLGHNGTGVKELRRLFLVDDLDVSLKFAV 589
QY 1110 LMWVFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQK 1169
Db 590 LMWVFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQK 649
QY 1170 IPGLKRKAE 1178
Db 650 IPGLKRKTE 658

RESULT 11
Q6JRV1 PRELIMINARY; PRT; 1055 AA.
AC Q6JRV1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RTN4.1-A2.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Wholemount embryos;
RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis."
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AY316196; BAQ82645.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1055 AA; 115426 MW; F583A19F9BA51EDF CRC64;

Query Match 25.9%; Score 1534.5; DB 2; Length 1055;
Best Local Similarity 36.9%; Pred. No. 4.7e-48;
Matches 463; Conservative 157; Mismatches 353; Indels 281; Gaps 49;

QY 5 DOSPLVSSSDS-----PPRP-----OPAFKYQVVRPEDEE 35
Db 3 EUSPDISSSHSGDERREPAQGERKXPWDDLDDVLDTGGAGQFSQFSGSHPARDIEEE 62
QY 36 EEEEEEEDEDELEVLKPAAGLSAAPV-PTAPAGAPLMDFGNDFFVPPAPRGL 94
Db 63 EDEEEERGAKWDSLEPSPV-EPEPGSIDISVSPSHSPA-----V 101
QY 95 PAAPVAPERQSWDPSPSVSVTPAPSLSAAVSPSKLPEDDEPPARPPPPASVSQ 154
Db 102 PSAPMEEPERP-----APCTAPSGSVATFLARLPLEED----- 136
QY 155 AEPVMTVPAPAPAPPPSTPAAPKPRGSGCAVXXKKKIMDLKQEPGNTISAGQEDPFSVL 214
Db 137 -ENLFTLPA-----ASAHLMHASADKIM---EPYSTVSTQGEERFASVL 175

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Qy 215 LETAASPSLSPLSAASPKHEHYLGNLSTVLPTGCTLQENVSEASKEVSEKAKTLLIDRD 274
D 176 LOSTASLSLSLSTDSKHAETVAFTGLAATEALQEPD----- 217
Qy 275 LTFESELEYSMGSGSFVSVPKASGAVIVANPREIIVKNKDEEEKLVNNILHXQBLPT 334
D 218 ---NMYSVSRITSHLPLSDNLKAL-DQVKEEVIFSEK-----YVVDHPT 260
Qy 335 ALTKLVKEDV-VSEKAKOSFNEKRVAVEAPMEE-----YADKPF-----E 377
D 261 SQQETISEEHAKLYSQAKEMFSGMLQSV-APPHEEFTDIKEVDYVPYDFKPFMSKSGD 319
Qy 378 RVMEVKDSKSDMLAAGGKLESNKVDKCKCPADSLQTNHKKDSESSNDTSPFPSTP 437
D 320 VGYEVDVAEKFOVDV-GRLL-NLESVKHE-----EKSEWEIDSLSDDIS-PLTP 368
Qy 438 EGIKDRGAYITCAPNPAATESIATNI-PLPESDPTSENKTDKKEEKAQIVTKNT 496
D 369 ELLPDST-----DYDMFAT--VEQNIPTFGGHRVAGNKTDEKKTIDIEAQ-----KT 414
Qy 497 S-----TKTSNPF-VAADSETDYVTDNLTKVTEEVANMPEGLTPDLVOACSESEL 549
D 415 SVGGLKATVNPFPNESAQSE--YVTHVATHVSTK-----PEGTPDILVQAYSEA 467
Qy 550 NEVTGKIAYETKMDLVQT-SEVMQESLYPAAQLCPSESEATPSPVLPIVMEAPLNS 608
D 468 YDTGIPKQKYESNDLVQTAANSQVEKVSPTAQAPARLEETDSVSSPVLPIVMEAPLAS 527
Qy 609 AVPSGASVIOPPSSPLEAS-SVNYESIKHEPNPPYEEAMSVLSKVGSIKEIKPEN 667
D 528 ALETV---ALKPDISPVGKIPARVEKTKABPEKPPSYEEAVT-----EVLQND 574
Qy 668 INAAL-----QTEAPYISTACDLIKETKLSAEPADPDSYSEMAKVEQP--VPDH 716
D 575 LAAALGSKGAVVEETPTPYISACDLIKGTESVA-----SGTFBSKLKQNEFSQF 628
Qy 717 SELVEDSPSEPVDLFSDDSDIPVQKQDVTMLVKESLT---ETSFSMIEYENKEK 772
D 629 MEPSDESPPSE-----CSEPSYKQWDSVVQ--KEAFSIKTESVNAQSIIPEQKV 679
Qy 773 LSALPPRG--GKPYLESFKLSLONTKDT--LLPDEVSTLSKKEKIPLOMELSTAVYSND 828
D 680 FDQKSESSPSKSYLDSFQPEICVSKATSDFAKGLATLLQEK--PLQMBELDRGL-SLE 736
Qy 829 DLFISKAAQIRETTFSDSPILIEDFPTLISKTDSPSK--LAREYTDLEVSHKSEI 885
D 737 KIPCTKYSPVSE-----SPEPRSPVPEDLSKLGDIOKEVLIQAKQEDKQVKNRSNL 789
Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISPSDDFSKNGSATSQVLLLPDVSALGH 945
D 790 DFPVENTEFTPAVQKPDGSG-----KAVSDTFGLDITTKGSAVHEV----- 832
Qy 946 TQABIESIVRPKVLKAE-KKLPDSTEKEDRSPSAIFSADLGTSTVVDLLYWRDIKKTG 1004
D 833 -----KVDRPKPPSKEDDGSKLP---KKESKASTVSSSDP-MNSVVDLIYWRDIKRS 881
Qy 1005 VVFGASIFLLLSLTVFVSIVSTAVIALALISVTISFRIYKGVQIAQKSDSEGHFPFRAYLE 1064
D 882 VVFGASIFLLLSLTVFVSIVSTAVIALALISVTISFRIYKGVQIAQKSDSEGHFPFRILE 941
Qy 1065 SEVAISELVOKYNSALGHVNCITKELRLRFLVDLVDLSLKPAVLMMVFTYVGCALFNGL 1124
D 942 SNLAVPEDLVOKYCNVALNHVNCITKELRHLFLVEDLVDSLKFVLMVMVFTYIGALFNGL 1001
Qy 1125 TLLIALISLFSVPVYERHOAQIDHYGLGNKVNKDAMAKIQKIPGLKRKAE 1178
D 1002 TLLIALISLFSIPVYERHQTQVDHYLALVNKLKSTSDILSKVPLKRAE 1055
PRT; 392 AA.
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RESULT 12  
Q96B16  
ID Q96B16

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AC Q96B16;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Reticulon 4, isoform D (RTN4 isoform B2).
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay D.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalley D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rt4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016165; AAH16165.1; -
DR EMBL; AY102278; AAM64247.1; -
DR EMBL; AY102285; AAM64242.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 25.8%; Score 1531; DB 2; Length 392;
Best Local Similarity 32.4%; Pred. No. 1.9e-48;
Matches 382; Conservative 7; Mismatches 3; Indels 786; Gaps 4;

Qy 1 MEDLDQSPLVSSSDSPRPQPAFKYQVREPEDEEEDEDEDEDELEVLERKPA 60
D 1 MEDLDQSPLVSSSDSPRPQPAFKYQVREPEDEEEDEDEDEDELEVLERKPA 60
Qy 61 AGLSAAFPVPTAPAAAGAPLMDFGNDVFPAPRGPLPAPPAAPPVAPRQPSWDSVSSSTVPAP 120
D 61 AGLSAAFPVPTAPAAAGAPLMDFGNDVFPAPRGPLPAPPAAPPVAPRQPSWDSVSSSTVPAP 120
Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSQAEVPTTPPAPAPAAPSTPAAPKRRG 180
D 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSQAEVPTTPPAPAPAAPSTPAAPKRRG 180
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Db 121 SFLSAAAAPSFKLPEDDEPPARPPPPPPASVSQAEVWTPPAPAPAAPSTPAAPKRRG 180  
Qy 181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPVSVLLTAASXPSLSPLSAASPKHEYLGN 240  
||:|  
Db 181 SSGSV----- 185  
Qy 241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRLDTEFSELEYSEMGSSFSVSPAESAV 300  
Db 186----- 185  
Qy 301 IVANPREEEIIVKNDBEEKLVSNILHXQQLPTALTCLVKEDEVVSSEKAKDSFNKRV 360  
Db 186----- 185  
Qy 361 AVEAPMREYADFKPFRVMEVKDSKEDSDMLAAGKIBSNLESKVDKCFADSLQTNH 420  
Db 186----- 185  
Qy 421 EKDSSESSNDTSPSTPEGIKORSAGYITCAPNPAPATESIATNIFPPLLEDPTSENXTDE 480  
||:|  
Db 186----- 190  
Qy 481 KKIEEKKAOIVTEKNTSTKTSNPFVAAQDSEYVTTDNLTKVTEVVANMPGEGITPDL 540  
Db 191----- 190  
Qy 541 VOEACESELNEVTGKIAVETKMDLVQTSSEVMQESLYPAAQLCPSESEATPSPVLPDI 600  
Db 191----- 190  
Qy 601 VMEAPLNSAVPAGASVIOQSSPLEASSVNYESIKHEPENPPPYEAMSVSLKVGIKE 660  
||:|  
Db 191----- 195  
Qy 661 EIKEPENINAALQETAPVISIACDLIKETKLSABAPDFSDYSEMAKVEQVPDHSILV 720  
Db 196----- 195  
Qy 721 EDSSPDSEPDVLFSDDSIPDVQKQDETVMVKESLTETSFESMIEYENKEKLSALPPEG 780  
|||  
Db 196----- 199  
Qy 781 GRPYLESFKLSLNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVYNSDDLFISKEAQIRE 840  
Db 200----- 199  
Qy 841 TETFSDSPIEIIDEPFTLISSTKDSFKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900  
Db 200----- 199  
Qy 901 PHDLSKNTQPKVEEKISFSDFSKNGSATSXVLLPPDVSALGHTQABIESIVKPKVLE 960  
Db 200----- 199  
Qy 961 KEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVF 1020  
||:|  
Db 200----- 234  
Qy 1021 SIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNS 1080  
|||  
Db 235 SIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNS 294  
Qy 1081 ALGHVNCTIKELRRFLVDDLVDSLKFAVLMMVFTYVVGALFNGLLTLLILALISLSPVPI 1140  
Db 295 ALGHVNCTIKELRRFLVDDLVDSLKFAVLMMVFTYVVGALFNGLLTLLILALISLSPVPI 354  
Qy 1141 YERHOAQIDHYLGANKNVKDAWKIQAIPGLKRAE 1178  
Db 355 YERHOAQIDHYLGANKNVKDAWKIQAIPGLKRAE 392

RESULT 13  
Q6JRV8

ID Q6JRV8 PRELIMINARY; PRT; 1044 AA.  
AC Q6JRV8;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE RTN4.2-A2;  
GN Name=RTN4;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Wholemount embryos;  
RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;  
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,  
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;  
RT Identification of two NOGO/RTN4 genes and analysis of Nogo-A  
RT expression in Xenopus laevis";  
RL Mol. Cell. Neurosci. 25:205-216(2004).  
DR EMBL; AY316189; AAQ82638.1;  
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1044 AA; 115088 MW; 34PB48351A6C9888 CRC64;  
Query Match 25.6%; Score 1518.5; DB 2; Length 1044;  
Best Local Similarity 37.3%; Pred No. 1.8e-47;  
Matches 459; Conservative 165; Mismatches 346; Indels 261; Gaps 52;  
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Db 21 EDLDD-VLDLTGGAGQSPFPVSYPARHMEKEEENEDEEEDSKNKSLEASPVLE- 77  
Qy 58 KPAAGLSAAPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPEROPSPVSTV 117  
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Db 78 DFGSTGSSSTPHSP-----PEPSAPTEEPERP-----ATC 109  
Qy 118 PAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPK 177  
||:|  
Db 110 TAPSSSLAYTLAQRLKED-----NLFLPAA----- 138  
Qy 178 RRGSGAVVXXXXKIMDLKEQPGNTISAGQEDFPVSVLLTAASXPSLSPLSAASPKHEY 237  
||:|  
Db 139 ---SAHMLHLSADKIM---EPSSTVSTGQEDFASVLLQSTASLSLPSLSS---KEHVQ 188  
Qy 238 LGNLSVLPTEGTLQE---NVSEASKEVSEKAKTLLIDRLDTEFSELEYSEMGSSFSVSP 294  
||:|  
Db 189 TVAFSTGLAANEALQEPDNTYSASRSLLDTLETKALD---QF----- 228  
Qy 295 KAESAVIVANPREEEIIVKNDBEEKLVSNILHXQQLPTALTCLVKEDEV-VSSEKAKD 353  
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Qy 354 SFNEKRVAVEAPMRE-----EYADFKPF-----ERVVEVKDSKEDSDMLAAGKI 398  
||:|  
Db 266 MFGSMQLQVAPPHEEFTDIKEVDVQYVDFKPFIFSSNSRDIGYEVKDAEKLHV-----GRL 321  
Qy 399 ESNLESKVDKCFADSLQTNHEKDSSESSNDTSPSTPEGIKORSAGYITCAPNPAP 456  
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||:|  
Db 371 -----FSLGSRVAGNKTDEKKIEDFAQ-----KTSVGFLKVATVNFYDESAQ 416  
Qy 510 DSETDYVTTDNLTKVTEEVANMPGEGITPDLVQEAACESELNEVTGKIAVETKMDLVQTS 569  
||:|  
Db 417 ESE--YVTTG---ATRVQVSTKABGPTPDIVQEAYESAYDTGIGSKLNYEPNIDLVTQA 470  
Qy 570 EV-MQESLYPAAQLCPSESEATPSPVLPDVI VMEAPLNSAVPAGASVIOQSSPLEAS 628

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Db 471 ATSMQKVSPTAQVPALLES--VSSPVLVDVMEAPLASTIL-CLETWALKPDISPVRTE 527
Qy 629 -SVNYESIHEPENPPPEEAMSVSLKVS--IKEEIKPENINAAOETE--PYIS 681
Db 528 PPARDEKTAEPKPEPSYSEAEVTEVLQDGPAAADLGDQKQ-GAVVKEAEAPYISPYIS 586
Qy 682 IACDLIKETKLSAEPAPDSYSEMAKVRQVPDHS--ELVDSQSPDSEPVDFSDDSIP 739
Db 587 IACDLIKGTQSA--SDTFESKFKQHEFDQFMEPSDESSEPDSE-----LS 631
Qy 740 DVPQKQDETVMVLKESLT-----ETSFESMIETENKESALPPEG--GKPYLESFKLSLD 793
Db 632 EPSYQWDSVVYKETFITIKTESAMAQSFVPEQKPGIDQKSESSPKPYLASQPEIY 691
Qy 794 NTKDT-LLPDEVST-LSKKEKIPLOMEELSTAVYNSDDLFISKEAQIRETETFSOSSPIE 851
Db 692 VSKATDLFAKGLDTEISIPQERHLMEEFDEGLYS--KLPGSKYSPVSESPEFRLS---- 746
Qy 852 IIDEPTLTISSKTSF-SKLAREYTDLEVSHKSEIANAPDAGAGSLPCTELPHDLSLKNIQ 910
Db 747 -----PEELTSKHEBIOTHIAGHPEDKQKNDKLDLPE-----NIE 784
Qy 911 --PKVEKISFSDSKNGSATSQVLLPPDVVSALGHTQAEITESIVKPKLEKAE--KX 967
Db 785 FTPIVQK---ADDFEKAASATHGV---DTTAKGASEVHEEKVTKPEPPSKDEVSXL 836
Qy 968 PSDTEKEDRSAPSAISADLGKTSVVDLLYWRDIIKTVGVGASLFLILSLTVFSIVSTA 1027
Db 837 P--KESKAPSTVPSSDFRNSVVDLIYWRDIKRSVGVGASLFLILSLTVFSIVSLA 893
Qy 1028 YIALALLSVTISFRIYKGVIOAIQKSDGHPHPRAYLESEVALSEBELVOKYSNLSALGHVNC 1087
Db 894 YIALALLSVTISFRIYKGVIOAIQKSEGHPRFRIESENALPVEDVQKHCTVALNQNR 953
Qy 1088 TIKELRRLFLVDLVDLSKFAVLMVFTYVGVLFNGLTLLILALISLFSVPVYERHOAQ 1147
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Qy 1148 IDHYGLANKVNDKAMAKIOKIPGLKBAE 1178
Db 1014 VDHYLALINKNLKNTSDILAKVPLGRKSE 1044

RESULT 14
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AC Q6JRV0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
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Name=RTN4;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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RP SEQUENCE FROM N.A.
RC TISSUE=Wholemount embryos;
RX PubMed=15019938; DOI=10.1016/j.j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RL Mol. Cell. Neurosci. 25:205-216 (2004).
DR EMBL; AY316197; AAQ82646.1;
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1043 AA; 113994 MW; 6AF170C14DD2CB1A CRC64;

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Query Match 25.6%; Score 1517.5; DB 2; Length 1043;
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Qy 5 DQSPVSSSDS-----PPRP-----QPAFKYQVFRPEDEE 35
Db 3 EQSPDISSSHSGDERREPAQGERKPPWDDLDVLDLTGGAGQFSQPFSGSHPARDEEE 62
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Db 63 EDEEERGAWKDLSRSPV-EPEPGSIDSI SPVSPHSPA-----VPSAPM--- 106
Qy 95 PAAPVAPERQSPWDPSPVSTVPAPSPLSAAAVSPKLPEDEDEPPAPPPPPASVSQ 154
Db 107 -----EPEPPAPCTAPSGSV 123
Qy 155 ABPVMTPAPAPAPPPPTAAPAKRGSGAVVXXXXKIMDKQPGNTISAGQEPFVS 214
Db 124 DENLFTLPA-----ASAHLMHASADKIM---EPVSTVSTQGEFASVL 163
Qy 215 LETASXPSLSPLSNAASPKHEHYLGNLSTVLPTEGLQENVSEASEKAKTLLIRD 274
Db 164 LQSTASLSLSPLSLTSDSSKHAETVAFPTGLAATEALQEPD----- 205
Qy 275 LTFSELBYSBMGSSFSVSPKASAVIVANPREBIIKVKODEEKLVSNNILHXQOELPT 334
Db 206 ----NWYSVSRITSHLPUSDNLESKAL--DQVKEVIFSEK-----YVDHPT 248
Qy 335 ALTKLVKDEEV-VSEKAKDSFNKRVAVEAPMREE-----YADFKP-----E 377
Db 249 SQQETISEEHAKLYSQSAKEMFSGMLQSV-APPHSEFTDIKEVYDVPYDFKPFMSKSGD 307
Qy 378 RVWEKDSKESDMLAAGKLESNLSKVKCPADSLBQTNHEKXSSNDTDFPSTP 437
Db 308 VGYEVDVAERFQVDV--GRL--NLESAVRHE-----EKSEMEIDSISDIS-PLTP 356
Qy 438 EGIDORSICAYITCAPFNPAAATESATNI-FPLEDPTSENXTDEKIKKEKKAQIVTEKT 496
Db 357 ELLPDST-----DYDMFAT--VEQNI PFSGGHVAGNKTDEKIIDIEAQ-----KT 402
Qy 497 S-----TKTSNPPF-VAAQDSETDYVTTDNLTKVTEEVVANMPGLTDLVQEA 549
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Qy 550 NEVTGKTIAETKMDLVOT-SEVMQESLYPAQALCPSESESEATSPVLPDIVMEAPLNS 608
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Qy 668 INAAL-----QTEAPYISACDLIKETKLSAEPAPDSYSEMAKVEQP--VPDH 716
Db 563 LAAALGSGKQGA VVEETETPYISACDLIKGTESVA-----SGTFESKLQNEFESQF 616
Qy 717 SELVEDSPDSEPVDFSDDSIPDPVQKQDETVMVLKESLT-----ETSFESMIETENK 772
Db 617 MEPSDESSEPDSE-----CSEPSYKQWDSVVQ--KEAFSIKTESVNAQSIIPQEQV 667
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QY 1005 VVFGASLFLLLSLTVFSIVSVYAYIALALLSVTISFRIYKGVTOATQKSDGEGHPPRAYLE 1064
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QY 1125 TLLILALISLFSVPVYIERHQAIQIDHYGLANKNVKDMAKIQAQKIPGLKRAE 1178
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DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Wholemount embryos;
RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AV316195; AAQ82644.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
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Db 61 EEEDEEEEE-----RGAW----- 72
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Db 73 -----KSLFSPVEE-----EPGSDISIP-----VSPHSAPVS 103
QY 161 PPAPAPAAPSTPAAPKRRGSGAVVXXXKIMDLKEQGNITISAGQEDFPVSLLETAAS 220
Db 104 APMEEPERPAPCTAP-----SGSV-----DKIM-----EPYSTVSTQEEFPASVLLQSTAS 150
QY 221 XPSLPLSAAASFKEHYLGNLSVTLPTGTLQENVSEASKEVSEKATLLIDRLTFSE 280
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Search completed: June 16, 2005, 13:17:42  
Job time : 167.813 secs

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QY 384 DSKEDSDMLAAGKTESNLESKVKKCADSLSEQNHEKDSSESDNDTSPSTPEGIKOR 443
Db 295 DVAEKFOVDV--GRL--NLESVAKHE-----EKSSEMEIDSIDDSI-PLTPELLPDS 343
QY 444 SGAYITCAPFNPAAETSIATNI-FPLEDPTSENKTDEKKIEEKAQIVTEKNTS----- 497
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QY 498 -TKTSNPF--VAAQDSEDTYVTTNLTNLTKVTEEVANMPPEGLTDLVQEAECESLNEVTG 555
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Db 604 SSPDSE-----CSEPSYKQWDSVWQ--KEAFSIKTESVNAQSIIPQEQVDFQKSE 654
QY 779 EG--CKPYLESFKLSLMDTKDT--LLPDEVSTLSKKEKIPLQWEELSTAVYNDLDFISK 834
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Db 917 EDLVQKYNALNHVNTIKELRRLFLVDLVDLSLKFPAVLMMVFTYVGFALFNGLTLILA 976
QY 1131 LISLSFSPVYIERHQAIQIDHYGLANKNVKDMAKIQAQKIPGLKRAE 1178
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ORIGIN
Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 1628 AGCCTATTCTGCTGCTTTTCATTGACAGTATTACAGCATTTGTGAGCGTAAACAGCTTACATT 1687

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 1688 GCCTTGCCCTGCTCTCTGACCATCAGCTTTAGATATACAGGCTGTGATCCAGCT 1747

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 1748 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATA 1807

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 1808 TCTGAGGAGTTGGTTGAGAGTACAGATAATCTGCTCTTGGTCAATGGAAGTCAAGTAA 1867

QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 1868 AAGGAATCAGGCGCTCTCTTAGTTAGTATGATTGATTGATTTCTCTGAAGTTGAGTG 1927

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 1928 TTGATGTTGGTATTTACCTATGTTGGTGGCTTGTAAATGCTTGACACTACTGATTTTG 1987

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 1988 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTATGACGGCATCAGGCACAGATAGAT 2047

QY 161 HisTyrLeuGlyLeuAlaLeuLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 2048 CATTATCTAGGACTTGCNAATAGATGTTAAGATGCTATGCTAAATCCAGCAGAAA 2107

QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 2108 ATCCCTGGATTGAAGCGCAAGCTGAA 2134

RESULT 2
AF320999 2883 bp mRNA linear PRI 18-DEC-2000
LOCUS Homo sapiens Nogo-A protein short form mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF320999
VERSION AF320999.1 GI:11878277
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polyA\_signal  
ORIGIN

Pred. No.:	9,11e-87	Length:	3491
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-830-972-29 COPY 990 1178 (1-189) x AF3333336 (1-3491)

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Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 2630 AGCCTATTCCCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATT 2689

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 2690 GCCTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 2749

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

D<sub>b</sub> 2750 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATACTCGGAATCTGAAGTTGCTATA 2809

81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Qy

DB 2810 TCTGAGGAGTTGGTTCAGAAAGTACAGTAAATCTGCTCTTGGTCAATGACACGATA 2869

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DD 2870 ATAGGACACAGGCGCCCTCTCTTAGTTCATGATGATTCCTGAGATTCGAGTGTGCAGTG 2929

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AX766050	AX766050	3576 bp	DNA	Linear	P&T 25-JUN-2003
LOCUS					

DEFINITION	Sequence 5 from Patent WO03002602.
ACCESSION	AY766050

VERSION AX766050.1 GI:32260129  
KEYWORDS

SOURCE	HOMO SAPIENS (human)
ORGANISM	Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCES**  
**AUTHORS**  
Eisenbach-Schwartz, M. and Hauben, E.

# neuroprotection



## YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL)

FEATURES  
source  
Location/Qualifiers  
1..3576  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
exon  
1..3576  
ORIGIN

Alignment Scores:  
Pred. No.: 9,38e-87 Length: 3576  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AX766050 (1-3576)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysGlyThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTCTGACCATCAGTAAAGAGACTGGAGTGGTGGTGGCC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrile 40  
Db 3070 AGCCTATTCTGCTGCTTCAATGACAGTATTCAGCATTTGAGCTAAGCTACAGCTACAT 3129  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db 3130 GCCTGGCCCTGCTCTGTGACCATCAGTAAAGAGACTGGAGTGGTGGTGGCC 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATCAAGGCCACCCATTCAGGCATATCTGCAATCTCAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrile 100  
Db 3250 TCTGAGGAGTGGTTCAGAGTACAGTAAATCTGCTTGGTCAATGAGTCAAGCTACAGATA 3309  
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAATCAGGCGCTCTCTGACCATCAGTAAAGAGACTGGAGTGGTGGTGGCC 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3370 TTGATGCGGTATTTACCTATGTTGGTGGCTTGTAAAGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3430 GCTCTCAATTTCACTCTTCAGTGTCTCTGTTATTTATGACGGCATCAGCGCAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
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RESULT 5  
LOCUS BD249446  
DEFINITION Protein similar to neuroendocrine-specific protein, and encoding  
cDNA.  
BD249446 3579 bp DNA linear PAT 17-JUL-2003

ACCESSION BD249446  
VERSION BD249446.1 GI:33059216  
KEYWORDS JP 2002522016-A/1.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3579)  
AUTHORS Michalovich, D. and Prinjha, R. K.

TITLE  
JOURNAL

## COMMENT

Protein similar to neuroendocrine-specific protein, and encoding  
Patent: JP 2002522016-A 1 23-JUL-2002;  
SMITHKLINE BEECHAM PLC  
OS Homo sapiens (human)  
PN JP 2002522016-A/1  
PD 23-JUL-2002  
PF 21-JUL-1999 JP 2000561310  
PR 22-JUL-1998 GB 9816024.5, 19-JUL-1999 GB 9916898.1 PI  
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA  
PC

C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC  
G01N33/566//  
PC C12P21/08, C12N15/00, C12N5/00  
CC Protein similar to neuroendocrine-specific protein, and CC  
encoding cDNA

PH Key Location/Qualifiers  
FT source 1..3579 /organism="Homo sapiens (human)".

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Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD249446 (1-3579)

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QY 181 IleProGlyLeuIysArgLysAlaGlu 189  
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DEFINITION Homo sapiens mRNA for Nogo-A protein (Nogo gene).  
ACCESSION AJ251383  
VERSION AJ251383.1 GI:9408095  
KEYWORDS Nogo gene; Nogo-A protein.  
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ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R.,  
Christie, G., Michalovich, D., Simmons, D.L. and Walsh, F.S.  
TITLE Inhibitor of neurite outgrowth in humans  
JOURNAL Nature 403 (6768), 383-384 (2000)  
MEDLINE 20129242  
PUBMED 10667780

REFERENCE 2 (bases 1 to 3579)  
AUTHORS Michalovich, D.  
TITLE Direct Submission  
JOURNAL Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline  
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND  
HERZEGOVINA

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ALIGNMENT Scores:  
Pred. No.: 9,39e-87 Length: 3579  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0

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DEFINITION Sequence 4 from Patent WO2004052932.  
ACCESSION CQ829486  
VERSION CQ829486.1 GI:49732808  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Barske, C., Mir, A.K., Oertle, T., Schnell, L., Schwab, M.E.,  
Vitaliti, A. and Zurini, M.  
TITLE Nogo a binding molecules and pharmaceutical use thereof  
JOURNAL Patent: WO 2004052932-A 4 24-JUN-2004;  
Novartis AG (CH)

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 DB: 6 Gaps: 0

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 VERSION AX195249.1 GI:15385809  
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 ORGANISM Homo sapiens  
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 Strittmatter, S. M.  
 Nogo receptor-mediated blockade of axonal growth  
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 YALE UNIVERSITY (US)  
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LOCUS
DEFINITION Homo sapiens RTN4 isoform G (RTN4) mRNA, complete cds;
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ACCESSION AY123250
VERSION AY123250.1 GI:26800589
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4060)
Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
JOURNAL
MEDLINE
PUBMED 22376540
12488097
REFERENCE
2 (bases 1 to 4060)
Van der Putten, H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
3 (bases 1 to 4060)
Oertle, T. and Schwab, M.E.
Direct Submission
Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
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Pred. No.:
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Best Local Similarity: 100.00% Mismatches: 0
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LOCUS Homo sapiens RTN4 isoform F (RTN4) mRNA, complete cds;
DEFINITION alternatively spliced.
ACCESSION AY123249
VERSION AY123249.1 GI:26800586
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4070)
Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
JOURNAL
MEDLINE
PUBMED 22376540
12488097
REFERENCE
2 (bases 1 to 4070)
Van der Putten, H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
3 (bases 1 to 4070)
REFERENCE
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD270070 (1-4093)

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Db 3220 AGCCTATTCTGCTGCTTTCAATGACAGTATTGAGCATTTGAGCGTAACAGCCTACATT 3279  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
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QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3400 TCTGAGGAGTTGCTTCTGAGAGTACAGTAATCTGCTCTTGGTCACTGGAACGCAGATA 3459  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3460 AAGAACTCAGGCGCCTCTCTTAGTTGATGATTTTAGTTGATTTCTGAAAGTTGCGAGT 3519  
QY 121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
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QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
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QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3640 CATTATCTAGGACTTCCAATAGAATGTTAAAGATGCTATGGCTAAATTCACAGCAAAA 3699  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3700 ATCCCTGGATTGAGCGCAAGCTGAA 3726

RESULT 13  
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ACCESSION AY123245  
VERSION AY123245.1 GI:26800574  
KEYWORDS  
SOURCE Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.  
Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4  
J. Mol. Biol. 325 (2), 299-323 (2003)  
MEDLINE 22376540  
PUBMED 12488097  
REFERENCE  
2 (bases 1 to 4102)  
AUTHORS Van der Putten,H.  
TITLE Direct Submission  
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland  
3 (bases 1 to 4102)  
AUTHORS Oertle,T. and Schwab,M.E.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland

FEATURES  
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3'UTR

ORIGIN

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Db 2627 AGCCTATTCTGCTGCTTTCAATGACAGTATTGAGCATTTGAGCGTAACAGCCTACATT 2686  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 2687 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCT 2746  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 2747 ATCCAGAAATCAGATGAGCGCCACCCATTCAGGGCATATCTGGAATCTGAGTTGCTATA 2806  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 2807 TCTGAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCACTGTAACGCACGATA 2866  
QY 101 LysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

Db 2867 AAGGAACCTCAGCGCCTCTTCTAGTTCATGATTTAGTTCCTGAAGTTGCAGTG 2926  
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 ACCESSION  
 VERSION AY123248  
 KEYWORDS  
 SOURCE AY123248.1 GI:26800583

ORGANISM Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.  
 TITLE Genomic structure and functional characterisation of the promoters  
 of human and mouse nogo/rtn4  
 J. Mol. Biol. 325 (2), 299-323 (2003)  
 JOURNAL  
 MEDLINE 22376540  
 PUBMED 12488097  
 REFERENCE  
 AUTHORS Van der Putten,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma  
 Inc., Basel, Switzerland  
 3 (bases 1 to 4109)  
 REFERENCE  
 AUTHORS Oertle,T. and Schwab,M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of  
 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,  
 Switzerland

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gene

5' UTR

CDS

3' UTR

ORIGIN

Alignment Scores:  
 Pred. No.: 1,11e-86 Length: 4109  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x AY123248 (1-4109)

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 Db 2634 AGCCTATTCTCCGCTGCTTTCAATGACAGTATTCAGCATTTGGAGGTAAACAGCCTACAT 2693  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
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 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 2814 TCTCAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTCATGTGAACATGACAGATA 2873  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
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 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
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 alternatively spliced.  
 PRI 23-SEP-2003







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Percent Similarity:	1	4160	EYVAMPGLPDLVQACSESENEVTGKTIAYETKMDLVQTSVMQESLSLPAQLCP	
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			endoplasmic reticulum and reduces their anti-apoptotic activity	
Qy	1	4160	JOURNAL Oncogene 19 (50), 5736-5746 (2000)	
			MEDLINE 21010696	
Db	1	4160	PUBMED 11126360	
			REFERENCE 2 (bases 1 to 4166)	
Qy	1	4160	Eguchi Y., Tagami S. and Tsujimoto Y.	
			Direct Submission	
Db	1	4160	TITLE Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate	
			School of Medicine, Biomedical Research Center, Department of	
Qy	1	4160	Medical Genetics, Yamadaoka 2-2, Suita, Osaka 565-0871, Japan	
			(E-mail: eguchi@gene.med.osaka-u.ac.jp, Tel: +81-6-6879-3363,	
Db	1	4160	Fax: +81-6-6879-3369)	
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Db	1	4160	VWEVKDSKSDMLAAGKIESENLESKVDLQSDLSLEQTHHEKDSSESDNDTSPST	
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Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3691 ATCCCTGGATTGAAGCGCAAGCTGAA 3717

RESULT 19
CQ874017 Q0874017 4789 bp DNA linear PAT 27-SEP-2004
LOCUS Sequence 436 from Patent WO2004076622.
ACCESSION Q0874017
VERSION Q0874017.1 GI:52747609
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Taira, K. and Kawasaki, H.
TITLE Regulation of mammalian cells
JOURNAL Patent: WO 2004076622-A 436 10-SEP-2004;
National Institute of Advanced Industrial Science and Technology
(JP)
FEATURES
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Location/Qualifiers
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Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-830-972-29_COPY_990_1178 (1-189) x Q0874017 (1-4789)

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Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3314 AGCCTATTCTCTGCTTCTTACATGATTTACAGATTGTGAGCGTAACAGCCTACATT 3373
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Db 3494 TCTGAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTAAGTGCACGATA 3553
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3554 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3613
Qy 121 LeuMetTropValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 3614 TTGATGTGGGTATTTACCTATCTTGGTGGCTTTGTTAATGGTCTGACACTACTGATTTTG 3673
Qy 141 AlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
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Qy 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
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DEFINITION alternatively spliced.
ACCESSION AY102279
VERSION AY102279.1 GI:26800572
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4789)
AUTHORS Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.
TITLE Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 4789)
AUTHORS Oertle, T. and Schwab, M.E.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
REFERENCE 3 (bases 1 to 4789)
AUTHORS Van der Putten, H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
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ORIGIN
Alignment Scores:
Pred. No.: 1.34e-86 Length: 4789
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AY102279 (1-4789)
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DB 3254 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGC 3313
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3314 AGCCTATTCTCTGCTGCTTTCATTGACAGTATTGACAGTATTGAGCGCTAACAGCCTACATT 3373
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlySerGlyValIleGlnAla 60
DB 3374 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGGTGTGATCCAAAGCT 3433
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3434 ATCCAGAAATCAGATGAGGCCACCCATTACAGGCATATCTCGAATCTGAAGTTGCTATA 3493
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 3494 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTTGGTTCATGCACTGCACGATA 3553
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB 3554 AAGAACTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTAGTTGATTTAGTTGATTTG 3613
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 3674 GCTCTCATTTTCACTCTTCAGTGTTCCTGTTATTATTATGAAGCGCATCAGGCACAGATAGAT 3733
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Db      3805 ATCCCTGGATTGAGCGCAAGCTGAA 3831
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RESULT 22
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DEFINITION Homo sapiens reticulon 4, transcript variant 4, mRNA (cDNA clone IMAGE:3505850), complete cds.
ACCESSION BC016165
VERSION   BC016165.1 GI:16740575
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buotow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzyzinski, M.I., Skalek, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
TITLE    Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED  12477932
2 (bases 1 to 1784)
AUTHORS  Strausberg, R.
DIRECT SUBMISSION
TITLE    Submitted (29-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT  Contact: MGC help desk
        Email: cgapbs-remail.nih.gov
        Tissue Procurement: DCTD/DRP
        cDNA Library Preparation: Rubin Laboratory
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
        DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
        info@bcgsc.bc.ca
        Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Anura Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smalish, Jeff Stott, Miranda Teai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 23 Row: d Column: 19
This clone has the following problem: The cds is short compared to the longest cds in the locus.
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Query Match: 99.68% Indels: 0
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Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 977 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAAAGCT 1036
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Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 1097 TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTCTCATGTGAACTGCACGATA 1156
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
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Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 1277 GCTCTCTTTCACCTCTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 1336
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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ORIGIN
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 9 Gaps: 0

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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 94 CTATTCTCTGCTCTTTCATTGACAGTATTCACAGTATTCAGCATTTGAGCGTAAACGCTACATTGCC 153
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 154 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATATACAGGGTGTGATCCAGCTATC 213
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Db 274 GAGGAGTTGGTTCAGAGTACAGTAAATCTGCTCTTGGTCATGTGAACTGCACGATAAG 333
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Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
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DEFINITION Sequence 2 from patent US 5858708.
ACCESSION AR028522
VERSION AR028522.1 GI:5940495
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KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 799)
AUTHORS Bandman,O., Au-Young,J., Goli,S.K. and Hillman,J.L.
TITLE Polynucleotides encoding two novel human neuroendocrine-specific
proteins
JOURNAL Patent: US 5858708-A 2 12-JAN-1999;
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Query Match: 99.57% Indels: 0
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US-09-830-972-29_COPY_990_1178 (1-189) x AR028522 (1-799)
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Db 588 TATCTAGGACTTGCAGAAATGCTTAAAGATGCTATGGCTTAAATCCAGCAAAATC 647
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Db 648 CTGGATTGAAGCGCAAGCTGAA 671

RESULT 26
BC007109
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DEFINITION Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone
IMAGE:429112?), complete cds.
ACCESSION BC007109
VERSION BC007109.1 GI:13937989
KEYWORDS
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ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
1 (bases 1 to 1079)  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zerbach B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raja S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Schermer A., Schein J.E., Jones S.J. and Marra M.A.

TITLE  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932

REFERENCE  
2 (bases 1 to 1079)  
Strausberg R.

TITLE  
Direct Submission

JOURNAL  
Submitted (30-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT  
NIH-MGC project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
Tissue Procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 21 Row: h Column: 12  
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein  
This clone has the following problem: The cds is short compared to the longest cds in the locus.  
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ORIGIN  
Alignment Scores:  
Pred. No.: 5,628-87 Length: 1079  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: Gaps: 0

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Db 145 GTTGTGACCTCCTGCTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCCAGC 204  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
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Db 385 GAGGAGTTGGTTTTCAGAGTACAGTAACTCTGCTCTTGGTCACTGAACTGCAGATAAG 444  
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LOCUS  
DEFINITION  
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BD249448  
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KEYWORDS  
JP 2002522016-A/3.  
Homo sapiens (human)  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



REFERENCE 1 (bases 1 to 1122)  
AUTHORS Michalovich, D. and Prinjha, R.K.  
TITLE Protein similar to neuroendocrine-specific protein, and encoding  
JOURNAL Patent: JP 2002522016-A 3 23-JUL-2002;  
SMITHKLINE BEECHAM PLC  
COMMENT OS Homo sapiens (human)  
PN JP 2002522016-A/3  
PD 23-JUL-2002  
PF 21-JUL-1999 JP 2000561310  
PR 22-JUL-1998 GB 9816024.5 19-JUL-1999 GB 9916898.1 PI  
PC DAVID MICHALOVICH, RABINDER KUMAR PRINJHA  
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
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G01N33/566//  
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encoding cDNA  
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Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
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DB 556 GTTGTGACCTCCTCTACTGGAGACATTAAGAAGCTGGAGTGGTGTGGTCCAGC 615  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 616 CTATTCTGCTGCTTTCATTGACATATTGACATTTGAGCTGTGAGCTAACGCCTACATTGCC 675  
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DB 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
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HSA251384  
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DEFINITION Homo sapiens mRNA for Nogo-B protein (Nogo gene).  
ACCESSION AJ251384  
VERSION AJ251384.1 GI:9408097  
KEYWORDS Nogo gene; Nogo-B protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R.,  
Christie, G., Michalovich, D., Simmons, D.L. and Walsh, F.S.  
TITLE Inhibitor of neurite outgrowth in humans  
JOURNAL Nature 403 (6768), 383-384 (2000)  
MEDLINE 20129242  
PUBMED 10667780  
REFERENCE 2 (bases 1 to 1122)  
AUTHORS Michalovich, D.  
TITLE Direct Submission  
JOURNAL Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline  
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND  
HERZEGOVINA  
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ORIGIN  
Alignment Scores:  
Pred. No.: 5.89e-87 Length: 1122  
Score: 927.00 Matches: 188  
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QY 2 ValValAspLeuLeuTyrTrrArgAspIleValSerThrGlyValValPheGlyAlaSer 21  
DB 556 GTTGTGACCTCCTCTACTGGAGACATTAAGAAGCTGGAGTGGTGTGGTCCAGC 615  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
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Db	736	CAGAAATCAGATGAGGACCCATTCAGGCATATCTGGATCTGAAGTTGCTATATCT	795
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
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Qy	102	GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
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Db	1036	TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC	1095
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RESULT	29		
LOCUS	BC001035		
DEFINITION	Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone IMAGE:3139770), complete cds.		
ACCESSION	BC001035		
VERSION	BC001035.2	GI:33875905	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1151)		
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krywinski,M.I., Skalska,U., Smailus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1151)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	On Aug 19, 2003 this sequence version replaced gi:12654418. Contact: MGC help desk Email: cgapbs@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov Akter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,J., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,P.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: c Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5902015 This clone has the following problem: The cds is short compared to the longest cds in the locus. FEATURES Location/Qualifiers 1..1151 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3139770" /tissue_type="placenta, choriocarcinoma" /clone_lib="NIH MGC_21" /lab_host="DH10B-R" /note="Vector: pOTB7" 1..1151 /gene="RTN4" /note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X" /db_xref="LocusID:57142" /db_xref="MIM:604475" 186..785 /gene="RTN4" /codon_start=1 /product="reticulon 4, isoform C" /protein_id="AAH01035.1" /db_xref="GI:12654419" /db_xref="LocusID:57142" /db_xref="MIM:604475" /translation="MDGQKNWKKVLDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYTAYIALALSVTISFRIYKGIQAIQKSDGHPFRAYLSEVAISELVQKYSNALSCHVNTIKELRLRFLVDLVDLSKFAVLMVFTYVGVLFNGLLILALISLFSVPV IYERHQAIDHVLGLANKNVKDMAKIQAKIPLKRAE" ORIGIN Alignment Scores: Pred. No.: 6.08e-87 Length: 1151 Score: 927.00 Matches: 188 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 99.57% Indels: 0 DB: 9 Gaps: 0 US-09-830-972-29_COPY_990_1178 (1-189) x BC001035 (1-1151) Qy 2 ValValAspLeuLeuTyrTyrPheArgAspIleLysThrGlyValValPheGlyAlaSer 21 Db 219 GTTGTGACCTCTCTGCTGAGAGACATTAAGACATGAGTGTGTGGTGGCAGC 278 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41		

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## RESULT 30

BD194907 1213 bp DNA linear PAT 17-JUL-2003  
LOCUS 86 human secreted proteins.  
DEFINITION BD194907  
ACCESSION BD194907.1 GI:33004658  
VERSION JP 2002514090-A/78.  
KEYWORDS unidentifed  
SOURCE unidentifed  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1213)  
AUTHORS Moore,P.A., Shi,Y., Rosen,C.A., Ruben,S.M., Lafleur,D.W.,  
Olsen,H.S., Ebner,R., Brewer,L.A., Young,P., Greene,J.M.,  
Ferre,A.M., Yu,G.L., Ni,J. and Feng,P.  
TITLE 86 human secreted proteins  
JOURNAL Patent: JP 2002514090-A 78 14-MAY-2002;  
HUMAN GENOME SCIENCES INC  
COMMENT OS Unidentifed  
PN JP 2002514090-A/78  
PD 14-MAY-2002  
PR 11-JUN-1998 JP 1999503203  
PR 13-JUN-1997 US 60/049547,13-JUN-1997 US 60/049548 PR  
13-JUN-1997 US 60/049549,13-JUN-1997 US 60/049550 PR  
13-JUN-1997 US 60/050566,13-JUN-1997 US 60/049606 PR  
13-JUN-1997 US 60/049607,13-JUN-1997 US 60/049608 PR  
13-JUN-1997 US 60/049609,13-JUN-1997 US 60/049610 PR  
13-JUN-1997 US 60/049611,13-JUN-1997 US 60/050901 PR  
13-JUN-1997 US 60/052989,08-JUL-1997 US 60/051919 PR  
18-AUG-1997 US 60/055984,12-SEP-1997 US 60/058665 PR  
12-SEP-1997 US 60/058668,12-SEP-1997 US 60/058669 PR  
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12-SEP-1997 US 60/058972,12-SEP-1997 US 60/058975 PR  
02-OCT-1997 US 60/060834,02-OCT-1997 US 60/060841 PR  
02-OCT-1997 US 60/060844,02-OCT-1997 US 60/060865 PR  
02-OCT-1997 US 60/061059,02-OCT-1997 US 60/061060 PI PAUL A  
MOORE,YANGU SHI,CRAIG A ROSEN,STEVEN M RUBEN,DAVID W PI  
LAFLEUR,  
PI HENRIK S OLSEN,REINHARD EBNER,LAURIE A BREWER,PAUL YOUNG,JOHN  
PI M GREENE,

PI ANN M FERRIE,GUO LIANG YU,JIAN NI,PING FENG  
PC C07H21/02,C07H21/04,C12N5/00,C12N5/04,C12N5/06,C12N5/10 PC  
C12N5/16 C12N15/00  
PC C12N15/09,C12N15/10,C12N15/11,C12N15/12,C12P21/04,C12P21/06 CC  
CC Strandedness: Double;  
CC Topology: Linear;  
CC 86 human secreted proteins  
FH Key Location/Qualifiers  
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Pred. No.: 6.48e-87 Length: 1213  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 6 Gaps: 0  
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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 308 CTATTCCTGCTGCTTTCTATTGACAGATTTGACGATTTGAGCGTAACAGCCTACATTGCC 367  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAAGCTATC 427  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 428 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGGAAGTTGCTATATCT 487  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 488 GAGAGTTGGTTTTCAGAACTACAGTAATCTGCTCTTGGTCACTGGAAGTGCAGTAAG 547  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 548 GAATCAGCGGCTCTCTTCTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTG 607  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 608 ATGTGGGTATTACCTATGTTGGTGGCTTGTATTAATGCTCTGACACTACTGATTTGGCT 667  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 668 CTCATTTTCACTCTTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 727  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 728 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAATC 787  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 788 CTGGATTGAAGCGCAAGCTGAA 811  
RESULT 31  
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DEFINITION Sequence 79 from Patent EP1439189.  
ACCESSION CQ855235  
VERSION CQ855235.1 GI:51510663





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## CDS

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens cDNA FLJ27302 fis, clone TMS04776.

AK130812

AK130812.1 GI:34527696

oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

1 Suzuki, O., Sasaki, N., Matsuda, S., Shoji, T., Ichihara, T.,  
Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,  
Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H.,  
Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E.,  
Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,  
Terashima, Y., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K.,  
Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R.,  
Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B.,  
Nagai, K., Isogai, T. and Sugano, S.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 1525)

Sugano, S. and Suzuki, Y.

Direct Submission

Submitted (31-JUL-2003)

Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure, Human Genome  
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: fclhna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,  
Fax: 81-3-5449-5416)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction and 5'-end one pass sequencing: Institute of Medical  
Science, University of Tokyo, Laboratory of Genome Structure, Human  
Genome Center; 3'-end one pass sequencing: RAB; clone selection for  
full insert sequencing: RAB and Helix Research Institute.

FEATURES

Location/Qualifiers

1..1525

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="TMS04776"

/tissue\_type="thymus"

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## ORIGIN

Alignment Scores:

Pred. No.: 8,31e-87 Length: 1485

Score: 927.00 Matches: 188

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.57% Indels: 0

DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BC010737 (1-1485)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

DB 561 GTTGTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGAGACTGGAGTGGTGTGGTGGCCAG 620

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41

DB 621 CTAATCTGCTGCTTTCATTCAGAGTATTCAGATTTGTGAGCGTAAACAGCTCATATGTC 680

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

DB 681 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGAGTGGTGTGGTGGCCAGTATC 740

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

DB 741 CAGAAATCAGATGAGGCCACCATTCAGGGCATATCTGGAATCTGGAATGCTATATCT 800

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

DB 801 GAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTTGGTCACTGCACTGCAAGTAAAG 860

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

DB 861 GAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTAGTTGATTTAGTTGATTTG 920

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

DB 921 ATGTGGGTATTTACCTATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 980

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

DB 981 CTATTTTCACTTTCAGTGTCTCTGTTATTTATGACGGCATCAGGCACAGATAGATCAT 1040

QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 1041 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGCTTAAATCAAGCAAAATC 1100

QY 182 ProGlyLeuLysArgLysAlaGlu 189

DB 1101 CCTGGATTGAAGCGCAAGCTGAA 1124

RESULT 34

AK130812

LOCUS

AK130812 1525 bp mRNA linear PRI 10-SEP-2003

Alignment Scores:

Pred. No.: 8,59e-87 Length: 1525

Score: 927.00 Matches: 188

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.57% Indels: 0

DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AK130812 (1-1525)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

DB 615 GTTGTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGAGACTGGAGTGGTGTGGTGGCCAGC 674

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41

DB 675 CTAATCTGCTGCTTTCATTCAGAGTATTCAGATTTGTGAGCGTAAACAGCTCATATGTC 734

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

DB 735 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGAGTGGTGTGGTGGCCAGTATC 794

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

DB 795 CAGAAATCAGATGAGGCCACCATTCAGGGCATATCTGGAATCTGGAATGCTATATCT 854

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

Db 855 GAGGAGTTGGTTTCAGAACTACAGTAATTCCTGCTCTTGGTTCATGTGAACCTGCACGATAAAG 914  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 975 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGCACACTACTGATTTGGCT 1034  
 Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 1035 CTCATTCTCACTCTTCAGTCTCTCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 1094  
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 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 1155 CTGTGATTGAAGCGCAAGCTGAA 1178

## RESULT 35

CQ769577  
 LOCUS CQ769577 1599 bp DNA linear PAT 04-MAR-2004  
 DEFINITION Sequence 303 from Patent WO2003058021.  
 ACCESSION CQ769577  
 VERSION CQ769577.1 GI:45113880  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Koenig-Hoffman, K., Kazinski, M., Schaefer, R. and Kesper, B.  
 Novel apoptosis-inducing dna sequences  
 Patent: WO 2003058021-A 303 17-JUL-2003;  
 Xantos Biomedicine AG (DE)

## FEATURES

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## ORIGIN

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 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 6 Gaps: 0

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 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 731 CTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCTACATTGCC 790  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 791 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 850  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 851 CAGAAATCAGATGAAGGGCCACCCATTTCAGGCGCATATCTGGAATCTGGAATGTGCTATATCT 910  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

Db 911 GAGGAGTTGGTTTCAGAACTACAGTAATTCCTGCTCTTGGTTCATGTGAACCTGCACGATAAAG 970  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 1031 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGCACACTACTGATTTGGCT 1090  
 Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
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 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 1211 CTGTGATTGAAGCGCAAGCTGAA 1234

## RESULT 36

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 DEFINITION Bone marrow secreted proteins and polynucleotides.  
 ACCESSION BD231889  
 VERSION BD231889.1 GI:33041659  
 KEYWORDS JP 2002511231-A/3.  
 SOURCE Homo sapiens (human)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1610)  
 Lin, H. and Cao, L.  
 Bone marrow secreted proteins and polynucleotides  
 Patent: JP 2002511231-A 3 16-APR-2002;  
 CHIRON CORP

OS Homo sapiens (human)  
 PN JP 2002511231-A/3  
 PD 16-APR-2002  
 PF 18-DEC-1998 JP 2000526635  
 PR 30-DEC-1997 US 60/068958,24-SEP-1998 US 60/101603 PR  
 30-SEP-1998 US 60/102540  
 PI HAISHAN LIN, LI CAO  
 PC C12N15/09,A61K38/00,A61P43/00,C07K14/47,C07K16/18,C12N5/10, PC  
 C12Q1/68,  
 PC C12N15/00,A61K37/02,C12N5/00  
 CC Bone marrow secreted proteins and polynucleotides PH Key  
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 Location/Qualifiers  
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 DB: 6 Gaps: 0

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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaYrIleAla 41  
Db 747 CTATTCTCTGCTCTTTCAATTGACAGTATTTCAGCATTTGAGCGTAAACAGCTTACATGGC 806  
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Db 807 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGTGATCCAAGCTATC 866  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
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RESULT 37  
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ACCESSION AF087901.1 GI:10039642  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1617)  
AUTHORS Yang, J., Yu, L., Bi, A. D. and Zhao, S. Y.  
TITLE Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14-->2p13 by radiation hybrid mapping  
JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)  
MEDLINE 20237542  
PubMed 10773680  
REFERENCE 2 (bases 1 to 1617)  
AUTHORS Yang, J., Yu, L., Dai, F. Y., Cui, W. C., Zheng, L. H. and Zhao, S. Y.  
TITLE Direct Submission  
JOURNAL Submitted (27-AUG-1998) Lab of Human Gene Research, Institute of Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433, P.R.China

FEATURES  
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IYERHQAGIDHYGLANKVNDAMAKIOAKI PGLKRKAQ"  
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polya\_signal  
polya\_site  
1608  
ORIGIN  
Alignment Scores:  
Pred. No.: 9,23e-87 Length: 1617  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AF087901 (1-1617)  
QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 139 GTTGTGTGACCTCTCTGTCTGAGAGACATTAAAGAGACTGGAGTGTGTGTGGTCCAGC 198  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaYrIleAla 41  
Db 199 CTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCTTACAT 258  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 259 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGTGATCCAAGCTATC 318  
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Db 319 CAGAAATCAGATGAGCGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGATATCT 378  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 379 GAGGAGTTGGTTTCAGAGTACAGTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 438  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 439 GAACCTCAGCGGCTCTCTCTTAGTTGATGATTTAGTTGATTTCTCTCTCTCTCTCTCTCT 498  
QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
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QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
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DEFINITION AK129806  
ACCESSION AK129806  
VERSION AK129806.1 GI:34526422  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens (human)  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Suzuki, Y.,  
Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M.,  
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T.,  
Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.



**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**

NEDO human cDNA sequencing project  
 2 (bases 1 to 1619)  
 Sugano, S. and Suzuki, Y.  
 Direct Submission  
 Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,  
 University of Tokyo, Laboratory of Genome Structure, Human Genome  
 Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
 (E-mail: flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
 Fax:81-3-5449-5416)

**COMMENT**

NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction and 5'-end one pass sequencing: Institute of Medical  
 Science, University of Tokyo, Laboratory of Genome Structure, Human  
 Genome Center; 3'-end one pass sequencing: RAB; clone selection for  
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 BC012619.1 GI:15214977  
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 1 (bases 1 to 1654)  
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 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
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 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 2 (bases 1 to 1654)  
 Direct Submission  
 Strausberg, R.  
 TITLE  
 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: [amadan@systemsbiology.org](mailto:amadan@systemsbiology.org)  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
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ORIGIN
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Pred. No.: 9,49e-87 Length: 1654
Score: 927.00 Matches: 1654
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 9 Gaps: 0
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VERSION  
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REFERENCE  
1 (bases 1 to 1658)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1658)  
Straussberg, R.  
Direct Submission  
Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [angbcm.tmc.edu](mailto:angbcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H., Kowals, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 21 Row: h Column: 13  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein  
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FEATURES  
source



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 REFERENCE 1 (bases 1 to 1698)  
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Wuzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBLISHED 12477932  
 REFERENCE 2 (bases 1 to 1698)  
 AUTHORS Strausberg,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapsb-r@mail.nih.gov](mailto:cgapsb-r@mail.nih.gov)  
 Tissue Procurement: CLONTECH  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 Contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
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LOCUS AF177332 Homo sapiens clone SP1507 unknown mRNA. linear PRI 03-OCT-2000
DEFINITION AF177332
ACCESSION AF177332
VERSION AF177332.1 GI:10503960
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 1700)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
TITLE Novel human cDNA clone with function of inhibiting cancer cell
growth
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1700)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-1999) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai
200032, P.R. China
FEATURES
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Query Match: 99.57% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AF177332 (1-1700)

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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIleAla 41
Db 213 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCTACATGCC 272
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 393 GAGGAGTTGGTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACTGCACGATAAG 452
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 453 GAATCTAGGCGCTCTTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTGCTAGTTG 512
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141
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RESULT 44
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LOCUS AB040463 Homo sapiens mRNA for RTN-XS, complete cds. linear PRI 10-OCT-2001
DEFINITION AB040463
ACCESSION AB040463
VERSION AB040463.1 GI:11610576
KEYWORDS reticulon.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.
TITLE A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity
JOURNAL Oncogene 19 (50), 5736-5746 (2000)
MEDLINE 21010696
PUBMED 11126360
REFERENCE 2 (bases 1 to 1709)
AUTHORS Eguchi,Y., Tagami,S. and Tsujimoto,Y.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate
School of Medicine, Biomedical Research Center, Department of
Medical Genetics, Yamadaoka 2-2, Suita, Osaka 565-0871, Japan
(E-mail: eguchi@genome.med.osaka-u.ac.jp, Tel:+81-6-6879-3363,
Fax:+81-6-6879-3369)
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ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AB040463 (1-1709)

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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 860 CTATTCCTGCTCTCTCATGACAGATTAACAGCATTTGTCAGCGTAACAGCCTACATGGC 919  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
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QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
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RESULT 45

AY164744  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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Bos taurus  
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE  
1 (bases 1 to 1721)  
Oertle, F., Klinger, M., Stuermer, C.A. and Schwab, M.E.

TITLE A reticular rhapsody: phylogenic evolution and nomenclature of the  
RTN/Nogo gene family  
JOURNAL FASEB J. 17 (10), 1238-1247 (2003)  
PUBMED 12832288  
REFERENCE 2 (bases 1 to 1721)  
AUTHORS Oertle, F. and Schwab, M.E.  
TITLE Direct Submission  
JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department  
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,  
Zurich 8057, Switzerland  
REFERENCE 3 (bases 1 to 1721)  
AUTHORS Oertle, F. and Schwab, M.E.  
TITLE Direct Submission  
JOURNAL Submitted (27-OCT-2003) Brain Research Institute and Department  
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,  
Zurich 8057, Switzerland  
REMARK Sequence update by submitter  
COMMENT On Oct 27, 2003 this sequence version replaced gi:32331288.

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ORIGIN

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Query Match: 99.57% Indels: 0  
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Db 219 TTGTTCTGCTCTCTGCTGACAGTTCAGCATTTGAGTGTACAGGCTACATGGC 278  
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QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      1224 CTCATTTCACCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGCACAGATAGATCAT 1283
QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1284 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGCTAAATCCAGCAAAATC 1343
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RESULT 47
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DEFINITION Homo sapiens RTN4 isoform C (RTN4) mRNA, complete cds;
alternatively spliced.
ACCESSION AY102276
VERSION   AY102276.1 GI:26800564
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
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REFERENCE 1 (bases 1 to 1800)
AUTHORS   Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE     Genomic structure and functional characterisation of the promoters
          of human and mouse rtng4
JOURNAL   J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE   22376540
PUBMED   12488097
REFERENCE 2 (bases 1 to 1800)
AUTHORS   Oertle,T. and Schwab,M.E.
TITLE     Direct Submission
JOURNAL   Submitted (07-MAY-2002) Brain Research Institute, University of
          Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
          Switzerland
          3 (bases 1 to 1800)
REFERENCE Van der Putten,H.
AUTHORS   Direct Submission
TITLE     Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
          Inc., Basel, Switzerland
JOURNAL   Location/Qualifiers
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Pred. No.:      1,05e-86      Length:      1800
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Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    99.57%        Indels:      0
DB:             9            Gaps:        0

US-09-830-972-29_COPY_990_1178 (1-189) x AY102276 (1-1800)

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QY      122 MetTrrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141
Db      628 ATGTGGGTATTTACCTATGTTGGTGGCTTGTTTTAATGGTCTGACACTACTGATTTTGGCT 687
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
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QY      182 ProGlyLeuLysArgLysAlaGlu 189
Db      808 CCTGGATTGAAGCGCAAGCTGAA 831

RESULT 48
LOCUS   AB015639                      2052 bp      mRNA      linear      PRI 03-SEP-1999
DEFINITION Homo sapiens ASY mRNA, complete cds.
ACCESSION AB015639
VERSION   AB015639.1 GI:5821139
KEYWORDS  ASY.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2052)
AUTHORS   Yutsudo,M.
TITLE     Isolation of a cell death-inducing gene
JOURNAL   Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 2052)
AUTHORS   Yutsudo,M.
TITLE     Direct Submission
JOURNAL   Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of

```



Tumor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka, Suita, Osaka  
565-0871, Japan (E-mail: yuteudc@biken.osaka-u.ac.jp,  
Tel: 81-6-879-8313, Fax: 81-6-879-8315)

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    Pred. No.:      1,24e-86      Length:      2052
    Score:          927.00      Matches:      188
    Percent Similarity: 100.00%      Conservative: 0
    Best Local Similarity: 100.00%      Mismatches: 0
    Query Match:      99.57%      Indels:      0
    DB:              Gaps:      0

    US-09-830-972-29_COPY_990_1178 (1-189) x AB015639 (1-2052)

    QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
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Db      1162 CCTGGATTGAAGCGCAAAAGCTGAA 1185

RESULT 49
LOCUS      AF148538
DEFINITION Homo sapiens reticulon 4b mRNA, complete cds.
ACCESSION AF148538
VERSION    AF148538.1
KEYWORDS   GI:10039552
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 2235)
AUTHORS    Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
TITLE      Assignment of the human reticulon 4 gene (RTN4) to chromosome
           2p14--2p13 by radiation hybrid mapping
JOURNAL    Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
MEDLINE    20237542
PUBMED     10773680
REFERENCE  2 (bases 1 to 2235)
AUTHORS    Zhou,Y., Yu,L. and Zhao,S.Y.
TITLE      Direct Submission
JOURNAL    Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
           Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
           P.R.China
FEATURES   Location/Qualifiers
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            polyA_signal 2208..2213
            polyA_site    2225

    ORIGIN
    Alignment Scores:
    Pred. No.:      1,37e-86      Length:      2235
    Score:          927.00      Matches:      188
    Percent Similarity: 100.00%      Conservative: 0
    Best Local Similarity: 100.00%      Mismatches: 0
    Query Match:      99.57%      Indels:      0
    DB:              Gaps:      0

    US-09-830-972-29_COPY_990_1178 (1-189) x AF148538 (1-2235)

    QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
    Db      697 GTTGTGACCTCTCTGCTGAGACATTAAGAAGCTGGAGTGGTGTGGTCCAGC 756

    QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41
    Db      757 CTATTCTCTGCTCTCTGCTGACATGATTCAGCATTTGAGCGTAAACAGCTTACATTC 816

    QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
    Db      817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 876

    QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
    Db      877 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 936

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FEATURES	Inc., Basel, Switzerland	
	Location/Qualifiers	
source	1..2332	
	/organism="Homo sapiens"	
gene	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
5'UTR	/chromosome="2"	
	/map="2p16"	
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	/gene="RTN4"	
3'UTR	/note="synonym: NOGO"	
	1..244	
ORIGIN	/gene="RTN4"	
	/note="NOGO-B; RTN4-B1; alternatively spliced"	
FEATURES	/codon_start=1	
	/product="RTN4 isoform B1"	
source	/protein_id="AA064246.1"	
	/db_xref="GI:26800562"	
ORIGIN	/translation="MEDLDQSLVSSDSPRPQPAEKYQFVRPEDEEEEREEED	
	EDEDLEUEVLERKPAAGLSAPVETAPAGAPLMDFGNDFVPAPRGLPAAPFPAP	
FEATURES	ERQPSWDSPSVSTVPAPSPUSAAVSPKLPEDDEPPAPPPPPASVPOAEFPVIT	
	PPAPAPAPSTPAPAPKRRSGSVVVDLYWRDITKKTGVFGASFLLLSLITVSVIT	
FEATURES	SVTAYIALALLSVTISPIRYKIQVQAIQSDGHPFRAYLESEVAISELVOKYSNSA	
	LGHVNCITIKELRLFLVDLVDSLFKFAVLMMVFTVVGALFNGLTLLILALISLFSVPV	
FEATURES	IYERHQAIIDHYLGLANKNVKDMAKIQKIPGLKRAE"	
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	Score: 927.00	
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ORIGIN	Conservative: 0	
	Best Local Similarity: 100.00%	
ORIGIN	Mismatches: 0	
	Query Match: 99.57%	
ORIGIN	Indels: 0	
	DB: 9	
ORIGIN	Gaps: 0	
	US-09-830-972-29_COPY_990_1178 (1-189) x AV102277 (1-2332)	
ORIGIN	2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21	
	800 GTTGTGGACCTCTCTGAGGAGACATTAGAGAGCTGGAGTGTGTGGTCCAGC 859	
ORIGIN	22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41	
	860 CTATTCTGCTGCTCTTTCATTCAGATTTCAGATTTCAGATTTCAGATTTCAG 919	
ORIGIN	42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61	
	920 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTACCAAGCTATC 979	
ORIGIN	62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81	
	980 CAGAAATCAGATGAGGCCACCCATTACGGCATATCTGGAATCTGGAATCTGGAATCT 1039	
ORIGIN	82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101	
	1040 GAGGAGTGTGGTTTTCAGAGTACAGTAAATCTGCTCTTGGTTCATGTGAACCTGCACGATAAG 1099	
ORIGIN	102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121	
	1100 GAATCAGCGCGCTCTCTTAGTTAGTATTTAGTTAGTTAGTTAGTTAGTTAGTTAGTT 1159	
ORIGIN	122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141	
	1160 ATGTGGGTATTTACCTATGTTGGTCTGTTTATGTTGTTGTTGTTGTTGTTGTTGTT 1219	
ORIGIN	142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161	
	1220 CTCAATTCCTCTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCGCAGATGATCAT 1279	
ORIGIN	162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181	
	1280 TATCTAGGACTTGCATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1339	
ORIGIN	182 ProGlyLeuLysArgLysAlaGlu 189	
	1340 CCTGGATTGAAGCGCAAGCTGAA 1363	
ORIGIN	CQ783030	
	1694 bp DNA linear PAT 17-MAR-2004	
ORIGIN	Sequence 3170 from Patent EP1396543.	
	CQ783030	
ORIGIN	CQ783030.1	
	GI:45502969	
ORIGIN	Homo sapiens (human)	
	Homo sapiens	
ORIGIN	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
ORIGIN	Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,	
	Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and	
ORIGIN	Koga, H.	
	Primers for synthesizing full length cDNA clones and their use	
ORIGIN	Patent: EP 1396543-A 3170 10-MAR-2004;	
	Research Association for Biotechnology (JP)	
ORIGIN	Location/Qualifiers	
	1..1694	
ORIGIN	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
ORIGIN	/db_xref="taxon:9606"	
	479..1354	
ORIGIN	/note="unnamed protein product"	
	/codon_start=1	
ORIGIN	/protein_id="CAF86236.1"	
	/db_xref="GI:45502970"	
ORIGIN	/translation="MTSCRRRPDPGCRPLPPFAPERQSPWPSPVSVTPVAPSPLSAA	
	AVSPKLPEDDEPPAPPPPPASVPOAEFPVITPPAPAPSTPAPAPKRRSGSAA	
ORIGIN	VVDLLYWRDITKKTGVFGVSLFLLSLTVPESIVSVTAYIALALLSVTISPIRYKGI	
	QAIQSDGHPFRAYLESEVAISELVOKYSNSALGHVNCITIKELRLFLVDLVDSLF	
ORIGIN	KFAVLMMVFTVVGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGLANKNVKDMA	
	AKIQKIPGLKRAE"	
ORIGIN	2.55e-86	
	Length: 1694	
ORIGIN	Score: 923.00	
	Matches: 187	
ORIGIN	Percent Similarity: 99.47%	
	Conservative: 0	
ORIGIN	Best Local Similarity: 99.47%	
	Mismatches: 1	
ORIGIN	Query Match: 99.14%	
	Indels: 0	
ORIGIN	Gaps: 0	
	US-09-830-972-29_COPY_990_1178 (1-189) x CQ783030 (1-1694)	
ORIGIN	2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21	
	788 GTTGTGGACCTCTCTGAGGAGACATTAGAGAGCTGGAGTGTGTGGTCTCAGC 847	
ORIGIN	22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41	
	848 CTATTCTGCTGCTCTTTCATTCAGATTTCAGATTTCAGATTTCAGATTTCAGATTTC 907	
ORIGIN	42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61	
	908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTACCAAGCTATC 967	
ORIGIN	62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81	
	968 CAGAAATCAGATGAGGCCACCCATTACGGCATATCTGGAATCTGGAATCTGGAATCT 1027	
ORIGIN	82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101	
	1027 CTCAATTCCTCTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCGCAGATGATCAT	

Db 1028 GAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGGTCACTGAGCTGCAGGATAAAG 1087  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 1088 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 1147  
 QY 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 1148 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAAATGGTCTGCACACTACTGATTTTGGCT 1207  
 QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 1208 CTCATTTTCACTCTTTCAGTGTCTCTGTTATTTATGAACGCAATCAGGACAGATAGATCAT 1267  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 1268 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1327  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351

## RESULT 53

BD127437 1694 bp DNA linear PAT 18-SEP-2002  
 LOCUS  
 DEFINITION  
 Primer for synthesizing full-length cDNA and use thereof.

BD127437  
 ACCESSION  
 VERSION  
 BD127437.1 GI:23222382  
 J000000000  
 KEYWORDS  
 Homo sapiens (human)  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
 Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
 Koga, H.

TITLE  
 Primer for synthesizing full-length cDNA and use thereof

JOURNAL  
 Patent: JP 2002017375-A 2868 22-JAN-2002;

COMMENT  
 HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002017375-A/2868

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253172

PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO

PI ISHII,

PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI

SHINICHI KOJIMA,

PI TETSUJI OTSUKI, HISASHI KOGA

PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC

10,

PC C12P21/02, C12Q1/68/C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

FT CDS (479)..(1351).

Location/Qualifiers

1. .1694

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:

Pred. No.: 2,55e-86 Length: 1694

Score: 923.00 Matches: 187

Percent Similarity: 99.47% Conservative: 0

Best Local Similarity: 99.47% Mismatches: 1

Query Match: 99.14% Indels: 0

DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD127437 (1-1694)

QY 2 ValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 788 GTTGTGTACCTCTCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTGTGCAGC 847  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 848 CTAATTCCTGCTCTTTCATTGACAGTATTCAGCAATGTGAGCGTGAACAGCTACATTGCC 907  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATC 967  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 968 CAGAAATCAGATGAAGCGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 1027  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCythrIleLys 101  
 Db 1028 GAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGGTCACTGATGCAGATTAAG 1087  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 1088 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 1147  
 QY 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 1148 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAAATGGTCTGCACACTACTGATTTTGGCT 1207  
 QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 1208 CTCATTTTCACTCTTTCAGTGTCTCTGTTATTTATGAACGCAATCAGGACAGATAGATCAT 1267  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 1268 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1327  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351

## RESULT 54

AK075039 1694 bp mRNA linear PRI 03-SEP-2002  
 LOCUS  
 DEFINITION  
 Homo sapiens cDNA FLJ90558 fis, clone OVARC1001030.

AK075039  
 ACCESSION  
 VERSION  
 AK075039.1 GI:22760874

KEYWORDS  
 oligo capping; fis (full insert sequence).

SOURCE  
 Homo sapiens (human)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,

Sugiyama, T., Suzuki, Y., Sato, H., Nagai, K., Sugano, S., Ishii, S.,

Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,

Kojima, S., Nagahara, K., Masuko, Y., Ono, T., Okano, K., Yoshikawa, Y.,

Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and

Ninomiya, K.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 1694)

Isogai, T. and Otsuki, T.

Direct Submission

JOURNAL

Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1523-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology; cDNA library construction:

Institute of Medical Science, University of Tokyo, Laboratory of

Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass

sequencing and clone selection: Helix Research Institute (supported

by Japan Key Technology Center etc.).

FEATURES  
source

Location/Qualifiers  
1..1694  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="OVARC1001030"  
/tissue\_type="ovary, tumor tissue"  
/clone\_lib="OVARC1"  
/note="cloning vector: pME18SFL3"  
misc\_difference 531  
/note="compared to AF148538, AF132047 and AC016171.4"  
/replace=""

## ORIGIN

Alignment Scores:  
Pred. No.: 2,558-86 Length: 1694  
Score: 923.00 Matches: 187  
Percent Similarity: 99.47% Conservativity: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 99.14% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AK075039 (1-1694)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db GTTGTGACCTCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGCAGC 847  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db CTATTCTGCTGCTTTCATTGACAGTATTGACAGTATTGAGCGTAACAGCCCTACATTGCC 907  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db TGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAGCTATC 967  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db CAGAAATCAGATGAAGCCACCCATTCAGGCGCATCTGGAATCTGAAGTTGCTATATCT 1027  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
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Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db ATGTGGGTATTACCTATTGGTGCTCTTTTATATGCTGCTGACACTACTGNTTTGGCT 1207  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db CTCATTTCTCCTTTCAGTGTCTCTTATTAAGCGCATTCAGGCGACAGATGATCAT 1267  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db TATCTAGGACTTGCAAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1327  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db CCTGATTTGAGCGCAAGCTGAA 1351

## RESULT 55

BD083733

## LOCUS

BD083733 1980 bp DNA linear PAT 27-AUG-2002  
Nucleic acid sequence characterized in that expression is  
potentiated in human neuroblastoma with good prognosis, in  
comparison between human neuroblastoma with good prognosis and human  
neuroblastoma with bad prognosis.

## ACCESSION

BD083733

## VERSION

BD083733.1 GI:22629343

KEYWORDS  
SOURCEJP 2001321175-A/22.  
Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

Nucleic acid sequence characterized in that expression is  
potentiated in human neuroblastoma with good prognosis, in  
comparison between human neuroblastoma with good prognosis and human  
neuroblastoma with bad prognosis

## JOURNAL

## COMMENT

OS Homo sapiens (human)

PD 20-NOV-2001

PF 12-MAY-2000

PI AKIRA NAKAGAWARA

PC C12N15/09,C12Q1/02,C12Q1/68,G01N33/50,C12N15/00 CC Nucleic

acid sequence characterized in that expression is CC

potentiated in

CC human neuroblastoma with good prognosis, in comparison between

CC human

CC neuroblastoma with good prognosis and human

CC neuroblastoma with

CC prognosis bad

CC prognosis

FH Key

FT source

FT Location/Qualifiers

1..1980

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 4,98e-86 Length: 1980  
Score: 921.00 Matches: 187  
Percent Similarity: 99.47% Conservativity: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.93% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD083733 (1-1980)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db TCAGTTGTTGACCTCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGC 1065  
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db AGCCTATTCCAGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCTTACATT 1125  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAGCT 1185  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db ATCCAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 1245  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTCTCTTGGTTCATGTGAACCTGCACGATA 1305  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db AAGGAATCAGGCCCTCTCTTTAGTTGATGATTTAGTTGATTTCTGAGATTGTCAGTG 1365  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140

Db	1366	TTGATGTGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACACTACTGATTTTG	1425
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	1426	GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTAAGACGGCATCAGGCACAGATAGAT	1485
Qy	161	HisTyrLeuGlyLeuAlaSerValValIleTyrGluArgHisGlnAlaGlnIleAsp	180
Db	1486	CATTATCTAGGACTTGCAAAATGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA	1545
Qy	181	IleProGlyLeuIleArgLysAlaGlu	189
Db	1546	ATCCCTGGATTGAAGCGCAAGCTGAA	1572
RESULT 56	BD097380		
LOCUS	BD097380	1980 bp	DNA linear PAT 27-AUG-2002
DEFINITION	Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma.		
ACCESSION	BD097380		
VERSION	BD097380.1	GI:22642954	
KEYWORDS	WO 0166733-A/22.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1	(bases 1 to 1980)	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma.		
JOURNAL	Patent: WO 0166733-A 22 13-SEP-2001;		
COMMENT	CHIBA PREF.HISAMITSU PHARMACEUTICAL CO INC,AKIRA NAKAGAWARA		
	OS	Homo sapiens (human)	
	PN	WO 0166733-A/22	
	PD	13-SEP-2001	
	PF	02-MAR-2001	WO 2001JP001631
	PR	07-MAR-2000	JP OOP 159195,12-MAY-2000 JP OOP 140387 PI
	AKIRA NAKAGAWARA		
	PC	C12N15/12,C12Q1/68	
	CC	Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma	
	CC	human neuroblastoma and poor prognostic human neuroblastoma	
	CC	human neuroblastoma and poor prognostic human neuroblastoma	
	Key	Location/Qualifiers	
	FT	source	1..1980
	FT	Location/Qualifiers	/organism='Homo sapiens (human)'
FEATURES	source		
	1..1980		
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	/db_xref="taxon:9606"		
ORIGIN			
Alignment Scores:			
Pred. No.:	4..98e-86	Length:	1980
Score:	921.00	Matches:	187
Percent Similarity:	99.47%	Conservative:	1
Best Local Similarity:	98.94%	Mismatches:	1
Query Match:	98.93%	Indels:	0
DB:	6	Gaps:	0
US-09-830-972-29_COPY_990_1178 (1-189) x BD097380 (1-1980)			
Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla	20
Db	1006	TCAGTTGTTGACCTCTCTACTGACAGACATTAAAGACACTGGAGTGGTGGTGGTGGC	1065
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,39e-86 Length: 994  
 Score: 918.00 Matches: 187  
 Percent Similarity: 99.47% Conservative: 0  
 Best Local Similarity: 99.47% Mismatches: 1  
 Query Match: 98.60% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD132923 (1-994)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 68 GTTGTGACCTCTCTGACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 127  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 128 CTATTCTCTGCTCTTTCATTTGACAGTATTTCAGCATTTGTGAGCGGTAAACAGCTTACATTGCC 187  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 188 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATC 247  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 248 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGATCTGAAGTTGCTATATCT 307  
 QY 82 GluGluLeuValGlnLysTyrSerIleValSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 308 CAGGAGTTGGTTTCAGAAATGACAGTAAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAAG 367  
 QY 102 GluLeuArgAcGLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 368 GAACCTCAGCGCGCTCTCTTCTAGTATGATTTAGTGTATCTCTGAAGTTTGCAGTGTG 427  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 DB 428 ATGTGGGTATTACCTATGTTGCTGCTGCTTTTANTGCTGACACTACTGATTTGGCT 487  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 488 CTCATTTCTACTCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCGACAGATAGATCAT 547  
 QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 548 TATCTAGTACTTGCATAAATGAAGTGTAAAGATGCTATGGCTTAAATCCAGCAAAATC 607  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 608 CTGTGATTGAAGCGCAAGCTGAA 631

RESULT 58  
 AB049853  
 LOCUS 2162 bp mRNA linear PRI 14-OCT-2000  
 DEFINITION Macaca fascicularis brain cDNA, clone: QnpA-18952.  
 ACCESSION AB049853  
 VERSION AB049853.1 GI:10801643

KEYWORDS fis (full insert sequence).

SOURCE Macaca fascicularis (crab-eating macaque)

ORGANISM Macaca fascicularis  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Macaca.

REFERENCE 1 (sites)

AUTHORS Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M.,  
 Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.

TITLE Isolation of full-length cDNA clones from macaque brain cDNA  
 libraries

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2162)

AUTHORS Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.  
 TITLE Direct Submission

## JOURNAL

Submitted (11-OCT-2000) Katsuyuki Hashimoto, National Institute of  
 Infectious Diseases, Division of Genetic Resources, 23-1, Toyama  
 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
 (E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,  
 Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)

## COMMENT

Lab host: TOP10  
 Vector: pME18S-FL3 (Acc.No. AB009864)  
 R. Site1: DraIII (CACTGTTGTG)  
 R. Site2: DraIII (CACCATGTG)

Description: 1st strand cDNA was primed with an oligo(dT) primer  
 [ATGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized  
 using specific 5' and 3' primers and amplified by PCR. The PCR  
 product was digested with SfiI and size selection was performed to  
 exclude fragments <1.5kb. The SfiI-digested PCR product was cloned  
 into distinct DraIII sites of pME18S-FL3. XhoI sites just outside  
 the DraIII sites can be used to isolate the cDNA insert. Libraries  
 were constructed by Sugano et al. (University of Tokyo, Institute of  
 Medical Science). Custom primer used for sequencing  
 (5' end primer [CTTCTGCTCTAAAGCTGCG];  
 3' end primer [CGACCTGCAGCTCGACACA]).

## FEATURES

## source

1..2162  
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 /sex="male"  
 /tissue\_type="brain parietal lobe"  
 /clone\_lib="macaque brain cDNA library QnpA"  
 /dev\_stage="adult"  
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## CDS

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 KDAWKIAQKIPGLKRAE"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,14e-85 Length: 2162  
 Score: 918.00 Matches: 185  
 Percent Similarity: 100.00% Conservative: 3  
 Best Local Similarity: 98.40% Mismatches: 0  
 Query Match: 98.60% Indels: 0  
 DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AB049853 (1-2162)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 596 GTTGTGACCTCTCTCTGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 655  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 656 CTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGAGTGTAAACAGCTTACATTGCC 715  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 716 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGCTATC 775  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 776 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAATTCGCGATATCT 835  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 836 GAGGAGTTGGTTTCAGAAATGACAGTAAATCTCTCTTGTGTCATGTGAATCTGCACGATAAG 895  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121



DB:	10	Gaps:	0
US-09-830-972-29_COPY_990_1178 (1-189) x AB073672 (1-1738)			
QY	1	SerValValAapLeuLeuTyrTrpArgAspIleIleYsThrGlyValValPheGlyValA	20
DB	1169	TCAGTGTGTGACCTCTGCTGCTGAGAGACATTAAGAGAGCTGAGTGGTGTGGTGGCC	1228
QY	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
DB	1229	AGCTTATTCCTGCTGCTGCTGCTGAGAGTGTTCAGCATTCAGTGTAAACGGCTACATT	1288
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla	60
DB	1289	GCCTTGGCCCTGCTCTCTGCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCT	1348
QY	61	IleGlnIysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle	80
DB	1349	ATCCAGAAATCAGATGAAGGCCACCCATTTAGGGCATATTTTGAAGTCTGAAGTTGGCATA	1408
QY	81	SerGluGluLeuValGlnIleYsTrpSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
DB	1409	TCAGAGGAATTTGGTTTCAGAAATATAGTAATTCCTGCTCTTGTCTATGTGAACACACAN	1468
QY	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuIysPheAlaVal	120
DB	1469	AAAGAAATTTGAGCGCTCTCTCTTAGTTGATGATTTAGTTCCCTGAAAGTTTGCAGTG	1528
QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu	140
DB	1529	TTGATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTGTGACACTACTGATT	1588
QY	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
DB	1589	GCCTGTACTCTACTCTTCAGTATTCCTGTTATATATGAAACGATCAGGCGCATAGAT	1648
QY	161	HisTyrLeuGlyLeuAlaAsnValysAspAlaMetAlaIysIleGlnAlaLys	180
DB	1649	CATTATCTAGGACTTTGCAACAGAGTGTAAAGCATGCCATGCCAAATCCCAAGCAAAA	1708
QY	181	IleProGlyLeuLeuArgLysAlaGlu	189
DB	1709	ATCCCTGGATTGAAGCGCAAGCAGAA	1735
RESULT 60			
BC032192		2958 bp	linear
LOCUS			
DEFINITION		Mus musculus reticulon 4, mRNA (cdna clone MGC:38204	
		IMAGE:5323152), complete cds.	
ACCESSION		BC032192	
VERSION		BC032192.1	
KEYWORDS		GI:21618980	
SOURCE		MGC.	
ORGANISM		Mus musculus (house mouse)	
REFERENCE			
AUTHORS			
1 (bases 1 to 2958)			
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,			
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,			
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,			
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,			
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,			
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,			
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Tohiyuki, S.,			
Carninci, P., Prange, C., Raha, S., Igoe, L., Loquellano, N.A., Peters, G.J.,			
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,			
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,			
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,			
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,			
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,			
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,			
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,			
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,			
ORIGIN			
Alignment Scores:			
Pred. No.:	1,79e-85	Length:	1738
Score:	915.00	Matches:	186
Percent Similarity:	99.47%	Conservative:	2
Best Local Similarity:	98.41%	Mismatches:	1
Query Match:	98.28%	Indels:	0



Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,  
Schnercher, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REMARK

## COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hghri.nih.gov](mailto:nisc_mgc@hghri.nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgouon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 56 Row: k Column: 2.

## FEATURES

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KLSTPSPFNYSYIAKFEKSPDCELDVDDSSPESEFVDFSDSIPEYVQIQEEA  
VLMKESLVESEYVTOHKHKLRSASQEVGKPYLESFQPNLHTTKDAASNEIPTLT  
KKEITSLQMEENTAIYNDLDSKEDKMESETFSDSSPIEIIDPEPTVSADKDS  
PKETDLEVSNKSEIANVQSGANSLPCSELCDFLSFNKTYPKDAENHVSDEFSEKRSV  
SKVPLLPNLSALESQIEEMGNIVPKVLTKGAEEKLPDTEKDRSLTAVLSAENLKT  
SVVDLLYPRDITVGFAGFLLSLTIVFSIVSTAYIALALLSVTISFRYKGM  
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## misc\_feature

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1457. 2029  
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the three reticulon isoforms and their homologues"  
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## ORIGIN

## Alignment Scores:

Pred. No.: 3.44e-85 Length: 2958  
Score: 915.00 Matches: 186  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.41% Mismatches: 1  
Query Match: 98.28% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BC032192 (1-2958)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 1463 TCAGTTGTGTGACCTCTCTACTGGAGACACATTAAAGAGACTGGAGTGGTGTGGTGC 1522  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 1523 AGCTATTTCCTGCTGCTCTCTGACAGTTCACAGTTGTCAGTGTACGGCCTACAT 1582  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 1583 GCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCT 1642  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 1643 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATA 1702  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 1703 TCAGAGGAATGGTTTCAGAAATATAGTAATTTCTGCTCTTGGTCATGTGACAGCAATA 1762  
QY 101 LysGluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaVal 120  
DB 1763 AAAGAAATGAGGCGTCTCTCTTAGTTGATGATTTAGTTGATTCCTCCTGAAGTTTCAGTG 1822  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140  
DB 1823 TTGATGTGGGTATTTACTTACGTGGTGGTCCCTTGTTCATATGGTTTGACACTACTGATTTTA 1882  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 1893 GCTCTGATCTCAGTCTTCAGTATTTCTGTTATATATGAAACGGCATCAGCGGAGATAGAT 1942  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 1943 CATTATCTAGACTTGCACAAACAGAGCGTTAAGGATGCCATGGCCAAATCCACAGCAAA 2002  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
DB 2003 ATCCCTGGATTGAAGCGCAAGACGAA 2029

## RESULT 61

BC032272 LOCUS 3815 bp mRNA linear ROD 16-APR-2003  
DEFINITION Mus musculus reticulon 4, mRNA (cDNA clone IMAGE:536860), partial  
cde.  
ACCESSION BC032272  
VERSION BC032272.1 GI:22749634  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland

FEATURES Location/Qualifiers

source 1..4063

organism="Mus musculus"

mol\_type="mRNA"

strain="129/SvCJ7"

db\_xref="taxon:10090"

chromosome="11"

gene 1..4063

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 TESTAANI FVLSDHTSENKDEKKLEERKAOLITKTSPTKSNPLVAIHDSADYV  
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3'UTR 3174..4063

/gene="Rtn4"

ORIGIN

Alignment Scores:

Pred. No.:	5.07e-85	Length:	4063
Score:	915.00	Matches:	186
Percent Similarity:	99.47%	Conservative:	2
Best Local Similarity:	98.41%	Mismatches:	1
Query Match:	98.28%	Indels:	0
DB:	10	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AY102280 (1-4063)

Qy	1	SerValValAspLeuLeuTyrrTpArgAspIleLysLysThrGlyValValPheGlyVala	20
Db	2604	TCAGTTGTTGACCTCCTGTACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGTGC	2663
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrile	40
Db	2664	AGCTTATTCCTGCTGCTCTGACAGCTGTTGACAGTTCAGTGTAAACGGCTACATT	2723
Qy	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAla	60
Db	2724	GCCTTGCCCTGCTCTCTGAGCTATCAGCTTTAGGATATATAAGGGTGTGATCCAA	2783
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIle	80
Db	2784	ATCCAGAAATCAGATGAAGCCACCCATTGAGGCATATTTGGAACTGAAGTTGCATA	2843
Qy	81	SerGluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnCysThrile	100

Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu  
 Ronaldo.M.F., Akabogu,I., Baik,T., Bair,J., Crouch,K., Davis,A.,  
 Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,  
 Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,  
 Casavant,T., Soares,M.B.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

## FEATURES

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## ORIGIN

Alignment Scores:  
 Pred. No.: 5,78e-85 Length: 4518  
 Score: 915.00 Matches: 186  
 Percent Similarity: 99.47% Conservative: 2  
 Best Local Similarity: 98.41% Mismatches: 1  
 Query Match: 98.28% Indels: 0  
 DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BC056373 (1-4518)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 3039 TCAGTTGTTGACCTCTGCTACTGAGAGACATTAAAGAAGCTGAGTGGTGTGGTGGC 3098  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 3099 AGCTTATTCCTGCTGCTGCTGCTGACAGTGTTCAGCATGTTCAGTGAACGGCTACATT 3158  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3159 GCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGTTGATCCAAAGCT 3218  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80  
 Db 3219 ATCCAGAAATCAGATGAAGGCCACCCATTACGGGCATATTGGAATCTGAAGTTGCCATA 3278  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 3279 TCAGAGAAATGCTGTTAGAAATATAGTAATCTGCTCTGCTGCTGCTGCTGCTGCTGCT 3338  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuVal 120  
 Db 3339 AAAGAATTGAGCGGCTCTCTCTTCTTAGTTGATGATGATTTAGTTGATTTCCCTGAAGTTGCA 3398

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 3399 TTGATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATATGGTGTTCACACTACTGATTATTA 3458  
 QY 141 AlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 3459 GCTCTGAICTCACTTCTTCAGTATTCTGTATATATGAACGCATCAGCGGCAGATAGAT 3518  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3519 CATTATCTAGGACTTGCACCAAGAGCGTTAAGGATGTCATGCCCAAAATCCAAAGCAAAA 3578  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 3579 ATCCCTGGATTGAAGCGCAAGACAGAA 3605

RESULT 64  
 AY102284  
 LOCUS Mus musculus RTN4 (Rtn4) 4627 bp mRNA linear ROD 29-JAN-2003  
 DEFINITION Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.  
 ACCESSION AY102284  
 VERSION AY102284.1 GI:23379816  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 4627)  
 AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.  
 TITLE Genomic Structure and Functional Characterisation of the Promoters  
 of Human and Mouse nogo/rtn4  
 JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)  
 MEDLINE 22376540  
 PUBMED 12488097  
 REFERENCE 2 (bases 1 to 4627)  
 AUTHORS Oertle,T. and Schwab,M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of  
 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,  
 Switzerland  
 REFERENCE 3 (bases 1 to 4627)  
 AUTHORS Van der Putten,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma  
 Inc., Basel, Switzerland  
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 LPSLSPLSTVFEKHYGLNLSAVASTECTIEETNEASRELPERATNPFVNRSAEF  
 VLYESEMSSFNKSGPKESAMLVENTKEEIVRSKDEDLVCSAALHNPOQSPATLT  
 KVKEDGVMSPEKTMDFNEMKMSVAVPVREYADPKPEQAEVKDTEGSRDLVAA  
 RANMESKVDKKCFEDSLQKGHGKSESNNENASFPRTPELVKDSRAYITCDSPSSA

TESTAANIPVPLEDHTSENKTDKKEI EERKQAI I I EKTSPKTSNPFVLAHIDSEADYV  
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YDGIKLEPNPPPEAMSVALKTSDEKEIPEPSFNAQAQEAAPISACDLIKE  
TKLSTEPSFESNYSIEAKPEKSPDHCELVDSSPEFVDLPSDDSIPEVPQOE  
AVMLKESUTEVSEITVQHKHKBRLASQEVKPYLESFQPNHLITKDAASNEIPTL  
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3738..4627  
/gene="Rtn4"

3'UTR

ORIGIN

Alignment Scores:

Pred. No.: 5,95e-85 Length: 4627  
Score: 915.00 Matches: 186  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.41% Mismatches: 1  
Query Match: 98.28% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AY102284 (1-4627)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 3168 TCAGTGTGTGACCTCTGTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGC 3227  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3228 AGCTTATCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATT 3287  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3288 GCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCT 3347  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3348 ATCCAGAAATCAGATGAAAGCCACCATTTACGGGCATATTTGGAATCTGAAGTTGCCATA 3407  
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 3408 TCAGAGGAATGGTTCAGAAATATAGTAATCTCTGCTTCTTGGTCATGTGACAGCAATA 3467  
QY 101 LysGluLeuArgArgPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3468 AAGAATTCAGGCGCTCTCTTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTGCAGTG 3527  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrIleLeuLeu 140  
DB 3528 TTGATGTGGGTATTTACTTACGTTGGTGTGCTTGTTCATAGTGGTTTGACACTACTGATTTTA 3587  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 3588 GCTCTGATCTCACTCTTCAGTATTCCTGTTATATATGAAAGGCATCAGCGCGCATAGAT 3647  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAenValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3648 CATTATCTAGGACTTGCAACAAAGAGCGTTAAGGATGCCATGGCCAAATAATCCAAAGCA 3707  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
DB 3708 ATCCCTGGATTGAAGCGCAAGCAGAA 3734

RESULT 65

AR379837

LOCUS

DEFINITION

ACCESSION

VERSION

Sequence 382 from patent US 6607879.

AR379837

AR379837

AR379837.1

2610 bp

DNA

linear

PAT 18-DEC-2003

RESULT 66

AY102282

LOCUS

DEFINITION

ACCESSION

VERSION

Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.

AY102282

AY102282.1

2266 bp

mRNA

linear

ROD 29-JAN-2003

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2610)  
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.  
TITLE Compositions for the detection of blood cell and immunological  
response gene expression  
JOURNAL Patent: US 6607879-A 382 19-AUG-2003;  
FEATURES Location/Qualifiers  
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Alignment Scores:

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Best Local Similarity: 99.47% Mismatches: 0  
Query Match: 98.17% Indels: 1  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AR379837 (1-2610)

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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAl 41  
DB 1371 CTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACAGCCTACAATTCG 1430  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTAT 1490  
QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
DB 1491 CCAGAAATCAGATGAAAGCCACCATTCAGGCATATCTGGAACTGGAAGTTGCTATATC 1550  
QY 81 rGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 101  
DB 1551 TGAGGAGTTGGTTCAGAAAGTACAGTAATCTCTGCTCTGCTCATGTGAACCTGCACGATAA 1610  
QY 101 sGluLeuArgArgPheLeuValAspLeuValAspSerLeuLysPheAlaVal 121  
DB 1611 GGAACCTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 1670  
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrIleLeuAl 141  
DB 1671 GATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTAATGCTCTGACACTACTGATTTTGGC 1730  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 161  
DB 1731 TCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1790  
QY 161 sTyrLeuGlyLeuAlaAsnLysAenValLysAspAlaMetAlaLysIleGlnAlaLys 181  
DB 1791 TTATCTAGGACTTGCAATAAAGAATGTTAAAGATGCTATAGCTAAATCCAAAGCAAAAT 1850  
QY 181 eProGlyLeuLysArgLysAlaGlu 189  
DB 1851 CCTTGGTGAAGCGCAAGCTGAA 1875

RESULT 66

AY102282

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.

AY102282

AY102282.1

2266 bp

mRNA

linear

ROD 29-JAN-2003



DB:		10	Gaps:	0
US-09-830-972-29_COPY_990_1178 (1-189) x AF326337 (1-734)				
Qy	2	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21	
Db	100	GTGTTGACCTCCTGCTACTGGAGAGACATTAAAGAACTGGAGTGGTGTGTTGGTCCAGC	159	
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41	
Db	150	TTATTCCCTGCTGCTCTCTGACAGTGTTCAGATTGTCAAGTGAACGGCTACATATGCC	219	
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61	
Db	220	TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAAGCTATC	279	
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81	
Db	280	CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATTTGGAAATCTGAAGTTGCCATATCA	339	
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101	
Db	340	GAGGAATGGTTCAAGATATAGTAATTTCTGCTCTGTGTCATGTAACAGCACAAATAAA	399	
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121	
Db	400	GAATTGAGCGCTCTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTGCAGTGTG	459	
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla	141	
Db	460	ATGTGGGTATTTACTTACGTTGGTCCCTGTTCAATGGTTTGACACTACTGATTTAGCC	519	
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161	
Db	520	CTGATCTCACCTTCAGTATTTCTGTTATATATGAACGGCATCAGCGGCAGATAGATCAT	579	
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181	
Db	580	TATCTAGACTTGCACCAAGAGTTTAAGGATGCCATGCCCAATCCAGCAAAATC	639	
Qy	182	ProGlyLeuLysArgLysAlaGlu	189	
Db	640	CCTGATTTGAAGCGCAAGCAGAA	663	
RESULT 68				
AY102283				
LOCUS Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.				
ACCESSION AY102283				
VERSION AY102283.1 GI:23379814				
KEYWORDS Mus musculus (house mouse)				
SOURCE Mus musculus				
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.				
AUTHORS Genomic Structure and Functional Characterisation of the Promoters of Human and Mouse nogo/rtn4				
TITLE J. Mol. Biol. 325 (2), 299-323 (2003)				
JOURNAL MEDLINE 22376540				
PUBMED 12488097				
REFERENCE 2 (bases 1 to 1769)				
AUTHORS Oertle,T. and Schwab,M.E.				
TITLE Direct Submission				
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland				
REFERENCE 3 (bases 1 to 1769)				
AUTHORS van der Putten,H.				
TITLE Direct Submission				
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland				

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3'UTR		
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Pred. No.: 4,76e-85 Length: 1769		
Score: 911.00 Matches: 185		
Percent Similarity: 99.47% Conservative: 2		
Best Local Similarity: 98.40% Mismatches: 1		
Query Match: 97.85% Indels: 0		
DB: 10 Gaps: 0		
US-09-830-972-29_COPY_990_1178 (1-189) x AY102283 (1-1769)		
Qy	2	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db	313	GTGTTGACCTCCTGCTACTGGAGAGACATTAAAGAACTGGAGTGGTGTGTTGGTCCAGC 372
Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db	373	TTATTCTGCTGCTGCTCTGACAGTGTTCAGCATTGTCAAGTGAACGGCTACATGTC 432
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db	433	TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAAGCTATC 492
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db	493	CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATTTGGAAATCTGAAGTTGCCATATCA 552
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db	553	GAGGAATGGTTCAAGAAATATAGTAATTTCTGCTCTTGGTCAATGTAACAGCACAAATAAA 612
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db	613	GAATTGAGCGCTCTCTTTAGTTGATGATTTAGTTAGTTCCCTGAAAGTTGCAAGTGTG 672
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db	673	ATGTGGGTATTTACTTACGTTGGTCCCTTGTCAATGGTTTGACACTACTGATTTTAGCT 732
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db	733	CTGATCTCACTCTTCAGTATTTCTGTTATATATGAACGGCATCAGCGCGCAGATAGATCAT 792
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db	793	TATCTAGACTTGCACCAAGAGCGTTAAGGATGCCATGCCCAATCCAGCAAAATC 852



Qy	182	ProGlyLeuIysArgLysAlaGlu 189 
Db	853	CCTGGATTGAAGCGCAAGCAGAA 876 
RESULT 69		
LOCUS	AY102281	2209 bp mRNA linear ROD 29-JAN-2003
DEFINITION	Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.	
ACCESSION	AY102281	
VERSION	AY102281.1	GI:23379810
KEYWORDS	Mus musculus (house mouse)	
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E. Genomic Structure and Functional Characterisation of the Promoters of Human and Mouse nogo/rtn4 J. Mol. Biol. 325 (2), 299-323 (2003) 22376540 12488097	
REFERENCE	2 (bases 1 to 2209)	
AUTHORS	Oertle,T. and Schwab,M.E.	
TITLE	Direct Submission	
JOURNAL	Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland	
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CDS	249..1319	/genes="Rtn4" /note="Rtn4" /notes="NOCO-B; RTN4-B1; alternatively spliced" /codon_start=1 /product="RTN4" /protein_id="AAM73503.1" /db_xref="GI:23379811" /translation="MEDIDQSILVSSADSPPPPAPKQFVTPEDEEDEEEDDEE EDEDELEUEVRKPAGSAAPPAPALPDSSDVPAPRGELPAPPTAPER QPSEWSPASAPSPPAAPAVLPKLPDEDPPAPAPAGAPLAPAPPTAPAP RRGSGSVVDLLLYWRDIKKTVGFCSGLLSLTFSIVSTAYIALALLSVTISF RIYKGVIQAIKSDGHPRPAIVEVAISELVOKYSNSALGHVNSTIKELRLFLV DDVLDSLKPAVLMMVFYVGALFNGLITLILALSIFPIVERHQAQIDHYLGLAN KSKVDAMAKIQAIPLKERKA"
3'UTR	1320..2209	/genes="Rtn4"
ORIGIN	exon	
Alignment Scores:	Pred. No.: 6.26e-85	Length: 2209
Score:	911.00	Matches: 185
Percent Similarity:	99.47%	Conservative: 2
Best Local Similarity:	98.40%	Mismatches: 1
Query Match:	97.85%	Indels: 0
DB:	10	Gaps: 0
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US-09-830-972-29 COPY 990 1178 (1-189) x AY102281 (1-2209)



US-09-830-972-29\_COPY\_990\_1178 (1-189) x AX766046 (1-3489)

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Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2983 AGCTTATTCCTGCTGCTCTGACAGTTCACAGTTCAGTGTGAACGGCTACATT 3042

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
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Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
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Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
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Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140  
Db 3283 TTGATGTGGGTGTTTACTATTTATGTTGGTCCCTGTTCAATGCTGACACTACTGATTTTA 3342

Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3343 GCTCTGATCTACTCTTCAGTATTCCTGTTATTTATGAAACGGCATCAGTGCAGATAGAT 3402

Qy 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3403 CATTATCTAGGACTTGCAACAAGAGTGTGAAGATGCCATGGCCAAATCCAAAGCAAA 3462

Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3463 ATCCCTGGATTGAAGCGCAAGCAGAT 3489

RESULT 71  
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LOCUS CQ829507 3492 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 25 from Patent WO2004052932.  
ACCESSION CQ829507  
VERSION CQ829507.1 GI:49732820

KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 Barske,C., Mir,A.K., Oertle,T., Schnell,L., Schwab,M.E.,  
Vitaliti,A. and Zurini,M.  
Nogo a binding molecules and pharmaceutical use thereof  
Patent: WO 2004052932-A 25 24-JUN-2004;  
Novartis AG (CH)

FEATURES Location/Qualifiers

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RNO242961

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## ORIGIN

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Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 97.53% Indels: 0  
DB: 6 Gaps: 0

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Db 3163 TCAGAGGAATGGTTCAGAAATACAGTAATTCCTGCTCTGTCATGTGAACAGCACATA 3222

Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3223 AAAGAACTGAGCGGCTTTCTTAGTCATGATTTAGTTGATTCCTCGAAGTTGCGAGTG 3282

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140  
Db 3283 TTGATGTGGGTGTTTACTATTTATGTTGGTCCCTGTTCAATGCTGACACTACTGATTTTA 3342

Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3343 GCTCTGATCTACTCTTCAGTATTCCTGTTATTTATGAAACGGCATCAGTGCAGATAGAT 3402

Qy 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3403 CATTATCTAGGACTTGCAACAAGAGTGTGAAGATGCCATGGCCAAATCCAAAGCAAA 3462

Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3463 ATCCCTGGATTGAAGCGCAAGCAGAT 3489









QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuValAspPheAlaValLeu 121  
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 QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
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 DB 570 TATCTAGGACTTGCAACAAGAGTGTAAAGGATGCCCAAAATCCAAGCAAAATC 629  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
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 ACCESSION AJ242963  
 VERSION AJ242963.1 GI:6822250  
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 SOURCE Rattus norvegicus (Norway rat)  
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 Rattus.  
 REFERENCE 1  
 AUTHORS Chen, M.S., Huber, A.B., van der Haar, M.E., Frank, M., Schnell, L.,  
 Spillmann, A., Christ, F. and Schwab, M.E.  
 TITLE Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
 antigen for monoclonal antibody IN-1  
 JOURNAL Nature 403 (6768), 434-439 (2000)  
 MEDLINE 20129258  
 PUBMED 10667796  
 REFERENCE 2 (bases 1 to 1568)  
 AUTHORS Van der Haar, M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-JUN-1999) Van der Haar M.E., Department of  
 Neuromorphology, Brain Research Institute, University of Zurich,  
 Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND  
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## FEATURES

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 VERSION AY164740.1 GI:32331280  
 KEYWORDS  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
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 Rattus.  
 REFERENCE 1 (bases 1 to 2156)  
 AUTHORS Oertle, T., Klinger, M., Stuermer, C.A. and Schwab, M.E.  
 TITLE A reticular rhapsody: phylogenetic evolution and nomenclature of the  
 RTN/Nogo gene family  
 JOURNAL PNAS 100 (10), 1238-1247 (2003)  
 PUBMED 12832288  
 REFERENCE 2 (bases 1 to 2156)  
 AUTHORS Oertle, T. and Schwab, M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department  
 Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,

Pred. No.: 2,2e-84 Length: 1568  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.10% Indels: 0  
 DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x RNO242963 (1-1568)

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 DB 151 GTTGTGGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGTTGGTGGCCAGC 210  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 211 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAACGGCTTACATTCGC 270  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 271 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGTATCCAGGCTATC 330  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 331 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTAGATCTGAAGTTGCTATATCA 390  
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 DB 391 GAGGAAATTTGGTTTCAGAAATACAGTAATTCCTGCTCTTGGTCAATGTGAACACCAATAAAA 450  
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 VERSION AY164740.1 GI:32331280  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 2156)  
 AUTHORS Oertle, T., Klinger, M., Stuermer, C.A. and Schwab, M.E.  
 TITLE A reticular rhapsody: phylogenetic evolution and nomenclature of the  
 RTN/Nogo gene family  
 JOURNAL PNAS 100 (10), 1238-1247 (2003)  
 PUBMED 12832288  
 REFERENCE 2 (bases 1 to 2156)  
 AUTHORS Oertle, T. and Schwab, M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department  
 Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,

Alignment Scores:

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ORIGIN
Alignment Scores:
Pred. No.: 3,25e-84 Length: 2156
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Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.10% Indels: 0
DB: 10 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AY164740 (1-2156)

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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141
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DEFINITION Rattus norvegicus mRNA for Nogo-B protein.
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VERSION AJ242962.1 GI:6822248
KEYWORDS Nogo-B protein.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1
REFERENCE
AUTHORS Chen, M.S., Huber, A.B., van der Haar, M.E., Frank, M., Schnell, L.,
Spillmann, A.A., Christ, F. and Schwab, M.E.
TITLE Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1
JOURNAL Nature 403 (6768), 434-439 (2000)
MEDLINE 20129258
PUBMED 10667796
REFERENCE
2 (bases 1 to 2156)
Van der Haar, M.E.
Direct Submission
TITLE Submitted (14-JUN-1999) Van der Haar M.E., Department of
Neuromorphology, Brain Research Institute, University of Zurich,
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND
JOURNAL
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ORIGIN
Alignment Scores:
Pred. No.: 3,25e-84 Length: 2156
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.10% Indels: 0
DB: 10 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x RNO242962 (1-2156)

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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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Db 945 GAGGAATGGTTTCAGAAATACAGTAATCTGCTCTGTCATGTGACAGCACATATAA 1004

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VDDLVDSLKFAVLMMVFTYTGALFNGLTLLILALISLFSIPVIYERHOAQIDHVLGA
NKSVKDAMAKIQAIKPLKRAE"

ORIGIN
Alignment Scores:
Pred. No.: 3,95e-84 Length: 1276
Score: 900.50 Matches: 185
Percent Similarity: 98.94% Conservativeness: 2
Best Local Similarity: 97.88% Mismatches: 1
Query Match: 96.72% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x AY114153 (1-1276)
QY 2 ValValAspLeuLeuTyrTrrArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 890 GTTGTTGACCTCTCTACTGAGAGACATTAAAGAGCTGGAGTGGTGTGGTCCAGC 949
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 950 TTATTCCTGCTGCTCTGACAGCTGTTACGATTGTCAGTGAACGCTACATTCGC 1009
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1010 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 1069
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 1070 CAGAATCAGATGAAGGACCCCATTCAGGCGATATTTAGAAATCTGAAGTGTGTATATCA 1129
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 1130 GAGGAATTTGGTTCAGAAATACAGTAATCTGCTCTTGGTCATGTGAACAGCACAATAAAA 1189
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 1190 GAACCTGAGCGCGCTTTCTTAGTTAGTATTTAGTTGATTCCTGAAGTGTTCAGTGTG 1249
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 1250 ATGTGGGTGTTTACTATGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 1310 CTGATCTCCTCTCAGTATTCCTGTTATTTATGAACGCGATCAGTGCAGATAGATCAT 1369
QY 162 TyrLeuGlyLeuAlaAsnLysValLysPheAlaMetAlaLysIleGlnAlaLysIle 181
Db 1370 TATCTAGGACTTGCAACACAGAGTGTAAAGATGCGCATGGCCAAATCCAAAGCAAAATC 1429
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 1430 CTGGAATGAAGCGCAAGACGAT 1453

RESULT 82
AY114153 1276 bp mRNA linear ROD 17-JUL-2002
LOCUS Mus musculus nogo-B mRNA, complete cds.
DEFINITION AY114153.1 GI:21898578
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Jin, W., Li, R., Long, M., Shen, J. and Ju, G.
Cloning and expression of the mouse Nogo-B protein
Unpublished
REFERENCE
2 (bases 1 to 1276)
Jin, W., Li, R., Long, M., Shen, J. and Ju, G.
Direct Submission
TITLE Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi
Road, Xi'an, Shaanxi 710032, China
FEATURES
Location/Qualifiers
1..1276
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
120..1193
/feature="RTN4; foocen"
/codon_start=1
/product="nogo-B"
/protein_id="AAM77069.1"
/db_xref="GI:21898579"

CDS

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/translation="MEDIDSSLVSSADSPRPAPKQFVTEPEDESEDESEDE
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KRKRGSSVVLDLYRDIKKTGVVYFGASLFLUSLTVFSIVTAYTALALSTVTS
FRYTKYQAIQKSGDEGPPRAYLESVAISELVQKYSNSALGVNSTIKELRRFL
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NKSVKDAMAKIQAIKPLKRAE"

ORIGIN
Alignment Scores:
Pred. No.: 3,95e-84 Length: 1276
Score: 900.50 Matches: 185
Percent Similarity: 98.94% Conservativeness: 2
Best Local Similarity: 97.88% Mismatches: 1
Query Match: 96.72% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x AY114153 (1-1276)
QY 2 ValValAspLeuLeuTyrTrrArgAspIleLysThrGlyValValPheGlyAla 20
Db 624 GTTGTTGACCTCTCTACTGAGAGACATTAAAGAGCTGGAGTGGTGTATTTTGGTCC 683
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 684 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGCATTGTCAGTGAACGCGCTACATT 743
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 744 GCCTTGGCCCTGCTCTCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAACT 803
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 804 ATCAGAAATCAGATGAAGGCCACCATTCAGGCGATATTTGGAAATCTGAAGTGGCCATA 863
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 864 TCAGAGGAATTTGGTTCAGAAATATAGTAATCTGCTCTGCTGCTGCTGCTGCTGCTGCT 923
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 924 AAAGAAATTTGAGCGCTCTCTTCTTAGTTAGTATTTAGTATTCCTCGAAGTTTGCAGTG 983
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 984 TTGATGTGGGTATTTACTTACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1043
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 1044 GCTCTGATCTCAGTCTCTCAGTATTCCTGTTATATATGAACGCGCATCAGCGCAGATAGAT 1103
QY 161 HisTyrLeuGlyLeuAlaAsnLysValLysPheAlaMetAlaLysIleGlnAlaLys 180
Db 1104 CATTATCTAGGACTTGCAACACAGAGCTGTAAAGATGCGCATGGCCAAATCCAAAGCAAAA 1163
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 1164 ATCCCTGATTTGAAGCGCAAGACGAGAA 1190

RESULT 83
BD190738 2386 bp DNA linear PAT 17-JUL-2003
LOCUS Secreted proteins and polynucleotides encoding them,,
DEFINITION BD190738
ACCESSION BD190738.1 GI:33000477
VERSION JP 2002515751-A/5.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2386)
Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.

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TITLE      Secreted proteins and polynucleotides encoding them
JOURNAL    Patent: JP 2002515751-A 5 28-MAY-2002;
            GENETICS INSTITUTE INC
COMMENT    PN  JP 2002515751-A/5
            PD  28-MAY-2002
            PF  24-OCT-1997 JP 1998519738
            PR  25-OCT-1996 US  08/740274
            PI  KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
            DAVID MERBERG,
            PI  MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
            C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC  Strandedness:
            Double:
            CC  Topology: Linear;
            FH  Key  Location/Qualifiers.
FEATURES   source
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
  Pred. No.:      3.58e-83      Length:      2386
  Score:          894.50      Matches:      184
  Percent Similarity: 97.35%      Conservative: 0
  Best Local Similarity: 97.35%      Mismatches: 0
  Query Match:     96.08%      Indels:      5
  DB:              6          Gaps:          1
US-09-830-972-29_COPY_990_1178 (1-189) x BD190738 (1-2386)
QY      1  SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB      1476 TCAGTTGTTGACCTCTGCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 1535
QY      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB      1536 AGCCTATTCTGCTGCTTCATTGACAGATTTCAGCATTTGAGCGTAAACAGCTACATT 1595
QY      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
DB      1596 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 1655
QY      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB      1656 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGG-----GAAGTTGCTATA 1700
QY      81  SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB      1701 TCTGAGAGTTGGTTTCAGAGTACAGTAATTCCTGCTCTTGGTCATCTGAACTGCAGATA 1760
QY      101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB      1761 AAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 1820
QY      121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB      1821 TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAAATGGTCTGACACTACTGATTTTG 1880
QY      141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB      1881 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTATGACGGCATCAGGCACAGATAGAT 1940
QY      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB      1941 CATTATCTAGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 2000
QY      181 IleProGlyLeuLysArgLysAlaGlu 189
DB      2001 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2027
RESULT 84
AX099401
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LOCUS      AX099401      2386 bp      DNA      linear      PAT 02-APR-2001
DEFINITION Sequence 41 from Patent WO0119988.
ACCESSION  AX099401
VERSION     AX099401.1  GI:13538524
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Jacobs, K., McCoy, J.M., Lavallie, E.R., Collins-Racie, L.A., Evans, C.,
            Merberg, D., Treacy, M., Bowman, M.R., Spaulding, V. and Agostino, M.J.
TITLE       Secreted proteins and polynucleotides encoding them
JOURNAL     Patent: WO 0119988-A 41 22-MAR-2001;
            Genetics Institute, Inc. (US)
FEATURES   Location/Qualifiers
            1..2386
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
  Pred. No.:      3.58e-83      Length:      2386
  Score:          894.50      Matches:      184
  Percent Similarity: 97.35%      Conservative: 0
  Best Local Similarity: 97.35%      Mismatches: 0
  Query Match:     96.08%      Indels:      5
  DB:              6          Gaps:          1
US-09-830-972-29_COPY_990_1178 (1-189) x AX099401 (1-2386)
QY      1  SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB      1476 TCAGTTGTTGACCTCTGCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 1535
QY      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB      1536 AGCCTATTCTGCTGCTTCATTGACAGATTTCAGCATTTGAGCGTAAACAGCTACATT 1595
QY      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
DB      1596 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 1655
QY      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB      1656 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGG-----GAAGTTGCTATA 1700
QY      81  SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB      1701 TCTGAGAGTTGGTTTCAGAGTACAGTAATTCCTGCTCTTGGTCATCTGAACTGCAGATA 1760
QY      101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB      1761 AAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 1820
QY      121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB      1821 TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAAATGGTCTGACACTACTGATTTTG 1880
QY      141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB      1881 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTATGACGGCATCAGGCACAGATAGAT 1940
QY      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB      1941 CATTATCTAGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 2000
QY      181 IleProGlyLeuLysArgLysAlaGlu 189
DB      2001 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2027
RESULT 85
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BX934715
LOCUS      BX934715          1591 bp      mRNA      linear      VRT 02-FEB-2004
DEFINITION Gallus gallus finished cDNA, clone CHEST117m23.
ACCESSION  BX934715
VERSION    BX934715.1  GI:41635243
KEYWORDS
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE  1 (bases 1 to 1591)
            Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E.,
            Croning, M.D.R., Davies, R.M., Francis, M.D., Graham, D.V.,
            Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R.,
            Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G.,
            Tickle, C. and Wilson, S.A.
            Direct Submission
            Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
            BB SRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
            sequencing project.
            This sequence is from the
            BB SRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
            from a library constructed by Elizabeth Bosch. cDNA was prepared
            from RNA extracted from brain,
            and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the
            vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source           1..1591
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
                     /db_xref="taxon:9031"
                     /clone="CHEST117m23"
                     /clone_lib="CSEQCHL24"
                     /dev_stage="16 days"

ORIGIN
Alignment Scores:
Pred. No.:      8,146-83      Length:      1591
Score:          889.00      Matches:    178
Percent Similarity: 97.35%      Conservative: 6
Best Local Similarity: 94.18%      Mismatches: 5
Query Match:    95.49%      Indels:    0
DB:             5          Gaps:      0

US-09-830-972-29_COPY_990_1178 (1-189) x BX934715 (1-1591)

Qy      1  SerValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAla 20
Db      185 TCAGTTGTGTACCTCTTTACTGGCGACACATTAGAAAGACAGGAGTGGTGTGGTGCC 244

Qy      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      245 AGCTTGTTCTCTGCTCTCTATTACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATT 304

Qy      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleAla 60
Db      305 GCCTTGGCCCTCTTCTGTGACCATCAGCTTTAGGATATACAAAGGAGTTATCCAGCA 364

Qy      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      365 ATCCAAAAGTCCGATGAAGGCCCATCCATTAGGCGTTACTTGGAGTCTGTAGTGTG 424

Qy      81  SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db      425 TCTGAAGAGCTGATTACAGAAATACAGCAGTGTGTGCTTGTTCATCATCAACGGCACAGTC 484

Qy      101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db      485 AAGGAGCTGAGACGCGCTCTCTCTGCTTCATGACTTGGTTGATTCTCTGAAGTTGTCAGTG 544

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Qy      121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db      545 TTGATGTGGGTGTTTCACTTACGTGGTGGCTTGTTAATGGTCTGACATTACTGATCTG 604

Qy      141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db      605 GCTTTGATTTCCGTGTTCCAGTGTTCCTGTTATTATGAGAGACATCAGGCCAGATCGAC 664

Qy      161 HisTyrLeuGlyLeuAlaAsnLysAsnValysAspAlaMetAlaLysIleGlnAlaLys 180
Db      665 CATTATTGGGACTAGTGAACAAGAACGTCAAAGATGCGATGGCAAGATCCAGCAAG 724

Qy      181 IleProGlyLeuLysArgLysAlaGlu 189
Db      725 ATCCCTGGGCTGAAGCGCAAACTGAG 751

RESULT 86
AY494005
LOCUS      AY494005          2835 bp      mRNA      linear      VRT 16-FEB-2004
DEFINITION Gallus gallus neurite outgrowth inhibitor NOGO-A (NOGO) mRNA,
            partial cds.
ACCESSION  AY494005
VERSION    AY494005.1  GI:42528324
KEYWORDS
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE  1 (bases 1 to 2835)
            Caltharp, S.A., Pira, C.U., McNeill, D.S., Liwnicz, B.H. and Oberg, K.C.
            Expression and Regulation of NOGO-A During Development of the Avian
            Central Nervous System
            Unpublished
            JOURNAL
            REFERENCE 2 (bases 1 to 2835)
            Caltharp, S.A., McNeill, D.S., Pira, C.U. and Oberg, K.C.
            Direct Submission
            TITLE
            JOURNAL
            Submitted (02-DEC-2003) Anatomy, Loma Linda University, 24785
            Stewart St. Evans Hall B09, Loma Linda, CA 92350, USA
FEATURES             Location/Qualifiers
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                     /db_xref="GI:42528325"
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                     KPVTQLCPSEDESEAPSPVLPDIMEAPILSSGTAGAEASTVQLETSGLTFTTASY
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                     FPGKESDQTLILNGKSVENITDEQEERLVDLSLAATGKPYLESFQDELDSKIVTQ
                     PSEPTPAKAKAEKIPLQMBELNALAYSTDVSVAMEPKPGSKGLSPSSPVSVNVEKTV
                     MLVDPKTGTFTFAEVTDTETVHKNSKDIGNIEIRDEKROAPLTLPGLDLSVRNVEKTV
                     EDAHALKKSIOAIDREVPEVSMVSLPATGTSPSSTEKEIVSVCKPEAFKEAERGA
                     SAKEKEPTAFVSKNLNVSSVDLLIYWRDINKTGTVFGASLFLILLSLTVFVSVTAY
                     IALALLSVTISFRIYKGIQAIQKDSGHPFRAYLESADVASELLIKYISVSLIGHIN
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ORIGIN

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Db      1288 CCTGGATTGAAGCGCAAGCAGAT 1311
RESULT 88
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LOCUS   BX933922      1363 bp      mRNA      linear      VRT 02-FEB-2004
DEFINITION Gallus gallus finished cDNA, clone CHEST1198.
ACCESSION BX933922
VERSION  BX933922.1 GI:41634450
KEYWORDS Gallus gallus (chicken)
SOURCE  Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1363)
AUTHORS Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V.,
Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
Tickle,C. and Wilson,S.A.
DIRECT SUBMISSION
Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickens@bms.unist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Elizabeth Bosch. cDNA was prepared
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI
cut cDNA was then ligated into the vector. Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9031"
/clone="CHEST1198"
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ORIGIN
Alignment Scores:
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Score: 885.00 Matches: 177
Percent Similarity: 97.34% Conservative: 6
Best Local Similarity: 94.15% Mismatches: 5
Query Match: 95.06% Indels: 0
DB: 5 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BX933922 (1-1363)

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Db      177 GTTGTGTACCTCTTACTTGGCGAGACATTAAAGACAGAGGTGGTGTGGTCCAGC 236
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41
Db      237 TTGTTCTCGCTGCTCTCAATTAACAGTGTTCAGCATCGTGAGCGTACACATTCCTGCC 296
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyRysGlyValIleGlnAlaIle 61
Db      297 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTATCCAGGCATC 356
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyRLeuGluSerGluValAlaIleSer 81
Db      357 CAAAGTCCGATGAAGGCGCATCCATTAGGGCTTACTTGGAGTCTGTAGTGTGTCT 416
Qy      82 GluGluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      417 GAAGAGCTGATTGAGAAATACAGACAGTGTGTGCTTGTGTGCTACATCAACGGCACAGTCAAG 476
Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

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Db      477 GAGCTGAGACGCCCTCTCTCTGTTGATGCTTCTCTGAAGTTTGACGTGTTG 536
Qy      122 MetTrpValPheThrTyRValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141
Db      537 ATGTGGGTGTTTCACTTACGTGGTGGCTTGTATATGTTTATGATCTGACATTACTGATCGGT 596
Qy      142 LeuIleSerLeuPheSerValProValIleTyRGlueArgHisGlnAlaGlnIleAspHis 161
Db      597 TTGATTTCCGCTGTTCAAGTTCCTGTTTATTTATGAGACATCAGGCCAGATCGACCAT 656
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      657 TATTTGGGAGTAGTGAACAAGAACTCAAGATGCGTGGCAAGATCAACGCAAGATC 716
Qy      182 ProGlyLeuLysArgLysAlaGlu 189
Db      717 CCTGGCTGAAGCGCAAACTGAG 740
RESULT 89
CR353502
LOCUS   CR353502      1578 bp      mRNA      linear      VRT 11-MAR-2004
DEFINITION Gallus gallus finished cDNA, clone CHEST12704.
ACCESSION CR353502
VERSION  CR353502.1 GI:45424789
KEYWORDS Gallus gallus (chicken)
SOURCE  Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1578)
AUTHORS Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V.,
Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
Tickle,C. and Wilson,S.A.
DIRECT SUBMISSION
Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickens@bms.unist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Elizabeth Bosch. cDNA was prepared
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI
cut cDNA was then ligated into the vector. Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B.
FEATURES
Location/Qualifiers
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/organism="Gallus gallus"
/mol_type="mRNA"
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/db_xref="taxon:9031"
/clone="CHEST12704"
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/dev_stage="adult"

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Alignment Scores:
Pred. No.: 2.1e-82 Length: 1578
Score: 885.00 Matches: 177
Percent Similarity: 97.34% Conservative: 6
Best Local Similarity: 94.15% Mismatches: 5
Query Match: 95.06% Indels: 0
DB: 5 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CR353502 (1-1578)

Qy      2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      174 GTTGTGTACCTCTTACTTGGCGAGACATTAAAGACAGAGGTGGTGTGGTCCAGC 233

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QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
|
|
|
Db 294 TTGGCCCTGCTTCTCTGTGACCATCAGCTTTAGGATATACAGGAGGTTATCCAGGCAATC 353
|
|
|
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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|
|
Db 354 CAAAGTCCGATGAAGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTGCTGTCT 413
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|
|
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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|
|
Db 414 GAAGAGCTGATTTCAGAAATACAGCAGTGTGTGTCATCAACGCGCAGTCAAG 473
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|
|
QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db 474 GAGCTGAGAGCGCTCTCTCGTTGATGACTTGTGTTGATCTCTGAGGTTGCGAGTGTG 533
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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
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Db 534 ATGTGGGTGTTCATTACGTGTGCTGCTGCTGTTTAAATGTCAGACATTACTGATCTGGCT 593
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QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
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Db 594 TTGATTTCGCTGTTCAGTGTCTCTCGTTGATGACTTGTGTTGATCTCTGAGGTTGCGAGTGTG 653
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QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Db 654 TATTGGGACTAGTGAACAGAACGTCAAAGATGCGATGGCAAGATCCAGCAAGATC 713
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QY 182 ProGlyLeuLysArgLysAlaGlu 189
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Db 714 CCTGGGCTGAAGCGCAAACTGAG 737
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RESULT 90
AY164737 1597 bp mRNA linear VRT 30-JUN-2003
LOCUS Gallus gallus RTN4-C (RTN4) mRNA, complete cds.
DEFINITION
ACCESSION AY164737
VERSION AY164737.1 GI:32331274
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE
AUTHORS Certie,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
TITLE A reticular rhapsody: phylogenic evolution and nomenclature of the RTN/Nogo gene family
JOURNAL RTN/Nogo
PUBMED 12832288
REFERENCE
AUTHORS Certie,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Zurich 8057, Switzerland
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3'UTR
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Score: 882.00 Matches: 176
Percent Similarity: 97.34% Conservative: 7
Best Local Similarity: 93.62% Mismatches: 5
Query Match: 94.74% Indels: 0
DB: 5 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AY164737 (1-1597)

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Db 159 GTTGTGACCTCCTTTACTGGCGAGACATTAAGAGACAGGAGTGTGTGTCGCCAGC 218
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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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|
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Db 219 TTGTTCTGCTCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTCGC 278
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QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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Db 279 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGTGTATCCAGGCAATC 338
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|
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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Db 339 CAAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTGGAGTCTGATGTGTGTCT 398
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
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Db 399 GAAGACCTGATTACAGAAATACAGCAGTGTGTGTCATCATCAACGCGCAGTCAAG 458
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QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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|
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Db 459 GAGCTGAGAGCGCTCTTCTCTGATGACTTGTGTTGATCTCTGAAGTTTCAGTGTG 518
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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141
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Db 519 ATGTGGGTCTTCACCTACCTGCTGCTGCTTTAAATGCTGACATTTACTGATCTGCT 578
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QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
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Db 579 TTGATTTCGCTGTTTCTGATGTTTCTGTTTATGAGAGACATCAGGCCCGCAGTCCGACCAT 638
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QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Db 639 TATTGGGACTAGTGAACAAAGACGTCAAAGATGCGATGGCAAGATCCAAAGCAAGATC 698
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QY 182 ProGlyLeuLysArgLysAlaGlu 189
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Db 699 CCTGGGCTGAAGCGCAAAACTGAG 722
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RESULT 91
AY1616195 3967 bp mRNA linear VRT 25-MAY-2004
LOCUS Xenopus laevis RTN4.1-A3 (RTN4) mRNA, complete cds; alternatively
DEFINITION spliced.
ACCESSION AY1616195
VERSION AY1616195.1 GI:34809221
KEYWORDS
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.

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REFERENCE
AUTHORS      1 (bases 1 to 3967)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
TITLE        Identification of two NOGO/RTN4 genes and analysis of Nogo-A
JOURNAL      Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
PUBMED       15019938
REFERENCE    2 (bases 1 to 3967)
AUTHORS      Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
              Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
              Stuermer,C.A.O.
TITLE        Direct Submission
JOURNAL      Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
              Universitaetstrasse 10, Konstanz 78457, Germany
FEATURES
source       Location/Qualifiers
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              SKGHAETVAFTGLAATEALQEPDNNYSVRSITSLPLSDNLESKALDQKEVIF
              SEKGVVDPHTSQGETTSEEKALYSQSAKEMFSCMLQSVAPPHEEFTDIKEVDYV
              DFKEPMSKSGVGVSDVAEKQVDVGRNLRSVAKHEKSEMEIDSIDDISP
              LTPELLPSTDYDMFATVEONI PFSGGSHVAGNKTDEKKTIDEAKQTSVFGGLKVA
              TVNPFNSAESESVVTHVATHYSTKPEGTPDIVEAYSEAYDGIPIQKYESNI
              DLVQTAANSVEKSPVTAQPARLEETDSSVPDIVEAPLASLETVALKPDIS
              PVGKPPARVEKTAPEKPPSEYEAVTEVLQNDLAAALGSKQGAVERETPYIS
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              GLTLLOKPKLOMELDGLSLEKTPCTKYSPVSEPEPSPVPEDLSSKLGIOKE
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Score: 781.00 Matches: 151
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Best Local Similarity: 79.89% Mismatches: 18
Query Match: 83.89% Indels: 0
DB: 5 Gaps: 0
US-09-830-972-29_copy_990_1178 (1-189) x AY316195 (1-3967)

Qy      1 SerLeuValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db      2616 TCAGTTGTGCAGCTTATTACTGCGGACATTAAGAGATCCGGAGTGGTGTGGGGCA 2675
Qy      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

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QY 161 HistyLeuGlyLeuAlaAnlyAsnVallyAspAlaMetAlaLyslleGlnAlaLys 180
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QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3249 GTTCCGGGCTGAACGCAAGCTGAA 3275

RESULT 94
LOCUS AY316191
DEFINITION Xenopus laevis RTN4.1-N (RTN4) mRNA, complete cds; alternatively
spliced.
ACCESSION AY316191
VERSION AY316191.1 GI:34809213
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis
Xenopus laevis (African clawed frog)

REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
AUTHORS Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
TITLE Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
JOURNAL Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
PUBMED 15019938
REFERENCE
2 (bases 1 to 1467)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
Stuermer,C.A.O.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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Location/Qualifiers
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Alignment Scores:
Pred. No.: 2,61e-71 Length: 1467
Score: 778.00 Matches: 150
Percent Similarity: 90.48% Conservative: 21
Best Local Similarity: 79.37% Mismatches: 18
Query Match: 83.57% Indels: 0
DB: 5 Gaps: 0

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaThrIle 40
Db 193 AGCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 252
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrGlyValIleGlnAla 60
Db 253 GCCCTGGCCCTCTCTCCGTCCACCATCTTAAGGATATACAAAGGGATTCTGCAGGCC 312
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 313 ATCCAGAGTTCAGAGGAGGACACCATTCAGATCCATCTTGGAGTCCAACTGGCGGTG 372
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 373 CCAGAGGATCTGGTCCAGAAATACTGCAATGTGGCCCTGAACCATGTCAACTGCACAGTC 432
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 433 AAGGAGCTCGGCACCTCTCTCTTGTAGAAGACCTGGTGGATTCCTCTGAAGTTTCAGTA 492
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 493 TTGATGTGGGTCTTACCTATATTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 552
QY 141 AlaLeuileSerLeuPheSerValProValileTyrGluArgHisGlnAlaGlnileApp 160
Db 553 GCACGTATTTCCTGTTTCAGTATTCCTGTCATTTATGAAGGCATCAGACTCAAGTGGAT 612
QY 161 HistyLeuGlyLeuAlaAnlyAsnVallyAspAlaMetAlaLyslleGlnAlaLys 180
Db 613 CACTACCTGGCACTCGTAACAAGATCTCAAGAGCACATCAGACCTGATTCCTCTCTAAA 672
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 673 GTTCCGGGCTGAACGCAAGCTGAA 699

RESULT 95
LOCUS AY316193
DEFINITION Xenopus laevis RTN4.1-B2 (RTN4) mRNA, complete cds; alternatively
spliced.
ACCESSION AY316193
VERSION AY316193.1 GI:34809217
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 1758)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
TITLE Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
JOURNAL Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
PUBMED 15019938
REFERENCE
2 (bases 1 to 1758)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
Stuermer,C.A.O.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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Location/Qualifiers
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3'UTR

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Alignment Scores:
Pred. No.: 3,266-71 Length: 1758
Score: 778.00 Matches: 150
Percent Similarity: 90.48% Conservative: 21
Best Local Similarity: 79.37% Mismatches: 18
Query Match: 83.57% Indels: 0
DB: 5 Gaps: 0

US-09-830-972-29_copy_990_1178 (1-189) x AV316193 (1-1758)

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 484 AGCTTGTTCCTCCTCTCTCTGAGTGTGTTCAGTATGTTCAGGTGCTGCTTATATT 543
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 544 GCCTTGGCCCTGCTCTCCGTCACCATCAGTTTAAAGGATATACAAAGGAGTCTGCAGGCC 603
QY 61 IleGlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 604 ATCCAGAAAGTCAGAGGAAGGACCCATTCAGATCCATCTTGGAGTCCCAACCTGCGCGTG 663
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100
Db 664 CCAGAGGATCGTTCAGAAATACATGCAATGTGGCCCTGAACCATGTCACTGCACAGTC 723
QY 101 LysGluLeuArgArgLeuPheLeuValAlaAspLeuValAspSerLeuLysPheAlaVal 120
Db 724 AAGGAGTGGCGCACCTCTTCCTCTGAGAAGACCTGGTGGATTCCTCAAGTTTGCAGTA 783
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MGC.  
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 1512)  
Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.  
and Richardson, P.  
Genetic and genomic tools for Xenopus research: The NIH Xenopus  
Initiative  
Dev. Dyn. 225 (4), 384-391 (2002)  
12454917  
2 (bases 1 to 1512)  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
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Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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3 (bases 1 to 1512)  
Klein, S. and Strausberg, R.  
Direct Submission  
Submitted (10-OCT-2003) National Institutes of Health, Xenopus Gene  
Collection (XGC), National Institute of Child Health and Human  
Development, 6100 Executive Boulevard, Room 4801, Rockville, MD  
20892-7510, USA  
NIH-MGC Project  
Contact: XGC help desk  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Igor Dawid  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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VERSION	AY316192.1		
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ORGANISM	Xenopus laevis		
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AUTHORS	1 (bases 1 to 1543) Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrusch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.		
TITLE	Identification of two NOGO/RTN4 genes and analysis of Nogo-A expression in Xenopus laevis		
JOURNAL	Mol. Cell. Neurosci. 25 (2), 205-216 (2004)		
PUBMED	15019938		
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AUTHORS	Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von Hanwehr,S., Petrusch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.O.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz, Universitaetsstrasse 10, Konstanz 78457, Germany		
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Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von
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Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
JOURNAL
PUBMED
15019938
REFERENCE
2 (bases 1 to 3886)
Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von
Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and
Stuermer, C.A.O.
Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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AY316190.1 GI:34811716
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Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von
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Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
JOURNAL
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15019938
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2 (bases 1 to 3943)
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x AV316190 (1-3943)

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QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2708 AGCTTGTCTCTCTACTGCTCTGAGTGTGTGAGTATTGTCTGAGTACTCGCTTATATT 2767  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 2768 GCCCTGGCCCTGCTCTCCGTCACCATCAGCTTTAGGATATACAAAGGGTTCTACAGGCC 2827  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
Db 2828 ATCCAGAAGTCTCAGGAAGACACCCATTTCAGGTCCATCTTGGAGTCCAACCTGGCGCTG 2887  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 2888 CCGGAGGACGTGGTCCAGAAACACTGCACCGTGGCCCTGAATCAGGTCAATCCACAGTC 2947  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 2948 GCTGAGCTCGGGCGCTCTTCTCGTAGAAGACTTGGTGGATTCCCTCAAGTTTGCAGTA 3007  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3008 TTGATGTGGGTCTTCATCTATATATCGGTGCTCTTTAATGGCCCTGACCTCTCATTTGTG 3067  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
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Db 3068 GCTCTCATTTCCCTGTTCCAGTATTCTGTATTATGAAGGCATCAGACTCAAGTGGAT 3127  
QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3128 CACTATCTGGCGCTGATRAACAAGAACCCTGAAAAATACTTTCAGACCTGATTTTGGCTAAA 3187  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3188 GTCCCGGGGCTGAAGCGCAAAATCAGAA 3214
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Search completed: June 19, 2005, 08:52:40  
Job time : 2797 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 04:27:16 ; Search time 354 Seconds  
(without alignments)  
3160.540 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SWBLLYWRDIKKTGVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq\_16Dec04:\*

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2: geneseqn1990s:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	100.0	3579	3 AAZ56886	AAZ56886 Human MAG
2	931	100.0	3579	4 AAF90324	AAF90324 Human NOG
3	931	100.0	3579	6 ABK90134	ABK90134 DNA encod
4	931	100.0	3579	6 ABN86601	ABN86601 Human neu
5	931	100.0	3579	12 ADO07886	ADO07886 Human pol

6	931	100.0	3579	12 ADR13965	ADR13965 Human NOG
7	931	100.0	3833	3 AAD01174	AA011174 Bovine ne
8	931	100.0	3919	12 ADP45550	ADP45550 Human Nog
9	931	100.0	4053	4 AAS09453	AAS09453 Human cDN
10	931	100.0	4053	9 ACC81048	ACC81048 Human NOG
11	931	100.0	4053	12 ADP13574	ADP13574 Renal cel
12	931	100.0	4093	3 AAA23454	AA23454 cDNA enco
13	931	100.0	4632	6 ABV94680	ABV94680 Human pan
14	931	100.0	4632	10 ADG32772	ADG32772 Human DNA
15	931	100.0	4698	8 ABX34563	ABX34563 Human modd
16	931	100.0	4789	13 ADR83534	ADR83534 Human ret
17	931	100.0	4822	6 ABS70449	ABS70449 Human bon
18	928	99.7	1758	4 AAF32725	AAF32725 Human sec
19	927	99.6	600	4 AAF90323	AAF90323 Human NOG
20	927	99.6	770	3 AAF72983	AAF72983 Human NSP
21	927	99.6	799	2 AAV23695	AAV23695 Human NSP
22	927	99.6	1122	3 AAZ56888	AAZ56888 Human MAG
23	927	99.6	1122	4 AAF90325	AAF90325 Human NOG
24	927	99.6	1213	2 AAX04379	AAX04379 Human sec
25	927	99.6	1216	6 ABA05903	ABA05903 Human RTN
26	927	99.6	1599	10 ADI62860	ADI62860 Human apo
27	927	99.6	1610	3 AAZ36230	AAZ36230 cDNA enco
28	927	99.6	1785	12 ADK14166	ADK14166 Human aut
29	927	99.6	2052	6 ABK90133	ABK90133 DNA encod
30	927	99.6	2235	6 ABV94681	ABV94681 Human pan
31	927	99.6	2240	3 AAC64406	AAC64406 Human Nog
32	923	99.1	1694	4 AAX94408	AAX94408 Human ful
33	923	99.1	1694	12 ADL31137	ADL31137 Full leng
34	921	98.9	1980	4 AAI98079	AAI98079 Human neu
35	918	98.6	991	2 AAX97587	AAX97587 Extended
36	918	98.6	994	12 ADP18854	ADP18854 Human sec
37	914	98.2	2610	11 ADI31056	ADI31056 Human cDN
38	911	97.9	734	12 ADP42781	ADP42781 Mouse CYP
39	908	97.5	3492	12 ADP45571	ADP45571 Rat NogoA
40	908	97.5	4684	3 AAD01173	AA011173 Rat neuroi
41	908	97.5	4684	6 ABN86600	ABN86600 Rat neuro
42	905	97.2	2782	10 ADB85284	ADB85284 Rat foocce
43	904.5	97.2	3492	12 ADO07888	ADO07888 Mouse pol
44	904	97.1	1568	3 ADO01175	AA011175 Rat neuroi
45	894.5	96.1	2386	2 AAV30920	AAV30920 Human sec

#### ALIGNMENTS

RESULT 1  
AAZ56886  
ID AAZ56886 standard; DNA; 3579 BP.  
XX  
AC AAZ56886;  
XX  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human MAGI polypeptide encoding DNA.  
XX  
KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
KW psychiatric disorder; developmental disorder; inflammatory disorder;  
KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3579  
FT /\*tag= a  
FT /product= "MAGI polypeptide"  
XX  
XX  
PN WO200005364-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 21-JUL-1999; 99WO-GB002360.  
XX  
PR 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Michalovich D, Prinjha RK;  
 XX WPI; 2000-182693/16.  
 DR P-PSDB; AAY56967.  
 XX Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 treatment of cancer and neurological disorders.  
 XX Claim 5; Page 19-20; 35pp; English.  
 XX The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein  
 XX  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ56886 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3010 TCAGTGTGTTACCTCTCTGTACTGAGAGACATTAAGAAGACTGGAGTGTGTGTGGTGC 3069  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3070 AGCCTATTCTGCTGCTTTTCATTGACAGTATTGAGCATTTGTGAGCGTAACAGCCTACATT 3129  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGCATATACAAGGGTGTGATCCAAGCT 3189  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGTCTATA 3249  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 3250 TCTGAGGAGTGTGTTGAGAGTACAGTAATCTCTGCTTGTGATGTAAGTCCACGATA 3309  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3310 AAGGAATCAGGCGCCTCTCTTAGTTGATGATTAGTTGATTTCTGAGTTTGCAGTG 3369  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 3370 TTGATGTGGGTATTACCTATGTTGGTGCCTTCTTTAATGGTCTGACACTACTGATTTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3430 GCTCTCATTTCACTCTTCAGTGTTCTCTGTTATTATGAAGCGCATCAGGCGCAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3490 CATTATCTAGGACTTGCATAATAAGATGTTTAAAGATGCTATGCTTAAATCCCAACAAA 3549

QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
 RESULT 2  
 AAF90324  
 ID AAF90324 standard; cDNA; 3579 BP.  
 XX AAF90324;  
 XX 23-JUL-2001 (first entry)  
 XX Human NOGO-A cDNA.  
 XX NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.  
 XX Homo sapiens.  
 XX WO200136631-A1.  
 XX 25-MAY-2001.  
 XX 14-NOV-2000; 2000WO-GB004345.  
 XX 15-NOV-1999; 99GB-00026995.  
 PR 24-JAN-2000; 2000GB-00001550.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Michalovich D, Prinjha R;  
 XX WPI; 2001-343822/36.  
 DR P-PSDB; AAB82349.  
 XX New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.  
 XX Disclosure; Page 25-26; 25pp; English.  
 CC The present sequence is that of cDNA encoding human NOGO-A (see  
 CC AAB82349). NOGO-A is a previously known splice variant of the human NOGO  
 CC gene on chromosome 2p21. NOGO-A cDNA was obtained by PCR amplification of  
 CC human spinal cord cDNA. The invention relates to a novel splice variant,  
 CC NOGO-C (see AAF90323). It provides NOGO-C polypeptides and  
 CC polynucleotides, and methods for producing such polypeptides by  
 CC recombinant techniques. Also disclosed are methods for utilizing NOGO-C  
 CC polypeptides and polynucleotides in the treatment of diseases including  
 CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
 CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
 CC disorders, psychiatric disorders and developmental disorders. Also  
 CC provided are methods for identifying agonists and antagonists for use in  
 CC treating conditions associated with NOGO-C imbalance, and diagnostic  
 CC assays for detecting diseases associated with inappropriate NOGO-C  
 CC activity or levels  
 XX Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF90324 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

Db 3010 TCAGTTGTTGACCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC 3069  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40  
Db 3070 AGCCATTATCTCTGCTCTTCATTCAGACATTAATCAGCATTTGAGCGTAACAGCCTACATTT 3129  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlleGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 3189  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrlleLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATCAAGCCACCCATTCAGGCGATATCTGGAATCTCAAGTTGCTATA 3249  
Qy 81 SerGluGluLeuValGlnLysTyrlleSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3250 TCTGAGGAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTTCATGTGAAGTTCACGATA 3309  
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAATCAGCGGCTCTCTTCTAGTGTGATGATTAGTTGATCTCTCAAGTTTGCATG 3369  
Qy 121 LeuMetTrpValPheThrTyrlleValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3370 TTGATGGGTATTATACCTATGCTGGTCTGCTGTTGTTAATGGTCTGACACTACTGATTTTG 3429  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrlleGluArgHisGlnAlaGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGCGCGAGATAGAT 3489  
Qy 161 HisTyrlleGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATATCTAGGACTTGCATTAAGATGTTAAAGATGCTATGGCTAAATCCNAGCAAAA 3549  
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
RESULT 3  
ID ABK90134 standard; DNA; 3579 BP.  
XX AC ABK90134;  
XX AC  
XX DT 21-OCT-2002 (first entry)  
XX DE DNA encoding human NogoA protein.  
XX KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hyper trophy; central nervous system; axon regeneration; NogoA;  
KW Nogo-associated disease; metastasis; gene; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 1..3579  
FT FT /\*tag= a  
FT FT /product= "Human NogoA protein"  
XX  
XX WO200257483-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 18-JAN-2002; 2002WO-GB000228.  
XX  
XX 18-JAN-2001; 2001GB-00001312.  
XX (GLAX ) GLAXO GROUP LTD.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Blackstock WP, Hale RS, Prinjha R, Rowley A;  
XX WPI, 2002-599722/64.  
XX P-PSDB; ABG30938.  
PT Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprising  
PT providing and monitoring interaction between Nogo and BACE polypeptides.  
XX  
XX Disclosure; Page 53-58; 69pp; English.  
XX  
XX The present invention relates to a new method of identifying modulators  
XX of Nogo function or BACE activity. The method involves providing Nogo and  
XX BACE polypeptides capable of binding with each other, monitoring the  
XX interaction between these polypeptides, and determining if the test agent  
XX is a modulator of Nogo or BACE activity. The method is useful in treating  
XX acute neuronal injuries, such as spinal or head injury, stroke,  
XX peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
XX neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
XX cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
XX hypertrophy) of the central nervous system. The BACE polypeptide is  
XX useful in screening methods to identify agents that may act as modulators  
XX of BACE activity and in particular agents that may be useful in treating  
XX Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
XX and the polynucleotide encoding the BACE polypeptide are useful in  
XX manufacturing a medicament for the treatment or prevention of disorders  
XX responsive to the modulation of Nogo activity, in alleviating the  
XX symptoms or improving the condition of a patient suffering from this  
XX disorder, in axon regeneration, or in preventing metastasis or spreading  
XX of a cancer. The polynucleotide may also be an essential component in  
XX assays, a probe, in recombinant protein synthesis, and in gene therapy  
XX techniques. The present nucleic acid sequence encodes the human NogoA  
XX protein of the invention  
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1,01e-102 Length: 3579  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABK90134 (1-3579)  
Qy 1 SerValValAspLeuLeuTyrlleTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC 3069  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40  
Db 3070 AGCCATTATCTCTGCTCTTCATTCAGACATTAATCAGCATTTGAGCGTAACAGCCTACATTT 3129  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlleGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 3189  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrlleLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATCAAGCCACCCATTCAGGCGATATCTGGAATCTCAAGTTGCTATA 3249  
Qy 81 SerGluGluLeuValGlnLysTyrlleSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3250 TCTGAGGAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTTCATGTGAAGTTCACGATA 3309  
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAATCAGCGGCTCTCTTCTAGTGTGATGATTAGTTGATCTCTCAAGTTTGCATG 3369  
Qy 121 LeuMetTrpValPheThrTyrlleValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140



RESULT 5  
 ADO07886  
 ID ADO07886 standard; cDNA; 3579 BP.  
 XX  
 AC ADO07886;  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human polynucleotide #65.  
 XX  
 KW Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 KW anorectic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2004071700-A1.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 09-OCT-2002; 2002US-00267502.  
 XX  
 PR 09-OCT-2002; 2002US-00267502.  
 XX  
 PA (LIFE-) LIFE SCI DEV CORP.  
 XX  
 PI Kim J, Galant R;  
 XX  
 DR WPI; 2004-328526/30.  
 DR P-PSDB; ADO08103.  
 XX  
 PT Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX  
 PS Claim 1; SEQ ID NO 212; 275pp; English.  
 CC  
 CC The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC polypeptide or a change in an activity of the polypeptide, treating a  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC human cDNA used in the scope of the invention.  
 XX  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADO07886 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 DB TCAGTTGTTGACCTCTCTACTGGAGACACATTAAAGACATGGAGTGGTGTGGTGC 3069  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 40  
 DB AGCCTATTCTCTGCTCTTTCATTGACAGTATTTCAGCAATTGTGAGCGTAAACAGCTACATT 3129  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCAAGCT 3189  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB ATCCAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGATCTGAAGTTGCTATA 3249  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACCTGCACGATA 3309  
 QY 101 LysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB AAGGAACCTCAGCGCCCTCTCTTAGTTCATGATTTAGTTGATTTCTCTGAAGTTTCAGAG 3369  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB TTGATGGGTATTACCTATGTTGGTCTCTTTAATGTTCTGACACTACTGATTTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB GCTCTCAATTCCTCTTCAAGTCTCTCTGTTATTTATGAACGCATCAGCGCGCAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB CATTATCTAGACATTCGCAATTAAGAATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 3549  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
 RESULT 6  
 ADR13965  
 ID ADR13965 standard; cDNA; 3579 BP.  
 XX  
 AC ADR13965;  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human NOGO-A cDNA.  
 KW ss; gene; human; myelin-associated glycoprotein; MAG; neural growth;  
 KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW multiple sclerosis; Creutzfeldt-Jacob disease; kuru;  
 KW multiple system atrophy; Lou Gehrig's disease;  
 KW progressive supranuclear palsy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..3579  
 FT /\*tag= a  
 FT /product= "NOGO-A"  
 XX  
 FN US2004121341-A1.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 20-DEC-2002; 2002US-00327213.  
 XX  
 PR 20-DEC-2002; 2002US-00327213.  
 XX  
 PA (FILB/) FILBIN M T.

PA (DOME/) DOMENICONI M.  
 PA (CAOZ/) CAO Z.  
 PI Filbin MT, Domeniconi M, Cao Z;  
 XX  
 XX  
 DR WPI; 2004-479666/45.  
 DR P-PSDB; ADR13966.  
 XX  
 XX  
 PT New myelin-associated glycoprotein (MAG) derivative comprises a mutation  
 PT in or flanking MAG Ig-like domain 5 (Igds), excluding the MAG derivative  
 PT MAG (dl-3)-Fc, useful promoting neural growth and regeneration.  
 XX  
 XX  
 PS Disclosure; SEQ ID NO 8; 81pp; English.  
 XX  
 XX  
 CC The invention relates to a myelin-associated glycoprotein (MAG)  
 CC derivative comprising a mutation in or flanking MAG Ig-like domain 5  
 CC (Igds), excluding the MAG derivative MAG (dl-3)-Fc, where the mutation  
 CC reduces or eliminates the ability of the derivative to regulate neurite  
 CC outgrowth as compared to endogenous or soluble MAG without eliminating  
 CC binding to neuronal surfaces. The inhibitors of MAG are useful for  
 CC promoting neural growth and regeneration. They are also useful for  
 CC treating neural degeneration associated with injuries, disorders, or  
 CC diseases. The disorder, disease, or condition is associated with  
 CC apoptosis or results from a demyelinating disease and includes  
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,  
 CC Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease,  
 CC kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou  
 CC Gehrig's disease), or progressive supranuclear palsy. The present  
 CC sequence represents the human NOGO-A cDNA.  
 XX  
 XX  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR13965 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3010 TCAGTTGTTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGTTGCTGCC 3069  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3070 AGCTTATTCCTGCTGCTTTTCATTCAGACAGTATTCAGCATTTGTGAGCGTACAGCTACATT 3129  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlyGlyValIleGlnAla 60  
 DB 3130 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCT 3189  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleLeuGluSerGluValAlaIle 80  
 DB 3190 ATCCAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 3250 TCTGAGAGTTGGTTTTCAGAAAGTACAGTAATTCCTGCTTGTGCTGATGACTGCACGATA 3309  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3310 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTGCAGTG 3369  
 QY 121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 3370 TTGATGGGTATTTACCTATGTTGTGGCTCTTTTAATGGTCTGACACTACTGATTTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3430 GCTCTCATTTTCATCTCTTCAGTGTCTCTGTTTATTTATGACGGCATCAGGCGCAGATGAT 3489

QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGCTAAATAATCCAAGCAAA 3549  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
 RESULT 7  
 AAD01174  
 ID AAD01174 standard; cDNA; 3833 BP.  
 XX  
 XX  
 AC AAD01174;  
 XX  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Bovine neurite growth inhibitor Nogo cDNA.  
 XX  
 KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; ss.  
 OS Bos sp.  
 XX  
 XX  
 PN WO2000031235-A2.  
 XX  
 XX  
 PD 02-JUN-2000.  
 XX  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 XX (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Claim 26; Fig 12; 122pp; English.  
 XX  
 CC The present sequence is a cDNA encoding bovine Nogo protein which is a  
 CC potent neural cell growth inhibitor and is free of all central nervous  
 CC system (CNS) myelin material with which it is natively associated. The  
 CC present sequence was obtained from bovine spinal cord white matter cDNA  
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory  
 CC activity are used in the treatment of neoplastic disease of the CNS e.g.  
 CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,  
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,  
 CC meningioma, neuroblastoma or retinoblastoma and degenerative nerve  
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which  
 CC promote Nogo activity can be used to treat or prevent hyperproliferative  
 CC or benign dysproliferative disorders e.g. psoriasis and tissue  
 CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to  
 CC inhibit production of Nogo protein to induce regeneration of neurons or  
 CC to promote structural plasticity of the CNS in disorders where neurite  
 CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers  
 XX  
 XX  
 SQ Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.: 1,12e-102 Length: 3833
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AAD01174 (1-3833)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 2301 TCAGTTGTTGACCTCTCTACTCGAGAGACATTAGAAGACTGGAGTGGTGTGGTGCC 2360
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 2361 AGCTTGTTCCTGCTCTCTCGCTGACGATTTACGATTTGAGGTGAACGGCTTACATT 2420
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 2421 GCCTTGGCCCTGCTCTCTGTGACTATCATGCTTTAGGATATATAGGGTGTGATCCAGGCT 2480
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 2481 ATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATA 2540
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 2541 TCTGAGGAGTGGTTCAGAAAGTACAGCAATTTCTGCTTGTGTCATGTTAACTGCACAAATA 2600
Qy 101 LysGluLeuAlaArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 2601 AAAGAACTCAGACGCTCTCTTAGTTCATGATTTAGTTGATTTCTGAAAGTTGCAGTG 2660
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 2661 TTGATGTGGTATTTACCTATGTTGGTGCCTTGTTCATAGTCTGCACACTACTAATTTTG 2720
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 2721 GCTCTGATTTCACTCTTCAGTGTTCCTGCTGTTATTTATGAACGGCATTCAGCGCAATAGAT 2780
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 2781 CATATCTGGACTGGCAAAATAGATGTTTAAAGATGCTATGGCTTAAATTCAGCAAAA 2840
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 2841 ATCCCTGGATTGAAGCGTAAAGCTGAA 2867

RESULT 8
ID ADP45550 standard; cDNA; 3919 BP.
AC ADP45550;
XX
XX
DT 09-SEP-2004 (first entry)
DE Human NogoA encoding cDNA SEQ ID NO:4.
KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
KW nerve repair; neuroprotective; gene therapy;
KW central nervous system injury; CNS injury; neurodegenerative disorder;
KW gene; ss.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH 1..3579
FT CDS
FT /*tag= a
FT /product= "NogoA"
XX
```

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PN WO2004052932-A2.
XX
XX 24-JUN-2004.
XX
XX 09-DEC-2003; 2003WO-EP013960.
XX
XX 10-DEC-2002; 2002GB-00028832.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS PHARMA GMBH.
XX (UYZU-) UNIV ZUERICH.
XX
XX Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
XX Zurini M;
XX
XX WPI; 2004-468818/44.
XX P-FSDB; ADP45551.
XX
XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
XX D20 or NogoA623-640, useful in preparing a composition for treating CNS
XX injury or neurodegenerative disorders.
XX
XX Example 1; SEQ ID NO 4; 121pp; English.
XX
XX The present invention describes a binding molecule which binds to human
XX NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a
XX dissociation constant of less than 1000nM. Also described: (1) a
XX polynucleotide encoding the binding molecule; (2) an expression vector or
XX system comprising the polynucleotide; (3) a host cell comprising the
XX expression system; (4) a pharmaceutical composition comprising the
XX binding molecule and a carrier or diluent; and (5) treating diseases
XX associated with nerve repair. The binding molecule has neuroprotective
XX activity, and can be used in gene therapy. The binding molecule is useful
XX in preparing a composition for treating central nervous system (CNS)
XX injury or neurodegenerative disorders. The present sequence encodes human
XX NogoA, which is used in the exemplification of the present invention.
XX
XX Sequence 3919 BP; 1168 A; 857 C; 890 G; 1004 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.: 1,15e-102 Length: 3919
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x ADP45550 (1-3919)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTTGACCTCTCTACTCGAGAGACATTAGAAGACTGGAGTGGTGTGGTGCC 3069
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCTCTGCTCTTTCATTCACAGTATTTCAGCATTTGAGCGTAACAGCCTACATT 3129
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATATCAAGGGTGTGATCCAAGCT 3189
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAAGTTGCTATA 3249
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTGGTTCAGAAAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACCTGCACGATA 3309
Qy 101 LysGluLeuArgArgLeuPheLeuValAspIleValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTACGGCGCCTCTTCTTAGTTGATGATTTAGTTAGTTATCTCTGAAGTTGCAGTG 3369
```







KW ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 135..3713  
 FT /\*tag= a  
 FT /product= "Human NogoA"  
 XX  
 XX WO2003031462-A2.  
 XX  
 XX 17-APR-2003.  
 XX  
 XX 04-OCT-2002; 2002WO-US032007.  
 XX  
 XX 06-OCT-2001; 2001US-00972599.  
 XX  
 XX (UYVA ) UNIV YALE.  
 XX Strittmatter SM;  
 XX  
 XX WPI; 2003-393433/37.  
 XX P-PSDB; ABR59667.  
 XX  
 XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 XX decreasing inhibition of axonal growth by a central nervous system  
 XX neuron, or in treating central nervous system disease, disorder or  
 XX injury, e.g. spinal cord injury.  
 XX  
 XX Disclosure; Page 126-131; 148pp; English.  
 XX  
 XX The invention relates to a novel nucleic acid encoding a polypeptide  
 XX comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 XX human Nogo receptor (NGR) NTLRCT domain), or residues 27-309 of P1 with  
 XX 1-20 conservative amino acid substitutions, and less than a complete CTS  
 XX domain, provided that a partial CTS domain, if present, consists of no  
 XX more than the first 39 consecutive residues. The nucleic acid of the  
 XX invention has neuroprotective activity. The polynucleotide may have a use  
 XX in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 XX axonal growth by a central nervous system (CNS) neuron. The Ngr  
 XX polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 XX dependent signal transduction in the central nervous system neuron may be  
 XX used in treating central nervous system disease, disorder or injury, e.g.  
 XX spinal cord injury. Expression of an Ngr protein may be associated with  
 XX inhibition of axonal regeneration following cranial, cerebral or spinal  
 XX trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 XX monophasic demyelination, encephalomyelitis, multifocal  
 XX leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 XX sequence is used in the exemplification of the invention  
 XX  
 XX SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.21e-102 Length: 4053  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-830-972-29\_copy\_990\_1178 (1-189) x ACC81048 (1-4053)  
 QY 1 SerValValAlaPheLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 DB 3144 TCAGTTGTGACCTCTCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC 3203  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3204 AGCCTATTCTCTGCTCTTTCATTGACAGTATTGACATTGTGAGCTTAACAGCTACATT 3263  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3264 GCCTTGGCCCTGCTCTCTGTGACCATCATGCTTTAGGATATACAGGGTGTGATCCAGCT 3323

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3324 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3383  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 3384 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTCACTGTGAACCTGCAGATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaVal 120  
 DB 3444 AAGGAACCTCAGCGCCCTCTTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3503  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 3504 TTGATGTGGGTATTTTACCTATGTTGGTGCCCTGTTTAATGGTCTGACACTACTGATTTTG 3563  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3564 GCTCTCATTTTCACCTCTTCAGTGTCTCTGTTTATTAATGAACGGCATCAGGCACAGATAGAT 3623  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3624 CATTATCTAGGACTTGCATAATAAGAAATCTTAAAGATGCTATGGCTAAAAATCCAAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710  
 RESULT 11  
 ADP13574  
 ID ADP13574 standard; DNA; 4053 BP.  
 XX  
 AC ADP13574;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Renal cell carcinoma differentially expressed gene #310.  
 XX  
 KW ds; diagnosis; non-blood disease; solid tumor; gene expression;  
 KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
 KW head/neck cancer; differential expression.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004048933-A2.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 21-NOV-2003; 2003WO-US037481.  
 XX  
 PR 21-NOV-2002; 2002US-0427982P.  
 PR 03-APR-2003; 2003US-0459782P.  
 XX  
 PA (AMHP ) WYETH.  
 PA (TWIN/) TWINE N C.  
 PA (BURC/) BURCZYNSKI M E.  
 PA (TREP/) TREPICCHIO W L.  
 PA (DORN/) DORNER A.  
 PA (STOV/) STOVER J A.  
 PA (SLON/) SLONI D K.  
 XX  
 PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
 PI Sloni DK;  
 XX  
 DR WPI; 2004-460799/43.  
 XX  
 PT Diagnosing non-blood disease such as solid tumor, involves comparing  
 PT differential expression profile of specific genes in peripheral blood  
 PT sample of subject with reference expression profile of specific genes.  
 PS Disclosure; SEQ ID NO 310; 350pp; English.  
 XX

CC The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a gene that  
CC is differentially expressed and detected by the method of the invention.  
CC (Note: this sequence is not given as part of the printed specification  
CC but was obtained from WIPO in electronic format at  
CC ftp.wipo./pub/published\_pct\_sequences).

XX SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1-21e-102 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADP13574 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3144 TCAGTGTGTTGACCTCTCTACTGAGAGACATTAAGAGAGTGGTGTGTTGGTGC 3203  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3204 AGCCTATTCTGCTGCTTTTCATGACGATTCAGCATTTGTGAGCGTAACGCTACAT 3263  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCT 3323  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3383  
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenCysThrIle 100  
Db 3384 TCTGAGGAGTTGGTTGAGAGTACAGTAATTCCTCTTGGTCATGTGAAGTCCACGATA 3443  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAATCAGGCGCCTCTCTTAGTGTATGATGATTTAGTTGATCTCTGAAGTTTCAGTG 3503  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3504 TTGATGTGGGTATTACCTATGTTGGTGGCTCTTTTAATGCTGTGACACTACTGATTTTG 3563  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3564 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT 3623  
QY 161 HisTyrLeuGlyLeuAlaAenLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3624 CATATCTAGACTTGCATAATAGATGTTAAGATGCTATGCTGCTAAATCCCAAGCAAAA 3683  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710

RESULT 12  
AAA23454

ID AAA23454 standard; cDNA; 4093 BP.  
XX AAA23454;  
AC 19-JUN-2000 (first entry)  
DT cDNA encoding human secreted protein vb22\_1, SEQ ID NO:63.  
XX Human; secreted protein; cancer; tumour; cardiovascular disorder;  
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
KW neurodegenerative disease; asthma; contraceptive; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT 152..1006  
FT /tag= b  
FT /product= "Clone vb22\_1 ORF2"  
FT 1048..3729  
FT /tag= a  
FT /product= "Human secreted protein vb22\_1"  
XX WO200011015-A1.  
XX 02-MAR-2000.  
XX 24-AUG-1999; 99WO-US019351.  
XX 24-AUG-1998; 98US-0097638P.  
XX 24-AUG-1998; 98US-0097659P.  
XX 09-SEP-1998; 98US-0099618P.  
XX 28-SEP-1998; 98US-0102092P.  
XX 25-NOV-1998; 98US-0109978P.  
XX 23-DEC-1998; 98US-0113645P.  
XX 23-DEC-1998; 98US-0113646P.  
XX 23-AUG-1999; 99US-00379246.  
XX (ALPH-) ALPHAGENE INC.  
XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
XX WPI: 2000-224657/19.  
XX P-PSDB; AA195012, AA195030.  
XX New secreted or transmembrane proteins and polynucleotides encoding them,  
XX useful for treating neurodegenerative disorders, autoimmune diseases and  
XX cancer.  
XX Claim 72; Page 321-322; 357pp; English.  
XX The invention relates to 40 human secreted proteins (AA194981-Y95020),  
XX and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins  
XX of the invention include those that are thought to be only partially  
XX secreted, i.e., transmembrane proteins. The proteins of the invention may  
XX exhibit one or more activities selected from the following: cytokine  
XX activity; cell proliferation; differentiation; immune modulation;  
XX haematopoiesis regulation; tissue growth activity; activin/inhibin  
XX activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
XX activity; anti-inflammatory activity; and tumour inhibition activity. The  
XX proteins may be administered to patients as vaccines, and the nucleotides  
XX may be used as part of a gene therapy regime. Diseases or conditions that  
XX may be treated using the proteins or nucleotides of the invention include  
XX autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
XX diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
XX multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
XX Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
XX allergic reactions such as asthma and anaemia. They may also be used for  
XX treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
XX diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
XX and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
XX activity may additionally be useful as contraceptives. Nucleic acid  
XX sequences of the invention may be used in chromosome mapping, and as a

CC source of diagnostic primers and probes. The present sequence represents  
 CC cDNA encoding one of the 40 proteins of the invention  
 XX  
 SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.22e-102 Length: 4093  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAA23454 (1-4093)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLeuValValPheGlyAla 20  
 Db 3160 TCAGTGTGTGACCTCTCTGCTGAGGACATTAAGAAGACTGGAGTGGTGTGGTGC 3219  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 3220 AGCCTATTCTCTGCTCTTTCATTGACAGTATTCACAGTGTGAGGTAAACAGCTACATT 3279  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3280 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3339  
 Qy 61 IleGlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3340 ATCCAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3399  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 3400 TCTGAGGAGTGGTTCAGAGTACAGTAACTCTGCTTGTGATGTAAGTGTGACAGATA 3459  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3460 AAGGAACCTCAGCGGCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAGTTGTCAGTG 3519  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 3520 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTAATGGTCTGACACTACTGATTTTG 3579  
 Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 3580 GCTCTCATTTCACTCTTTCAGTGTCTCTGTTATTTATGAAAGGCATCAGGCACAGATAGT 3639  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3640 CATTATCTAGGACTTGGCAATAAAGAATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 3699  
 Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 3700 ATCCCTGGATTGAAGCGCAAGCTGAA 3726

RESULT 13

ABV94680

ID ABV94680 standard; cDNA; 4632 BP.

XX AC

XX ABV94680;

XX 14-JAN-2003 (first entry)

DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.

XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

KW cytostatic; tumour; gene; ss.

XX Homo sapiens.

OS WO200260317-A2.

XX 08-AUG-2002.

PN

XX

XX

XX

XX

XX

XX 30-JAN-2002; 2002WO-US002781.  
 XX  
 PR 30-JAN-2001; 2001US-0265305P.  
 PR 31-JAN-2001; 2001US-0265682P.  
 PR 09-FEB-2001; 2001US-0267568P.  
 PR 21-MAR-2001; 2001US-0278651P.  
 PR 28-APR-2001; 2001US-0287112P.  
 PR 16-MAY-2001; 2001US-0291631P.  
 PR 12-JUL-2001; 2001US-0305484P.  
 PR 20-AUG-2001; 2001US-0313999P.  
 PR 27-NOV-2001; 2001US-0333626P.  
 XX  
 XX (CORI-) CORIXA CORP.  
 XX  
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
 XX  
 XX WPI; 2002-627435/67.  
 DR P-PSDB; ABP68600.  
 XX  
 XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
 PT cancer.  
 XX  
 XX Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.  
 CC  
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)  
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
 CC complements of (a); (c) sequences consisting of at least 20 contiguous  
 CC residues of (a); (d) sequences that hybridize to (a), under moderately  
 CC stringent conditions; (e) sequences having at least 75% or 90% identity  
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
 CC in a patient and compositions comprising polypeptides, polynucleotides,  
 CC antibodies, fusion proteins, T cell populations and antigen presenting  
 CC cells expressing the polypeptide are useful in treating pancreatic cancer  
 CC and stimulating an immune response. The polynucleotides can be used as  
 CC probes or primers for nucleic acid hybridisation, in the design and  
 CC preparation of ribozyme molecules for inhibiting expression of the tumour  
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
 CC therapy. Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.46e-102 Length: 4632  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABV94680 (1-4632)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLeuValValPheGlyAla 20  
 Db 3151 TCAGTGTGTGACCTCTCTGCTGAGGACATTAAGAAGACTGGAGTGGTGTGGTGC 3210  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 3211 AGCCTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGCGTAAACAGCTACATT 3270  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3330  
 Qy 61 IleGlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3331 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATA 3390  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100

Db 3391 TCTAGGAGTTGTTTCAGAAAGTACAGTAATTCCTCTTGGTCATGTGAACGACGATA 3450  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGAACCTCAGGCGCTCTCTTAGTTGATTTAGTTGATCTCTGAAGTTGACGTG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3511 TTGATCGGGTATTTACCTATGTGTGGCTTGTGTTAAATGGTCTGACACTACTGATTTG 3570  
QY 141 AlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3571 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3630  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3631 CATTATCTAGGACTTCGAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3690  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3691 ATCCCTGGATTGAAGCGCAAGCTGAA 3717

## RESULT 14

ID ADG32772 standard; DNA; 4632 BP.

AC ADG32772;

XX 26-FEB-2004 (first entry)

DT Human DNA differentially expressed in patients with SLE SeqID96.

XX human; ds; autoimmune; chronic inflammatory disease; SLE;

KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;

KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;

KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;

KW diverticulitis; primary biliary sclerosis.

XX Homo sapiens.

OS WO2003090694-A2.

PN 06-NOV-2003.

XX 24-APR-2003; 2003WO-US013015.

PF 24-APR-2002; 2002US-00131827.

PR (EXPR-) EXPRESSION DIAGNOSTICS INC.

PA Wohlgemuth J, Fry K, Woodward R, Ly N;

XX WPI; 2003-877243/81.

XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases,

PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative

PT colitis, psoriasis and asthma by detecting the expression level of one or

PT more genes.

XX Claim 18; SEQ ID NO 96; 877pp; English.

XX This invention relates to novel methods for diagnosing and monitoring

CC autoimmune and chronic inflammatory diseases. Specifically, it refers to

CC the identification of genes that have a clinical utility as diagnostic

CC tools for the management of, in particular, patients with systemic lupus

CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the

CC present invention describes a method for determining the levels of

CC multiple differentially expressed genes of a patient, in a concerted

CC manner, in order to achieve an improved diagnostic assay with sensitivity

CC and specificity for the disease in question. As such, these genes are

CC useful for the diagnosis of various other inflammatory disorders

CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,

CC ankylosing spondylitis, ulcerative colitis, primary sclerosing  
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.  
CC This polynucleotide is a DNA sequence representing human mRNA that is  
CC differentially expressed in patients with SLE, used in an exemplification  
CC of the invention.

XX Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.466-102 Length: 4632  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADG32772 (1-4632)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

Db 3151 TCAGTTGTGTGACCTCCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGC 3210

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 3211 AGCCTATTCTGCTGCTTTTCATTGACAGTATTGACATTTGTGAGCGTAACAGCTACATT 3270

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 3271 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCT 3330

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 3331 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATA 3390

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100

Db 3391 TCTGAGAGTTGGTTTCAGAGTACAGTAATCTCTGCTCTTGGTCATGTGAACGACGATA 3450

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

Db 3451 AAGGAACCTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTTGAAGTTTGCAGTG 3510

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140

Db 3511 TTGATGTGGTATTTACCTATGTGTGGCTTGTGTTAAATGGTCTGACACTACTGATTTG 3570

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160

Db 3571 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3630

QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 3631 CATTATCTAGGACTTCGAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3690

QY 181 IleProGlyLeuLysArgLysAlaGlu 189

Db 3691 ATCCCTGGATTGAAGCGCAAGCTGAA 3717

RESULT 15

ID ABX34563

XX ABX34563 standard; cDNA; 4698 BP.

AC ABX34563;

XX 13-FEB-2003 (first entry)

DT Human mddt cDNA SEQ ID 124.

XX MDDT; human; disease detection and treatment molecule polypeptide;

XX anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;

XX haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;

XX gene therapy; protein replacement therapy; cell proliferative disorder;

XX cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; sarcoma;

anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
 Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
 psoriasis; hepatitis; gene; ss.  
 Homo sapiens.  
 WO200279449-A2.  
 10-OCT-2002.  
 27-MAR-2002; 2002WO-US009944.  
 28-MAR-2001; 2001US-0279619P.  
 29-MAR-2001; 2001US-0280067P.  
 29-MAR-2001; 2001US-0280068P.  
 16-MAY-2001; 2001US-0291280P.  
 17-MAY-2001; 2001US-0291829P.  
 17-MAY-2001; 2001US-0291849P.  
 19-JUN-2001; 2001US-0299428P.  
 20-JUN-2001; 2001US-0299776P.  
 20-JUN-2001; 2001US-0300001P.  
 (INCY-) INCYTE GENOMICS INC.  
 Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
 Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
 Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 WPI; 2003-058431/05.  
 P-PSDB; ABU11573.  
 New purified disease detection and treatment molecule proteins and  
 polynucleotides, useful for diagnosing, treating or preventing cancers  
 (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
 or hepatitis.  
 Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.  
 This invention describes a novel disease detection and treatment molecule  
 polypeptide (MDPR) which has anti-inflammatory, immunosuppressive,  
 osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
 antianemic, antipsoriatic and hepatotropic activity. The polynucleotides  
 and the polypeptides of the invention can be used for gene therapy,  
 protein replacement therapy and are useful for treating a variety of  
 diseases or conditions. These polypeptides or polynucleotides are  
 particularly useful for diagnosing, treating or preventing cell  
 proliferative disorders (e.g. cancers including adenocarcinoma,  
 leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
 disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
 syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
 hepatitis. ABX3440-ABX34835 encode the MDPR polypeptides represented in  
 ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
 The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences  
 SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,498-102 Length: 4698  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABX34563 (1-4698)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 3155 TCAGTTGTTGACCTCCTCTACTGAGAGACATTAGAGAGCTGGAGTGGTGTGTTGGTCC 3214

QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 3215 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAAAGCCCTACATT 3274  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3275 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3334  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3335 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAAGTTGCTATA 3394  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 3395 TCTGAGGAGTTGGTTTTCAGAGTACAGTAATTTCTGCTCTTGTTCATGTGAATGACGATA 3454  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3455 AAGAACTCAGGCGCTCTCTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 3514  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 3515 TTGATGTGGTATTTTACCTATGTTGGTGCCTTGTTTAATGTGCTGACACTACTGATTTTG 3574  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 3575 GCTCTCATTTTCATCTTCAGTGTTCCTGTTTATTTATGAAACGGCATCAGGCACAGATAGAT 3634  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3635 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAA 3694  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 3695 ATCCCTGGATTGAAGCGCAAGCTGAA 3721  
 RESULT 16  
 ADR83534  
 ID ADR83534 standard; DNA; 4789 BP.  
 AC ADR83534;  
 DT 02-DEC-2004 (first entry)  
 DE Human reticulon 4 DNA, target gene of miRNA.  
 KW human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;  
 KW immune disease; nerve disorder; amyotrophic lateral sclerosis;  
 KW Parkinson's disease; Alzheimer's disease; inflammatory disease;  
 KW siRNA silencing precursor; cytostatic; immunosuppressive; neuroprotection; antiinflammatory; immunotherapy; reticulon 4.  
 OS Homo sapiens.  
 PN WO2004076622-A2.  
 PD 10-SEP-2004.  
 XX 10-FEB-2004; 2004WO-JP001433.  
 PF 10-FEB-2003; 2003US-0445829P.  
 PR (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA Taira K, Kawasaki H;  
 PI WPI; 2004-653393/63.  
 DR Modulating expression of a target gene in a cell, for treating cancer, an  
 XX immune disease, or a nerve disorder, comprises introducing into the cell  
 PT a polynucleotide that forms a duplex region with an mRNA transcribed from  
 PT the target gene.

XX Claim 9; SEQ ID NO 436; 865pp; English.  
XX  
XX This invention relates to a novel method for modulating the expression of  
CC a target gene in a cell. Specifically, it refers to the introduction into  
CC a cell of a polynucleotide that forms a duplex region with an mRNA  
CC transcribed from the target gene, where the duplex region comprises a  
CC mammalian mRNA target region i.e. a non-coding microRNA (miRNA) that  
CC regulates mRNA at a post-transcriptional level. The present invention  
CC describes a method for controlling ontogenesis of a mammal, function of a  
CC mammalian cell, differentiation of a mammalian cell or viability of a  
CC mammalian cell in the post-transcriptional phase, which comprises  
CC introducing a plasmid vector comprising a promoter and nucleic acid  
CC molecule expressing an miRNA or siRNA silencing precursor to the miRNA.  
CC Accordingly, it provides a cell therapy method for treating cancer,  
CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,  
CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease  
CC by introducing into the cell the miRNA, siRNA silencing precursor to the  
CC miRNA or the plasmid vector. As such, they can be developed into  
CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,  
CC neuroprotective and antiinflammatory activities and hence can  
CC be used for immunotherapy. This polynucleotide sequence is a human target  
CC gene whose expression is modulated by miRNAs of the invention.  
XX  
XX Sequence 4789 BP; 1422 A; 1052 C; 1075 G; 1240 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.53e-102 Length: 4789  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR83534 (1-4789)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3254 TCAGTTGTTGACCTCTCTGACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3313  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3314 AGCCTATTCTGCTGCTTTCATTCAGCATTTTACAGCATTTGAGCGTAAACAGCTACATT 3373  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
DB 3374 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3433  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleLeuSerGluValAlaIle 80  
DB 3434 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3493  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 3494 TCTGAGAGATTGTTTTCAGAAAGTACAGTAATTCCTCTGCTGCTGATGACTGCACGATA 3553  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3554 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAATCTGAGTTGCTAGT 3613  
QY 121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140  
DB 3614 TTGATGGGATATTTACCTATGTTGGTGGCTTCTTAAATGGTCTGACACTGATGATTTTG 3673  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 3674 GCTCTCATTTCACTCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT 3733  
QY 161 HisTyrLeuGlyLeuAlaLeuLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3734 CATTATCTAGCACTTGCMAATAAGAAATGTTAAAGATGCTATGCTAAAAATCCCAAGCAAAA 3793  
QY 181 IleProGlyLeuLysArgLysAlaGlu 199

DB 3794 ATCCCTGGATTGAAGCGCAAGCTGAA 3820  
RESULT 17  
ABS70449  
ID ABS70449 standard; cDNA; 4822 BP.  
XX  
AC ABS70449;  
XX  
DT 27-NOV-2002 (first entry)  
XX  
DE Human bone remodelling gene #106.  
XX  
KW Bone remodelling; osteoporosis; human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6426186-B1.  
XX  
PD 30-JUL-2002.  
XX  
PF 18-JAN-2000; 2000US-00484970.  
XX  
PR 18-JAN-2000; 2000US-00484970.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Jones KA, Volkmut W, Walker MG;  
XX  
WPI; 2002-673014/72.  
XX  
PT A combination of polynucleotides which are co-expressed with genes known  
PT to be involved in bone remodeling and osteoporosis are useful in an array  
PT for the diagnosis of bone remodeling and osteoporosis associated  
PT disorders.  
XX  
PS Claim 1; Col 283-288; 206pp; English.  
XX  
CC The invention relates to a combination comprising a number of  
CC substantially purified and isolated polynucleotides which are co-  
CC expressed with genes known to be involved in bone remodeling and  
CC osteoporosis. The invention is used to diagnose disorders associated with  
CC bone remodeling or osteoporosis. ABS70344-ABS70512 represent human bone  
CC remodelling genes of the invention  
XX  
SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;

Alignment Scores:  
Pred. No.: 1.54e-102 Length: 4822  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABS70449 (1-4822)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3265 TCAGTTGTTGACCTCTCTGACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3324  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3325 AGCCTATTCTCTGCTGCTTTCATTCAGCATTTGAGCGTAAACAGCTACATT 3384  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3385 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3444  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3445 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3504

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrile 100  
 DB 3505 TCTGAGGAGTTGGTTTCAGAGGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCACGATA 3564  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3565 AAGGAACCTCAGCGCGCTCTCTTCTAGTGTATTTAGTATTTCTCTGAAGTTTGCAGTG 3624  
 QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 3625 TTGATGTGGGTATTTACCTATGTTGGTGCTGTTTAATGGTCTGACACTACTGATTTTG 3684  
 QY 141 AlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3685 GCTCTCAITTCACCTCTTCAGTGTCTCTGTTATTTATGAAGGCATCAGGCACAGATAGAT 3744  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3745 CATATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3804  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3805 ATCCCTGGATTGAAGCGCAAGCTGAA 3831

## RESULT 18

AAF32725/c

ID AAF32725 standard; cDNA; 1758 BP.

XX AC AAF32725;

XX DT 23-MAR-2001 (first entry)

XX DE Human secreted protein gene 27 SEQ ID NO:37.

XX KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;

XX KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;

XX KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;

XX KW fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;

XX KW hyperproliferative disorder; neoplasm; cardiovascular disorder;

XX KW cardiac arrest; cerebrovascular disorder; Alzheimer's disease; infection;

XX KW angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;

XX KW ocular disorder; corneal infection; wound healing; food additive;

XX KW preservative; ss.

XX OS Homo sapiens.

XX XX WO200077255-A1.

XX XX 21-DEC-2000.

XX XX 01-JUN-2000; 2000WO-US014926.

XX XX 11-JUN-1999; 99US-0138628P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Rosen CA, Ruben SM, Komatsoulis GA;

XX XX WPI; 2001-025337/03.

XX XX P-PSDB; AAB64448.

XX PT Isolated nucleic acid molecule encoding a human secreted protein is used

XX PT in preventing, treating or ameliorating a medical condition.

XX PS Claim 1; Page 495; 593pp; English.

XX CC The polynucleotide sequences given in AAF32699 to AAF32747 encode the

XX CC human secreted proteins given in AAB64422 to AAB64470. AAB64471 to

XX CC AAB64548 represent human secreted polypeptide sequences and proteins

XX CC homologous to them, which are given in the exemplification of the present

XX CC invention. Human secreted proteins have activities based on the tissues

XX CC and cells the genes are expressed in. Examples of activities include:

XX CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;

CC cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;

CC neuroprotective; antibacterial; virucide; fungicide; and

CC ophthalmological. The polynucleotides and polypeptides can be used to

CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,

CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used

CC in diagnosing a pathological condition or susceptibility to a

CC pathological condition. Disorders which are diagnosed or treated include

CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative

CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders

CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,

CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,

CC infections caused by bacteria, viruses and fungi and ocular disorders

CC e.g. corneal infection. The polypeptides can also be used to aid wound

CC healing and epithelial cell proliferation, to prevent skin aging due to

CC sunburn, to maintain organs before transplantation, for supporting cell

CC culture of primary tissues, to regenerate tissues and in chemotaxis. The

CC polypeptides can also be used as a food additive or preservative to

CC increase or decrease storage capabilities. AAF32690 to AAF32698 and

CC AAB64421 represent sequences used in the exemplification of the present

CC invention

XX SQ Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;

## Alignment Scores:

Pred. No.: 8.69e-103 Length: 1758

Score: 928.00 Matches: 188

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.47% Mismatches: 0

Query Match: 99.68% Indels: 0

DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF32725 (1-1758)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20

DB 1580 GCAGTTGTGACCTCCCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGC 1521

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

DB 1520 AGCTATTCTCCGCTGCTTTTCATTGACAGTATTGACATTGTGAGCTAACAGCTACATT 1461

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

DB 1460 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 1401

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

DB 1400 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAAGTTGCTATA 1341

QY 81 SerGluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100

DB 1340 TCTGAGGAGTTGGTTTACAGAGTACAGTAATTTCTCTCTTGTGTCATGTGAACTGCACGATA 1281

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

DB 1280 AAGGAACCTCAGCGCGCTCTTCTTAGTTGATTTAGTTGATTTCTCTGAACTTTGCAGTG 1221

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140

DB 1220 TTGATGTGGGTATTTACCTATGTTGGTGCTCTTGTAAATGCTGTCACACTACTGATTTTG 1161

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160

DB 1160 GCTCTCATTTTCCTTCAGGTGTTCTGTTTATTAATGAACGGCATCAGGCACAGATAGAT 1101

QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180

DB 1100 CATATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 1041

QY 181 IleProGlyLeuLysArgLysAlaGlu 189

DB 1040 ATCCCTGGATTGAAGCGCAAGCTGAA 1014



```
RESULT 19
AAF90323
ID AAF90323 standard; cDNA; 600 BP.
XX
AC AAF90323;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human NOGO-C cDNA.
XX
KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
KW neuromuscular disorder; psychiatric disorder; developmental disorder;
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200136631-A1.
XX
PD 25-MAY-2001.
XX
PF 14-NOV-2000; 2000WO-GB004345.
XX
PR 15-NOV-1999; 99GB-00069995.
PR 24-JAN-2000; 2000GB-00001550.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha R;
XX
WPI; 2001-343822/36.
DR P-PSDB; AAB82348.
XX
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.
PS Claim 1; Page 25; 25pp; English.
XX
CC The present sequence is that of cDNA encoding human NOGO-C (see
CC AAB82348). NOGO-C is a novel splice variant of the human NOGO gene on
CC chromosome 2p21. 2 Other splice variants, NOGO-A and NOGO-B, have
CC previously been identified. The invention provides NOGO-C polypeptides
CC and polynucleotides, and methods for producing such polypeptides by
CC recombinant techniques. Also disclosed are methods for utilising NOGO-C
CC polypeptides and polynucleotides in the treatment of diseases including
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular
CC disorders, psychiatric disorders and developmental disorders. Also
CC provided are methods for identifying agonists and agonists for use in
CC treating conditions associated with NOGO-C imbalance, and diagnostic
CC assays for detecting diseases associated with inappropriate NOGO-C
CC activity or levels
XX
SQ Sequence 600 BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,55e-103 Length: 600
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AAF90323 (1-600)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 34 GTTGTGACCTCTGTTACTGGAGACATTAAAGAGACTGGAGTGGTGGTGGTCCAGC 93
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
```

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Db 94 CTATTCCTGCTGCTCTTCAATGACAGTATTACAGCATTTGACGGTAAACAGCCTACATTGCC 153
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 213
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 214 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 273
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 274 GAGGAGTTGGTTCAAGAGTACAGTAATTTCTGCTCTTGGTCACTGTGAACTGCACGATAAG 333
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 334 GAACTCAGGCGCTCTCTCTAGTTGATTTAGTTGATTTCTCTGAAGTTTTCAGTGTG 393
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleAla 141
Db 394 ATGGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 453
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 454 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGTATCAT 513
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 514 TATCTAGGACTTGCAATAAGAATGTTAAAGATGCTATGGCTATAAATCCAAGCAAAATC 573
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 574 CCTGGATTGAAGCCGCAAGCTGAA 597

RESULT 20
AAF72983
ID AAF72983 standard; cDNA; 770 BP.
XX
AC AAF72983;
XX
DT 24-NOV-2000 (first entry)
XX
DE Human NSPH encoding cDNA sequence SEQ ID NO:3.
XX
KW Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC; ss.
XX
OS Homo sapiens.
XX
PN CN1253180-A.
XX
PD 17-MAY-2000.
XX
PF 30-OCT-1998; 98CN-00121473.
XX
PR 30-OCT-1998; 98CN-00121473.
XX
PA (UYFU-) UNIV FUDAN.
XX
PI Yu L, Zhao Y, Zhang H;
XX
WPI: 2000-466537/41.
DR P-PSDB; AAB12805.
XX
PT Specific protein of human neuroendocrine, coding sequence and its
PT preparing process and application.
XX
PS Claim 1; Page 14; 21pp; Chinese.
XX
CC The present invention relates to a new member of the human neuroendocrine
CC specific protein family, designated NSPH. The present sequence encodes
CC the human NSPH protein
XX
SQ Sequence 770 BP; 215 A; 136 C; 190 G; 229 T; 0 U; 0 Other;
```



Alignment Scores:  
 Pred. No.: 3,62e-103 Length: 770  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAA72983 (1-770)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 114 GTTGTGTGACCTCTCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 173  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIleAla 41  
 DB 174 CTATTCTCTGCTCTTCAATGACAGTATTCAGCATTTGAGCGTAACAGCTACATTGCC 233  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 234 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 293  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 294 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATATCT 353  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 354 GAGGAGTGGTTCAGAAGTACAGTAATCTCTGCTCTTGGTCACTGTAAGCTGCACGATAAG 413  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 414 GAACTCAGCGCGCTCTTCTTAGTATGATTTAGTTAGTTCTCTGAGTTGCAAGTTGCGTGTG 473  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 474 ATGTGGGTATTTACCTATGTGGTGGCTTGTAAATGGTCTGCACACTACTGATTTGGCT 533  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 534 CTCATTTCACTCTTCAGTGTTCCTCTGTATTTATGAACGGCATCAGGCGACAGATAGATCAT 593  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 594 TATCTAGGACTTGCAATTAAGATGCTTAAGATGCTATGGCTAAATCCAGCAAAATC 653  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 654 CCTGGATTGAAGCGCAAGCTGAA 677

RESULT 21  
 AAV23695  
 ID AAV23695 standard; cDNA; 799 BP.  
 AC AAV23695;  
 XX AAV23695;  
 DT 24-JUL-1998 (first entry)  
 XX Human NSPLP protein A coding sequence.  
 DE NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;  
 KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 75..674  
 FT /tag= a  
 FT /product= "NSPLPA"  
 XX  
 XX PN W09806841-A2.  
 XX

PD 19-FEB-1998.  
 XX  
 PF 24-JUL-1997; 97WO-US013469.  
 XX  
 PR 12-AUG-1996; 96US-00700607.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Bandman O, Au-Young J, Goli SK, Hillman J;  
 XX  
 DR WPI, 1998-159533/14.  
 DR P-PSDB; AAW53947.  
 XX  
 PT Human neuro-endocrine-specific protein-like proteins - useful for  
 PT diagnosis, monitoring and treatment of cancer and neuro-degenerative  
 PT disease.  
 XX  
 PS Claim 3; Page 38-39; 73pp; English.  
 XX  
 CC This sequence encodes a human neuroendocrine-specific protein-like  
 CC protein (NSPLP) of the invention. Recombinant cells transformed with the  
 CC DNA are used to express the NSPLP proteins, which are used to treat  
 CC cancer and neurodegenerative diseases such as amyotrophic lateral  
 CC sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be  
 CC used to inhibit activity of the NSPLP proteins. Antibodies specific for  
 CC NSPLP are used for diagnosis and monitoring treatment of diseases  
 CC associated with NSPLP expression, in usual immunoassays, and to isolate  
 CC NSPLP from natural sources. The NSPLP proteins, or their fragments can  
 CC also be used in drug screening to identify NSPLP antagonists. The nucleic  
 CC acid can be used diagnostically and for monitoring treatment (in  
 CC hybridisation or amplification assays); to isolate closely related  
 CC sequences; in gene therapy for both sense and antisense applications  
 CC (including use of ribozymes) and for mapping the natural genomic sequence  
 XX  
 SQ Sequence 799 BP; 218 A; 141 C; 196 G; 242 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 3,81e-103 Length: 799  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 2 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAV23695 (1-799)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 108 GTTGTGTGACCTCTCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 167  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 168 CTATTCTCTGCTCTTCAATGACAGTATTCAGCATTTGAGCGTAACAGCTACATTGCC 227  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 287  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 288 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATATCT 347  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 348 GAGGAGTGGTTCAGAAGTACAGTAATTTCTCTCTTGGTCACTGTAAGCTGCACGATAAG 407  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 408 GAACTCAGCGCGCTCTTCTTAGTATGATTTAGTTAGTTCTCTGAAAGTTGCGAGTGTG 467  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 468 ATGTGGGTATTTACCTATGTTGGTGGCTTGTAAATGGTCTGCACACTACTGATTTGGCT 527

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 528 CTCATTTCATCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 588 TATCTAGGACTTGCAAATAGAAATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAATC 647  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 648 CCTGGATTGAGCGCAAGCTGAA 671

## RESULT 22

AAZ56888  
 ID AAZ56888 standard; DNA; 1122 BP.

AC AAZ56888;

XX 25-APR-2000 (first entry)

DT Human MAGI polypeptide variant encoding DNA.

DE MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
 KW psychiatric disorder; developmental disorder; inflammatory disorder;  
 KW stroke; cytostatic; cerebroprotective; neuroprotective; variant; ds.  
 XX Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..1122

FT /\*tag= a

FT /product= "MAGI polypeptide"

PN WO200005364-A1.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-GB002360.

XX 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha RK;

XX WPI; 2000-182693/16.

DR P-PSDB; AAY56969.

XX Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.

XX Claim 5; Page 21-22; 35pp; English.

XX The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein variant

XX Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6.13e-103 Length: 1122  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ56888 (1-1122)

QY 2 ValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 556 GTTGTGACCTCCTGCTACTGAGAGACATTAGAGAGACTGGAGTGGTGTGTCGACG 615  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAla 41  
 DB 616 CTATTCCTGCTGCTTCATTGACAGTATTCAGCAATGTGAGCGTACACGCTACATGCC 675  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 676 TTGGCCCTGCTCTGCTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAGCTATC 735  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 736 CAGAAATCAGATGAAGGCCACCCATTTCAGGCAATATCTGGAATCTGAAATGTTGCTATCT 795  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 796 GAGGAGTTGGTTCAGAGGTACAGTAATCTCTGCTTGGTTCATGTGAACGACGATAAAG 855  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 856 GAACTCAGCGGCTCTCTTAGTGTAGTATTTAGTTGATTCTCTGAAGTTTCAGGTGTG 915  
 QY 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 DB 916 ATGTGGGTATTTACCTATGTTGGTGGCTTTTAAATGGTCTGACACTACTGATTTGGCT 975  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 976 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 1035  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 1036 TATCTAGGACTTGCAAATAGAAATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAATC 1095  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 1096 CCTGGATTGAGCGCAAGCTGAA 1119

## RESULT 23

AAF90325

ID AAF90325 standard; cDNA; 1122 BP.

XX AAF90325;

XX 23-JUL-2001 (first entry)

XX Human NOGO-B cDNA.

XX NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; neurotropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.

XX Homo sapiens.

XX WO200136631-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-GB004345.

XX 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

XX

(SMIK ) SMITHKLINE BEECHAM PLC.

Michalovich D, Prinjha R;

WPI; 2001-343822/36.

P-PSDB; AAB82350.

New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.

Disclosure; Page 27; 25pp; English.

The present sequence is that of cDNA encoding human NOGO-B (see AAB82350). NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel NOGO gene splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilizing NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels

Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6, 13e-103 Length: 1122  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF90325 (1-1122)

QY	2	ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer	21
DB	556	GTGTGTGACCTCTGTACGAGACATTAAAGACTGGAGTGGTGTGGTGCCAGC	615
QY	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
DB	616	CTATTCTCGCTGCTTTTCATTGACAGTATTACGATTGTGAGCGTAACAGCTTACATGCC	675
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
DB	676	TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATTCAGCTATC	735
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
DB	736	CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT	795
QY	82	GluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnCythrIleLys	101
DB	796	GAGGAGTGGTTTCAGAGTACAGTAAATCTGCTTTGTGTCATGTGAACCTGCACGATAAAG	855
QY	102	GluLeuAtgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
DB	856	GNACTCAGCGCCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAAGTTGCAGTGTG	915
QY	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla	141
DB	916	ATGTGGGTATTTACCTATGTTGGTCCCTGTTTATATGCTGTCGACACTACTGATTTGGCT	975
QY	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
DB	976	CTCATTTTCACCTTCAGTGTTCCTGTTTATTTATGAACGGCATTCAGGCACAGATAGATCAT	1035
QY	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181

DB	1036	TATCTAGGACITTCAAATAAGAAATGTTAAAGATGCTATGCTATAAATCCAGCAAAATC	1095
QY	182	ProGlyLeuLysArgLysAlaGlu	189
DB	1096	CCTGGATTGAAGCGCAAGCTGAA	1119
RESULT 24			
AAAX04379			
ID	AAAX04379	standard; DNA; 1213 BP.	
XX	AC	AAAX04379;	
XX	DT	13-APR-1999 (first entry)	
XX	DE	Human secreted protein gene 69 clone HAGFT48.	
XX	KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
XX	KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	
XX	KW	developmental abnormality; foetal deficiency; blood; allergy; renal; ds;	
XX	KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
XX	KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
XX	KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	
XX	KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
XX	KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
OS		Homo sapiens.	
XX	FN	WO9856804-A1.	
XX	PD	17-DEC-1998.	
XX	PF	11-JUN-1998; 98WO-US012125.	
XX	PR	13-JUN-1997; 97US-0049547P.	
XX	PR	13-JUN-1997; 97US-0049548P.	
XX	PR	13-JUN-1997; 97US-0049549P.	
XX	PR	13-JUN-1997; 97US-0049550P.	
XX	PR	13-JUN-1997; 97US-0049556P.	
XX	PR	13-JUN-1997; 97US-0049606P.	
XX	PR	13-JUN-1997; 97US-0049607P.	
XX	PR	13-JUN-1997; 97US-0049608P.	
XX	PR	13-JUN-1997; 97US-0049609P.	
XX	PR	13-JUN-1997; 97US-0049610P.	
XX	PR	13-JUN-1997; 97US-0049611P.	
XX	PR	13-JUN-1997; 97US-0050901P.	
XX	PR	13-JUN-1997; 97US-0052989P.	
XX	PR	08-JUL-1997; 97US-0051919P.	
XX	PR	18-AUG-1997; 97US-0055984P.	
XX	PR	12-SEP-1997; 97US-0058665P.	
XX	PR	12-SEP-1997; 97US-0058668P.	
XX	PR	12-SEP-1997; 97US-0058669P.	
XX	PR	12-SEP-1997; 97US-0058710P.	
XX	PR	12-SEP-1997; 97US-0058711P.	
XX	PR	12-SEP-1997; 97US-0058722P.	
XX	PR	12-SEP-1997; 97US-0058975P.	
XX	PR	02-OCT-1997; 97US-0060834P.	
XX	PR	02-OCT-1997; 97US-0060841P.	
XX	PR	02-OCT-1997; 97US-0060844P.	
XX	PR	02-OCT-1997; 97US-0060865P.	
XX	PR	02-OCT-1997; 97US-0061059P.	
XX	PR	02-OCT-1997; 97US-0061060P.	
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olesen HS;	
XX	PI	Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;	
XX	PI	Feng P;	
XX	XX		
DR	WPI; 1999-080881/07.		
DR	P-PSDB; AAW78194.		
XX		New isolated human genes and the secreted polypeptides they encode -	

PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.

XX  
XX  
XX Claim 1; Page 235-236; 380pp; English.

XX This sequence represents a nucleic acid molecule which encodes a secreted  
CC human protein. The gene number, and the clone it is derived from, are  
CC detailed in the descriptor line. The gene can be used to generate fusion  
CC proteins by linking to the gene to a human immunoglobulin Fc portion  
CC (e.g. AAX04302) for increasing the stability of the fused protein as  
CC compared to the human protein only. The invention relates to 86 novel  
CC genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino  
CC acid sequences AAW8126-W8225) which are useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,  
CC pathological conditions can be diagnosed by determining the amount of the  
CC new polypeptides in a sample or by determining the presence of mutations  
CC in the new polynucleotides. Specific uses are described for each of the  
CC 86 polynucleotides, based on which tissues they are most highly expressed  
CC in (see AAX04311 for described uses)

XX SQ Sequence 1213 BP; 335 A; 222 C; 297 G; 355 T; 0 U; 4 Other;

#### Alignment Scores:

Pred. No.:	6.84e-103	Length:	1213
Score:	927.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.57%	Indels:	0
DB:	2	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAX04379 (1-1213)

QY	2	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21
DB	248	GTGTGACCTCTCTGCTGACAGACATTAAGACATGAGTGGTGTGGTGGCCAGC	307
QY	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
DB	308	CTATTCTCTGCTTTTCATTGACAGATTACAGATTGTGAGCGTAAACGCCATCATGTC	367
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
DB	368	TTGGCCCTCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATC	427
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
DB	428	CAGAAATCAGATGAGGCGCCACCATTTCAGGCGATATCTGGAATCTCGAAGTTGCTATATCT	487
QY	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
DB	488	GAGGAGTTGGTTTCTGAGAGTACAGTAATCTGCTTTGGTCATGTGAAGTGCAGATPAAAG	547
QY	102	GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
DB	548	GAATCAGGCGCTCTTCTTAGTTGATGATTAGTTGATCTCTGAAGTTGCGAGTTG	607
QY	122	MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla	141
DB	608	ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGCACACTACTGATTTTGGCT	667
QY	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
DB	668	CTCATTTTCACTCTTCAGTGTCTCTGTTATTATTAAGCGGATCAGGACAGATAGATCAT	727
QY	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
DB	728	TATCTAGGACTTCGCAATTAAGATGTTAAAGATGCTATGCTAAATCCAAGCAAAATC	787
QY	182	ProGlyLeuLysArgLysAlaGlu	189
DB	788	CCTGGATTGAAGCGCAAGCTGAA	811

RESULT 25

ABA05903

ID ABA05903 standard; cDNA; 1216 BP.

XX AC ABA05903;

XX DT 04-MAR-2002 (first entry)

XX DE Human RTN4B encoding cDNA SEQ ID NO 3.

XX KW Human; RTN4B; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 5..1126

XX FT /\*tag= a

XX FT /product= "RTN4B"

XX PN CN1311439-A.

XX PD 05-SEP-2001.

XX PF 02-MAR-2000; 2000CN-00111791.

XX PR 02-MAR-2000; 2000CN-00111791.

XX PA (UYFU-) UNIV FUDAN.

XX PI Yu L, Fu Q, Zhao Y;

XX DR WPI: 2002-049934/07.

XX DR P-PSDB; AAM47954.

XX Human RTN 4B protein and coding sequence, its preparation and use.  
XX Claim 9; Page 20 (Disclosure); 27pp; Chinese.  
XX The invention relates to human RTN4B protein and coding sequence, useful  
CC for providing a cDNA members. The present invention also refers to  
CC RTN4 with RTN family members. The present invention also refers to  
CC polypeptide encoded by a nucleotide sequence and manufacturing method and  
CC application of the polypeptide and polynucleotide  
XX SQ Sequence 1216 BP; 256 A; 354 C; 341 G; 265 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	6.86e-103	Length:	1216
Score:	927.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.57%	Indels:	0
DB:	6	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABA05903 (1-1216)

QY	2	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21
DB	560	GTGTGACCTCTCTGCTGACAGACATTAAGACATGAGTGGTGTGGTGGCCAGC	619
QY	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
DB	620	CTATTCTCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACGCCATCATGTC	679
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
DB	680	TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATC	739
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
DB	740	CAGAAATCAGATGAGGCGCCACCATTTCAGGCGATATCTGGAATCTGAAGTTGCTATATCT	799
QY	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101

Db 800 GAGGAGTGGTTTCAGAGTACAGTAATTCCTGCTTGGTGTGATGTGAACCTGCAGCAGATAAAG 859  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLeuPheAlaValLeu 121  
 Db 860 GAACCTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTCAGTGTG 919  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 920 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAATGGTCTGCACACTACTGATTTGGCT 979  
 Qy 142 LeuLeuSerLeuPheSerValProValLeuTyrGluArgHisGlnAlaGlnLeuAspHis 161  
 Db 980 CTCATTTTCACCTCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 1039  
 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 1040 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATTCAGCAAAATC 1099  
 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 1100 CTGGATTGAGCGCAAGCTCAA 1123  
 RESULT 26  
 ADI62860  
 ID ADI62860 standard; cDNA; 1599 BP.  
 XX AC ADI62860;  
 XX DT 22-APR-2004 (first entry)  
 XX Human apoptosis-associated cDNA SEQ ID 303.  
 DE KW apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;  
 DE KW antirheumatic; antiarthritic; dermatological; antiinflammatory;  
 DE KW hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;  
 DE KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;  
 DE KW autoimmune disease; degenerative disease; viral infection; leukaemia;  
 DE KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;  
 DE KW lupus; hepatitis; influenza viruses; Alzheimer's disease;  
 DE KW Huntington's disease; Parkinson's disease; reperfusion injury; stroke;  
 DE KW alcoholic liver disease; human; gene; ss.  
 OS Homo sapiens.  
 XX OS  
 PN WO2003058021-A2.  
 XX PD 17-JUL-2003.  
 XX PF 13-JAN-2003; 2003WO-EP000270.  
 XX PR 11-JAN-2002; 2002DE-01000856.  
 XX XX (XANT-) XANTOS BIOMEDICINE AG.  
 XX Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;  
 XX WPI; 2003-542134/51.  
 XX New nucleic acids involved in apoptosis, useful for diagnosis and  
 PT treatment of e.g. tumors and degenerative disease, also related proteins,  
 PT antibodies and modulators.  
 XX PS Claim 1b; SEQ ID NO 303; 517pp; German.  
 XX This invention describes novel nucleic acid molecules that are associated  
 CC with apoptosis and encode a polypeptide and are derived from a normalised  
 CC gene library (embryonic or liver) or clone collections, and the extent of  
 CC apoptosis measured by cell death detection assay or the CPRG assay  
 CC (measuring loss of membrane integrity). The products of the invention  
 CC have cytostatic, neuroprotective, immunosuppressive, antirheumatic,  
 CC antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,  
 CC nootropic, anticonvulsant, antiparkinsonian, vasotropic,  
 CC cerebroprotective and antialcoholic activity and can be used for gene

CC therapy. The polynucleotides also related vectors, hosts (or their  
 CC extracts), encoded polypeptide (or their receptors) and/or agents that  
 CC inhibit their activity (including antisense sequences) are used for  
 CC treatment or prevention of tumours, autoimmune or degenerative diseases  
 CC and viral infections, specifically leukaemia, carcinoma, sarcoma,  
 CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection  
 CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or  
 CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver  
 CC disease. Detection of the polynucleotides and derived polypeptides can  
 CC also be used for diagnosis of these diseases. This sequence encodes an  
 CC apoptosis-associated protein described in the disclosure of the  
 CC invention.  
 XX Sequence 1599 BP; 354 A; 452 C; 422 G; 371 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.01e-102 Length: 1599  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADI62860 (1-1599)  
 Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 671 GTTGTGACCTCCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAGC 730  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 731 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTCGC 790  
 Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 791 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 850  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 851 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATCTCGAATCTGGAAGTTGCTATATCT 910  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 911 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTCTTGGTTCATGTGAACCTGCACGATAAG 970  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 971 GAACCTCAGCGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTGTG 1030  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 1031 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTAATGGTCTGCACACTACTGATTTGGCT 1090  
 Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnLeuAspHis 161  
 Db 1091 CTCATTTTCACCTCTTCAGTGTTCCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 1150  
 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 1151 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATTCAGCAAAATC 1210  
 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 1211 CTGGATTGAGCGCAAGCTCAA 1234  
 RESULT 27  
 AAZ36230  
 ID AAZ36230 standard; cDNA; 1610 BP.  
 XX AC AAZ36230;  
 XX DT 22-FEB-2000 (first entry)  
 XX



XX Aune TW, Olsen NJ;  
PI WPI; 2004-061002/06.  
XX  
DR  
XX  
PT Detecting an autoimmune disorder in a subject comprising comparing the  
PT expression level of each gene determined with a standard, where the  
PT comparing detects the presence of an autoimmune disorder in the subject.  
XX  
XX  
PS Claim 10; SEQ ID NO 62; 86pp; English.  
XX  
XX The invention relates to a method of detecting an autoimmune disorder in  
CC a subject comprising obtaining a biological sample, preferably a  
CC peripheral blood mononuclear cell, from a subject, determining expression  
CC levels of at least two genes in the biological sample, and comparing the  
CC expression level of each gene determined with a standard, where the  
CC comparison detects the presence of an autoimmune disorder in the subject.  
CC The method is useful for detecting or diagnosing an autoimmune disorder,  
CC e.g. rheumatoid arthritis, systemic lupus erythematosus, multiple  
CC sclerosis, or type 1 (insulin-dependent) diabetes. The present sequence  
CC represents one of seventy genes used to detect autoimmune disorders with  
CC the described method.  
XX  
SQ Sequence 1785 BP; 520 A; 316 C; 402 G; 547 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1, 18e-102 Length: 1785  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 12 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADK14166 (1-1785)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 247 GTTGTGACCTCCTGCTGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 306  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 307 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGGAGCGTAACAGCCTACATTC 366  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 367 TTGGCCCTGCTCTCTGTGACCATCATGCTTTAGGATATACAGGGTGTGATCATAGCTATC 426  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 427 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 486  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101  
DB 487 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTTGTGTCATGTGAACCTGCACGATAAG 546  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 547 GAATCAGCGCCCTCTTCTTGTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 606  
QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB 607 ATGTGGGTATTACCTATGTTGGTCTTGTATTAATGCTGTGACACTACTGATTTGGCT 666  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 667 CTCATTTTCACCTTCAGTGTTCCTGTTATTTATGAACGGCATTCAGGCACAGATAGATCAT 726  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaIle 181  
DB 727 TATCTAGACCTTGCAATTAAGATGTTAAAGATGCTATGGCTTAAATCAAGCAAAATC 786  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
|||||

Db 787 CCTGGATTGAAGCGCAAGCTGAA 810  
RESULT 29  
ABK90133  
ID ABK90133 standard; DNA; 2052 BP.  
XX  
XX AC ABK90133;  
XX  
XX DT 21-OCT-2002 (first entry)  
XX  
XX DE DNA encoding human NogoB protein.  
XX  
XX KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hypertrophy; central nervous system; axon regeneration; NogoB;  
KW Nogo-associated disease; metastasis; gene; ds.  
XX  
XX OS Homo sapiens.  
XX  
XX FH Key Location/Qualifiers  
FT CDS 67..1188  
FT FT /\*tag= a  
FT FT /product= "Human NogoB protein"  
XX  
XX FN WO200257483-A2.  
XX  
XX PD 25-JUL-2002.  
XX  
XX PF 18-JAN-2002; 2002WO-GB000228.  
XX  
XX PR 18-JAN-2001; 2001GB-00001312.  
XX  
XX PA (GLAX ) GLAXO GROUP LTD.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
XX  
XX DR WPI; 2002-599722/64.  
XX P-PSDB; ABG30937.  
XX  
PT Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
PT providing and monitoring interaction between Nogo and BACE polypeptides.  
XX  
PS Disclosure; Page 50-52; 68pp; English.  
XX  
XX The present invention relates to a new method of identifying modulators  
XX of Nogo function or BACE activity. The method involves providing Nogo and  
XX BACE polypeptides capable of binding with each other, monitoring the  
XX interaction between these polypeptides, and determining if the test agent  
XX is a modulator of Nogo or BACE activity. The method is useful in treating  
XX acute neuronal injuries, such as spinal or head injury, stroke,  
XX peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
XX neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
XX cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
XX hypertrophy) of the central nervous system. The BACE polypeptide is  
XX useful in screening methods to identify agents that may act as modulators  
XX of BACE activity and in particular agents that may be useful in treating  
XX Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
XX and the polynucleotide encoding the BACE polypeptide are useful in  
XX manufacturing a medicament for the treatment or prevention of disorders  
XX responsive to the modulation of Nogo activity, in alleviating the  
XX symptoms or improving the condition of a patient suffering from this  
XX disorder, in axon regeneration, or in preventing metastasis or spreading  
XX of a cancer. The polynucleotide may also be an essential component in  
XX assays, a probe, in recombinant protein synthesis, and in gene therapy  
XX techniques. The present nucleic acid sequence encodes the human NogoB  
XX protein of the invention  
XX  
XX Sequence 2052 BP; 511 A; 512 C; 506 G; 523 T; 0 U; 0 Other;



```
Alignment Scores:
Pred. No.: 1.43e-102 Length: 2052
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x ABK90133 (1-2052)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 622 GTTGTGACCTCTCTGTGACGACATTAAGAGACTGGAGTGTGTGGTCCAGC 681
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 682 CTATTCTGCTGCTTTCATTCAGAGTATTGAGCATTTGAGCGTAAACAGCCTACATTGCC 741
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
DB 742 TTGGCCCTGCTCTCTGTGACCATCTTGTAGGATATACAGGGGTGTGATCCAAAGCTATC 801
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 802 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGATCTGGAATCTGATCTATATCT 861
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 862 GAGGAGTGTGTTCCAGAAATACAGTAAATTCCTGCTTGTGTCATGTGAAGTGCACGATAAG 921
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 922 GAACCTCAGGCGCTCTCTTAGTGTGATGATTTAGTTGATTTCTCTGAAGTTGCGTGTG 981
QY 122 MetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 982 ATGTGGGTATTTACCTATGTTGTGCTGCTTTGTTTAAATGGTCTGACACTGATTTGGCT 1041
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 1042 CTCATTTCACTTTCAGTGTCTGCTGTTATTTATGAACGGCATTCAGGCACAGATAGATCAT 1101
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 1102 TATCTAGGACTTCGAATTAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1161
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 1162 CCTGGATTGAGCGCAAGCTGAA 1185

RESULT 30
ABV94681
ID ABV94681 standard; cDNA; 2235 BP.
XX
AC ABV94681;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 54.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US0002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR
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PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX P-PSDB; ABP68601.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
XX cancer.
XX
XX Claim 1; SEQ ID NO 54; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a); under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridisation, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 1.61e-102 Length: 2235
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x ABV94681 (1-2235)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 697 GTTGTGACCTCTCTGTGACGACATTAAGAGACTGGAGTGTGTGGTCCAGC 756
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 757 CTATTCTGCTGCTTTCATTCAGCATTTGAGCGTAAACAGCCTACATTGCC 816
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 817 TTGGCCCTGCTCTCTGTGACCATCTGATATACAGGGTGTGATCCAAAGCTATC 876
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 877 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGATATCT 936
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 937 GAGGAGTGTGTTCCAGAAATGATAGTAAATCTGCTTGTGGTCAATGAGTGCACGATAAG 996
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
```



Db 997 GAACCTAGCCGCTCTCTTCTAGTGTGATGATTTAGTGTGATTTCTCTGAAGTTGTCAGTGTG 1056  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1057 ATGCGGTATTTACTATGTTGGTCCCTGTTTAAATGTCGTGACACTACTGATTTGGCT 1116  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1117 CTCATTTTCACTCTTTCAGTGTTCCTCTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1176  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1177 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAATC 1236  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1237 CTGGATTGAAGCGCAAGCTGAA 1260  
RESULT 31  
AAC64406  
ID AAC64406 standard; cDNA; 2240 BP.  
XX  
AC AAC64406;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human Nogo B nucleotide sequence SEQ ID NO:1.  
XX  
KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;  
KW stress-phosphorylated endoplasmic reticulum protein; cytoskeletal;  
KW gene therapy; cell growth; cellular stress response; neuron growth;  
KW regulator of oxidative stress; inhibitor of neurite outgrowth;  
KW axon regeneration; diagnosis; cancer; identification; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200060083-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 07-APR-2000; 2000WO-US009383.  
XX  
PR 08-APR-1999; 99US-0128372P.  
PR 21-JUN-1999; 99US-0140331P.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
XX Wei D, Halenbeck R, Williams LT;  
XX  
XX WPI; 2000-665007/64.  
DR P-PSDB; AAB24242.  
XX  
XX Novel protein associated with cell stress response useful for modulating  
PT stress levels, cell growth, diagnosis and treatment of cancer and  
PT malignant growth and for identifying agonists and antagonists.  
XX  
PS Claim 2; Page 63-64; 68pp; English.  
XX  
CC The present sequence encodes a human stress-phosphorylated endoplasmic  
CC reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and  
CC is a modulator of the storage and exchange of calcium, cell growth and  
CC cellular stress response. It can: regulate oxidative stress; inhibit  
CC neurite outgrowth, neuron growth and axon regeneration. Nogo B  
CC polypeptides and polynucleotides are useful for modulating stress levels  
CC and cellular stress-response, cell growth and viability, diagnosis and  
CC treatment of cancer, malignant growth and other Nogo B related diseases.  
CC Nogo B polypeptides are also useful to screen combinatorial libraries to  
CC identify agonist or antagonist. Antibodies against Nogo B polypeptides  
CC are useful for affinity chromatography and distinguishing Nogo B  
CC polypeptides  
XX  
SQ Sequence 2240 BP; 570 A; 558 C; 536 G; 576 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.62e-102 Length: 2240  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAC64406 (1-2240)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 693 GTTGTGACCTCTCTGTTACTGAGAGACATTAAAGACTGGAGTGTGTTTGGTCCAGC 752  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 753 CTATTCTCTGCTGCTTTTCAATGACAGTATTGAGCATTTGAGCGTAACAGCCTTACATTGCC 812  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAAGCTATC 872  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 873 CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGAAAGTTGCTATATCT 932  
Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCythrIleLys 101  
Db 933 GAGGAGTGGTTCAGAAAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACCTGCACGATAAG 992  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 993 GAATCAGGCCCTCTCTTAGTTGATGATTTAGTTAGTTCTCTGAAAGTTGCAAGTGTG 1052  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 1053 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTCTGACACTACTGATTTGGCT 1112  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1113 CTCATTTTCACTCTTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1172  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1173 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAATC 1232  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1233 CCTGGATTGAAGCGCAAGCTGAA 1256  
RESULT 32  
AAK94408  
ID AAK94408 standard; cDNA; 1694 BP.  
XX  
XX AAK94408;  
AC  
DT 06-NOV-2001 (first entry)  
XX  
DE Human full-length cDNA, SEQ ID NO: 3170.  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX  
OS Homo sapiens.  
XX  
FN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
DR P-PSDB; AAM93484.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX  
XX Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.  
XX  
CC The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesized by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly  
CC from EPO  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 3,36e-102 Length: 1694  
Score: 923.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 99.14% Indels: 0  
DB: 4 Gaps: 0  
  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAK94408 (1-1694)  
  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGACCTCTGTTACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGTGACG 847  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 848 CTATTCCTGCTGCTTTTCATTCAGCAGTATTGAGCATTTGAGCGTAAACGCCTACATTGC 907  
  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCTATC 967  
  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 968 CAGAAATCAGATCAGAGCCACCCATTCAGGCATATCTGGAATCTCAGATGCTATATCT 1027  
  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 1028 GAGGAGTTGGTTGAGAGTACAGTAATCTGCTCTTGGTCATGTGAACGTCAGTAAG 1087  
  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1088 GAACCTCAGCGCCCTCTCTTAGTGTAGTATGATTTAGTTGATCTCTGAAGTTGACGTTGG 1147  
  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 1148 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1207  
  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 1208 CTCAATTCATCTCTCAGTGTCTCTGTATTATTAATGAACGGCATCAGGCATAGATCAT 1267  
  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 1268 TATCTAGGACTTGCATAATAAGAAATCTTAAAGATGCTATCGTAAATCCAGCAAAATC 1327  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 1328 CCTGGATTGAGCGCAAGACTGAA 1351  
  
RESULT 33  
ADL31137  
ID ADL31137 standard; cDNA; 1694 BP.  
XX  
AC ADL31137;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Full length human cDNA clone SeqID 3170.  
XX  
KW human; medicine; signal transduction; glycoprotein; transcription;  
KW oligo-capping method; ss; gene.  
XX  
OS Homo sapiens.  
XX  
PN EP1396543-A2.  
XX  
PD 10-MAR-2004.  
XX  
PF 07-JUL-2000; 2003EP-00025638.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX  
(REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
WPI; 2004-204755/20.  
DR P-PSDB; ADL31138.  
XX  
PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
PT length human cDNAs.  
XX  
PS Example 1; SEQ ID NO 3170; 1340pp; English.  
XX  
CC This invention relates to a novel primers useful for synthesizing full  
CC length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction,  
CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
CC ends using the oligo-capping method. This polynucleotide sequence is a  
CC full length human cDNA clone of the invention.  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 3,36e-102 Length: 1694  
Score: 923.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 99.14% Indels: 0  
DB: 12 Gaps: 0  
  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADL31137 (1-1694)  
  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGACCTCTGTTACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGTGACG 847  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 848 CTATTCTCTCTCTTCAATGACAGTATTGACAGTATTGAGCGTAAACAGCCTACATTTGCC 907  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAAAGGTTGATCCAAAGCTATC 967  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 968 CAGAAATCAGATCAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 1027  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 1028 GAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGGTCAATGTGAAGTGCACGATAAG 1087  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 1098 GAACTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTGACGTGTTG 1147  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1148 ATGTGGGTATTTACCTATGTTGGTGGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 1207  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1208 CTCATTTTCACCTCTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCACAGATGATCAT 1267  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1268 TATCTAGAGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1327  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351

RESULT 34

AAI98079  
ID AAI98079 standard; cDNA; 1980 BP.

AC AAI98079;

DT 04-DEC-2001 (first entry)

XX Human neuroblastoma expressed polynucleotide SEQ ID NO 22.

DE Human; neuroblastoma; ss.

OS Homo sapiens.

XX WO200166733-A1.

PD 13-SEP-2001.

XX 02-MAR-2001; 2001WO-JP001631.

XX 07-MAR-2000; 2000JP-00159195.

PR 12-MAY-2000; 2000JP-00140387.

XX (CHIB-) CHIBA PREFECTURE.

PA (HISM) HISAMITSU PHARM CO LTD.

XX Nakagawara A;

XX WPI; 2001-602630/68.

XX Nucleic acids for prognosis of human neuroblastoma comprise nucleic acids expressed by human neuroblastomas.

XX Claim 1; Page 69-70; 159pp; Japanese.

XX The invention relates to nucleic acids (AAI98058-AAI98161) or their homologues expressed by human neuroblastomas useful for detecting genes expressed by neuroblastoma and for analysing their structure and function. The nucleic acids are useful for the diagnosis and prognosis of

CC neuroblastoma  
XX SQ Sequence 1980 BP; 601 A; 373 C; 423 G; 583 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 7.34e-102 Length: 1980  
Score: 921.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 1  
Best Local Similarity: 98.94% Mismatches: 0  
Query Match: 98.93% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAI98079 (1-1980)  
Qy 1 SerValValAspLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 1006 TCAGTTTGTGACCTCTCTGCTACTGGAGAGACATTAAGAAGCTGGAGTGGTGTGGTGGC 1065  
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 1066 AGCCTATTCCAGCTGCTTTTCATTGACAGTATTGACAGTATTGAGCGTAAACAGCCTACATT 1125  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 1185  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 1186 ATCCAGAANTCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 1245  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 1246 TCTGAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGGTCAATGTAACCTGCACGATA 1305  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 1306 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAGTTTGCAGTG 1365  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 1366 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGGTCTGACACTACTGATTTTG 1425  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 1426 GCTCTCATTTTCACCTTCAGTGTTCCTGTTATTTATGAACGCGCATCAGGCACAGATAGAT 1485  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1486 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 1545  
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572

RESULT 35

AAAX97587  
ID AAAX97587 standard; DNA; 991 BP.

XX AAAX97587;

DT 13-SEP-1999 (first entry)

XX Extended human secreted protein coding sequence, SEQ ID NO. 51.

XX Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory; haematopoiesis regulator; tissue growth regulator; tumour inhibitor; KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy; genetic disease; ss.

OS Homo sapiens.

XX WO9931236-A2.

XX PD 24-JUN-1999.  
XX PF 17-DEC-1998; 98WO-IB002122.  
XX PR 17-DEC-1997; 97US-0069957P.  
PR 09-FEB-1998; 98US-0074121P.  
PR 13-APR-1998; 98US-0081563P.  
PR 10-AUG-1998; 98US-0096116P.  
XX (GEST ) GENSET.  
XX Bougueleret L, Duclert A, Dumas Milne Edwards J;  
PI P-PSDB; AA35903.  
DR New isolated human secreted proteins.  
XX Claim 1; Page 185-186; 516pp; English.  
XX This sequence represents an extended human secreted protein coding  
CC sequence of the invention. The secreted proteins can be used in treating  
CC or controlling a variety of human conditions. The secreted proteins may  
CC act as cytokines or may affect cellular proliferation or differentiation  
CC or may act as immune system regulators, haematopoiesis regulators, tissue  
CC growth regulators, regulators of reproductive hormones or cell movement  
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or  
CC tumour inhibition activity. The DNAs can be used in forensic procedures  
CC to identify individuals or in diagnostic procedures to identify  
CC individuals having genetic diseases resulting from abnormal expression of  
CC the genes corresponding to the extended cDNAs. They are also useful for  
CC constructing a high resolution map of the human chromosomes. They can  
CC also be used for gene therapy to control or treat genetic diseases  
XX SQ Sequence 991 BP; 280 A; 175 C; 232 G; 304 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6,46e-102 Length: 991  
Score: 918.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 98.60% Indels: 0  
DB: Gaps: 2  
  
US-09-830-972-29\_COPY\_990\_1178 (1-188) x AAX97587 (1-991)  
  
QY 2 ValValAspLeuLeuThrTrpArgAspIleLeuLysThrGlyValValPheGlyAlaSer 21  
DB 68 GTTGTGACCTCTCTGTGACCATCAGTATTAGAGACATTAAGACATGGAGTGTGTGGTCCAGC 127  
  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaThrIleAla 41  
DB 128 CTTATTCCTGCTGCTTTCAITGACAGTATTACAGATTGTGAGCGTAACAGCTACATGCC 187  
  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGTCAAGCTATC 247  
  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 248 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 307  
  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 308 GAGGAGTTGGTTCAGAGTACAGTAACTTCTGCTCTTGGTCACTGAGTGAAGTGAAGTAAAG 367  
  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 368 GAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 427  
  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141

DB 428 ATGTGGGTATTTTACCTATGTTGGTGCCTTGTGTTTAATGGTCTGACACTACTGATTTTGGCT 487  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 488 CTCATTTCACTCTCTCAGTGTCTCTGTTATTAAGCGCATCGGCACAGATAGTATCAT 547  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 548 TATCTAGTACTTGCACAAATGAAGTCTTAAAGATGCTATGGCTTAAATCCAGCAAAATC 607  
  
QY 182 ProGlyLeuLeuArgLysAlaGlu 189  
DB 608 CCTGGATTGAGCGCAAGCTGAA 631  
  
RESULT 36  
ADP18854  
ID ADP18854 standard; cDNA; 994 BP.  
XX  
XX ADP18854;  
AC  
XX 26-AUG-2004 (first entry)  
DT Human secreted polynucleotide #110.  
XX  
XX Human; secreted protein; gene; ss; genetic disease.  
KW Homo sapiens.  
OS  
PN US2004110939-A1.  
XX 10-JUN-2004.  
PD  
XX 15-OCT-2001; 2001US-00978360.  
PF  
XX 17-DEC-1998; 98WO-IB002122.  
PR 09-FEB-1999; 98WO-IB000282.  
PR 21-JUN-2000; 2000WO-IB000951.  
PR 15-SEP-2000; 2000US-00663600.  
XX (GEST ) GENSET SA.  
Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;  
PI Duclert A;  
XX WPI; 2004-440404/41.  
DR P-PSDB; ADP19259.  
XX New isolated polynucleotide encoding secreted polypeptide, useful for  
PT gene therapy, or in diagnostic procedures to identify individuals having  
PT genetic diseases resulting from abnormal expression of the genes.  
XX  
PS Claim 1; SEQ ID NO 110; 113pp; English.  
XX  
XX The invention relates to human cDNA sequences that encode human secreted  
CC proteins. The invention also relates to an antibody that specifically  
CC binds to a polypeptide of the invention and a method of binding the  
CC polypeptide to an antibody. The polynucleotides are useful for expressing  
CC the entire secreted proteins which they encode and for distinguishing  
CC human tissues and cells from non-human tissues and cells, and for  
CC distinguishing between human tissues and cells that do or do not express  
CC the polynucleotides comprising the cDNAs. The polynucleotides and  
CC polypeptides are useful in forensic procedures or diagnostic procedures  
CC to identify individuals with genetic diseases resulting from abnormal  
CC expression of the genes corresponding to the cDNAs. The sequences are  
CC also useful in gene therapy to control or treat genetic diseases. This  
CC sequence represents a human secreted polynucleotide of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.gov was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 994 BP; 283 A; 175 C; 232 G; 304 T; 0 U; 0 Other;  
  
Alignment Scores:

```
Pred. No.: 6.48e-102 Length: 994
Score: 918.00 Matches: 187
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 98.60% Indels: 0
DB: 12 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x ADP18854 (1-994)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValSerThrGlyValValPheGlyAlaSer 21
Db 68 GTTGTGACCTCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 127

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 128 CTATTCTGCTGCTTTCATTCAGCATTTTCAGCATTTGAGCGTAACAGCCTACATGCC 187

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 188 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAGCTATC 247

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 248 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 307

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLys 101
Db 308 GAGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTGTCATGTGAACTGCACGATAAG 367

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 368 GAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGCAAGTTTGCAGTGTG 427

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 428 ATGCGGTATTTACCTATGTTGGTGGCTTGTATTAATGCTGTCGACACTACTGATTTGGCT 487

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 488 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGACGGCATCAGGCACAGTATGATCAT 547

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 548 TATCTAGTACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 607

Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 608 CCTGGATTGAAGCCGAAAGCTGAA 631

RESULT 37
AD131056
ID AD131056 standard; cDNA; 2610 BP.
XX AC AD131056;
XX DT 17-JUN-2004 (first entry)
XX DE Human cDNA #382.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypersensinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX OS Homo sapiens.
XX FN US6607879-B1.
XX PD 19-AUG-2003.
XX PF 09-FEB-1998; 98US-00023655.
XX
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PR 09-FEB-1998; 98US-00023655.
XX (INCY-) INCYTE CORP.
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 382; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypersensinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2610 BP; 773 A; 434 C; 557 G; 820 T; 0 U; 26 Other;
```

```
Alignment Scores:
Pred. NO.: 7.73e-101 Length: 2610
Score: 914.00 Matches: 188
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 0
Query Match: 98.17% Indels: 1
DB: 11 Gaps: 0
```

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AD131056 (1-2610)

```
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValSerThrGlyValValPheGlyAlaSer 21
Db 1311 GTTGTGACCTCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 1370

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41
Db 1371 CTATTCTGCTGCTTTCATTCAGCATTTTCAGCATTTGAGCGTAACAGCCTACAAATGC 1430

Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1431 CTTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAGCTAT 1490

Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 1491 CCAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC 1550

Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLys 101
```

Db 1551 TGAGGAGTTGGTTACAGAGTACAGTAATTTCTGCTTGTGTCATGTGAACCTGCAGCATATAA 1610  
Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValle 121  
Db 1611 GGAACCTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAAGTGT 1670  
Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAl 141  
Db 1671 GATGTGGTATTACCTATGTTGGTCCCTTTTATGCTCTGACACTACTGATTTTGGC 1730  
Qy 141 aleuileSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
Db 1731 TCTCAITTCACCTTCAGTGTCTCTGTTATTTATGAACCGCATCAGCGACAGATATCA 1790  
Qy 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 1791 TTATCTAGGACITGGCAATAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAAT 1850  
Qy 181 eProGlyLeuLysArgGlyAlaGlu 189  
Db 1851 CCTGGGTTGAAGCGCAAAAGCTGAA 1875

RESULT 38  
ADP42781  
ID ADP42781 standard; cDNA; 734 BP.  
XX  
AC ADP42781;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Mouse CYP27 nucleotide sequence SEQ ID NO:87.

XX diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy;  
KW diabetes; insulin resistance; metabolic disease; mouse; gene; ss.  
XX  
XX Mus sp.  
XX  
XX WO2003102163-A2.  
XX  
XX 11-DEC-2003.  
XX  
XX 04-JUN-2003; 2003WO-US017825.  
XX  
XX 04-JUN-2002; 2002US-0385957P.  
XX  
XX 04-JUN-2002; 2002US-0386013P.  
XX  
XX 04-JUN-2002; 2002US-0386074P.  
XX  
XX 05-JUN-2002; 2002US-0386107P.  
XX  
XX 05-JUN-2002; 2002US-0386314P.  
XX  
XX 05-JUN-2002; 2002US-0386326P.  
XX  
XX 05-JUN-2002; 2002US-0386332P.  
XX  
XX 05-JUN-2002; 2002US-0386481P.  
XX  
XX 05-JUN-2002; 2002US-0386512P.  
XX  
XX 05-JUN-2002; 2002US-0386513P.  
XX  
XX 05-JUN-2002; 2002US-0386558P.  
XX  
XX 05-JUN-2002; 2002US-0386600P.  
XX  
XX 05-JUN-2002; 2002US-0386615P.  
XX  
XX 05-JUN-2002; 2002US-0386654P.  
XX  
XX 06-JUN-2002; 2002US-0386838P.  
XX  
XX 06-JUN-2002; 2002US-0386861P.  
XX  
XX 06-JUN-2002; 2002US-0386944P.  
XX  
XX 06-JUN-2002; 2002US-0386955P.  
XX  
XX 06-JUN-2002; 2002US-0387017P.  
XX  
XX 06-JUN-2002; 2002US-0387026P.  
XX  
XX 06-JUN-2002; 2002US-0387039P.  
XX  
XX 20-JUN-2002; 2002US-0386865P.

XX (META-) METABOLEX INC.  
XX  
XX PA Allan B, Gregoire F, Lavan B, Moodie S, Waters S, Wong C;  
XX PI WPI; 2004-053469/05.  
XX DR P-PSDB; ADP42782.  
XX  
XX

PT Identifying an agent for treating diabetic or pre-diabetic individuals  
PT comprises contacting an agent with a polypeptide, e.g., human ceramidase,  
PT and selecting an agent that modulates the expression or activity of the  
PT polypeptide.  
XX  
PS Disclosure; SEQ ID NO 87; 209pp; English.  
XX  
CC The present invention describes a method for identifying an agent for  
CC treating a diabetic or pre-diabetic individual. The method comprises  
CC contacting an agent to a mixture comprising a polypeptide encoded by a  
CC nucleic acid that hybridises under stringent conditions to a nucleic acid  
CC encoding any of the 23 fully defined amino acid sequences given in the  
CC specification, and selecting an agent that modulates the expression or  
CC activity of the polypeptide. Also described: (1) a method of treating a  
CC diabetic or pre-diabetic animal, comprising administering to the animal a  
CC therapeutic amount of an agent identified by the method described above;  
CC (2) a method of introducing an expression cassette into a cell,  
CC comprising introducing into the cell an expression cassette comprising a  
CC promoter operably linked to a polynucleotide encoding a polypeptide,  
CC where the polynucleotide hybridises under stringent conditions to a  
CC nucleic acid encoding the above amino acid sequences; and (3) a method of  
CC diagnosing an individual who has Type 2 diabetes or is pre-diabetic,  
CC comprising detecting in a sample from the individual the level of a  
CC polypeptide or the level of the above-mentioned polynucleotide encoding  
CC the polypeptide, where a modulated level of the polypeptide or  
CC polynucleotide in the sample compared to a level of the polypeptide or  
CC polynucleotide in either a lean individual or a previous sample from the  
CC individual indicates that the individual is diabetic or pre-diabetic. The  
CC method is useful in diagnosing and treating diabetes, insulin resistance  
CC or related metabolic diseases in human subjects. The method may also be  
CC used in identifying agents for treating diabetic or pre-diabetic  
CC individuals. The present sequence is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 734 BP; 202 A; 138 C; 179 G; 215 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3.03e-101 Length: 734  
Score: 911.00 Matches: 185  
Percent Similarity: 99.47% Conservatve: 2  
Best Local Similarity: 98.40% Mismatches: 1  
Query Match: 97.85% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADF42781 (1-734)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 100 GTTGTGGACCTCTCTACTGAGACACATTAAAGAGACTGGAGTGGTGTGGTGCACG 159  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 160 TTATTCCTGCTGCTCTCTGACAGTTCAGCAITTCAGTGTAAACGGCTTACATTCGC 219  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 220 TTGGCCCTGCTCTCTGCTACTATCAGCTTTAGATATATAAGGGTGTGATCAAGCTATC 279  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 280 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATTTGGATCTGAGTTCGCATATCA 339  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 340 GAGGAATGGTTTCAGAAATATAGTAATTCCTGCTCTTGGTTCATGTGAACACGCAATAAAA 399  
Qy 102 GluLeuArgArgLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaValLeu 121  
Db 400 GAAATTTGAGCGGTCTCTCTTAGTATGATTTAGTTGATTCCTCCCTGAGTTGAGTTG 459  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 460 ATGTGGGTATTTACTTACGTGGTGGCTTGTTCATGTGTTGACACTACTGATTTTAGCC 519

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 520 CTGATCTACCTCTTCTAGTATCTCTGTATATATGAAAGCGCATCAGCGCAGATAGATCAT 579  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 580 TATCTAGGACTTGCAAAACAAGAGTGTAAAGGATGCCATGGCCAAATCCAAAGCAAAATC 639  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 640 CCTGGATTGAAGCGCAAGCAGAA 663  
 RESULT 39  
 ID ADP45571 standard; cDNA; 3492 BP.  
 XX  
 AC ADP45571;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Rat NogoA encoding cDNA SEQ ID NO:25.  
 XX  
 KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;  
 KW nerve repair; neuroprotective; gene therapy;  
 KW central nervous system injury; CNS injury; neurodegenerative disorder;  
 KW rat; gene; ss.  
 XX  
 OS Rattus norvegicus.  
 XX  
 FH Location/Qualifiers  
 FT 1..3492  
 FT /\*tag= a  
 FT /product= "NogoA"  
 XX  
 WO2004052932-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 09-DEC-2003; 2003WO-EP013960.  
 XX  
 PR 10-DEC-2002; 2002GB-00028832.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 PA (UYZU-) UNIV ZUERICH.  
 XX  
 PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;  
 PI Zurini M;  
 XX  
 DR WPI; 2004-468818/44.  
 DR P-PSDB; ADP45572.  
 XX  
 PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.  
 XX  
 PS Disclosure; SEQ ID NO 25; 121pp; English.  
 XX  
 CC The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes rat NogoA, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 3492 BP; 1031 A; 804 C; 822 G; 835 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6,27e-100 Length: 3492  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservatives: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 97.53% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADP45571 (1-3492)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 2923 TCAGTTGTGACCTCCTCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGC 2982  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 2983 AGCTTATTCCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCCCTACAT 3042  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3043 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGCAGGCT 3102  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3103 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA 3162  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 3163 TCAGAGGAATTTGGTTTCAGAAATACAGTAATTTCTGCTCTGTGTCATGTGAACAGCAATA 3222  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3223 AAAGACTGAGCGCGCTTTCTTCTAGTTGATGATTTAGTTGATTCCTGAAGTTGTCAGTG 3282  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 3283 TTGATGTGGTGTGTTTACTTATGTTGGTGCCTTGTTCATGTGCTGACACTACTGATTTTA 3342  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 3343 GCTCTGATCTCACCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGAT 3402  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3403 CATATCTAGGACTTGCAAAACAAGAGTGTAAAGGATGCCATGGCCAAATCCAAAGCAAA 3462  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 3463 ATCCCTGGATTGAAGCGCAAGCAGAT 3489  
 RESULT 40  
 ID AAD01173 standard; cDNA; 4684 BP.  
 XX  
 AC AAD01173;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat neurite growth inhibitor Nogo A cDNA.  
 XX  
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; ss.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key  
 FT CDS Location/Qualifiers  
 FT 253..3744



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FT      /*tag= a
FT      /product= "Nogo A"
FT      /transl_except= (pos:1462..1464, aa:ile)
XX      WO200031235-A2.
PD      02-JUN-2000.
XX      05-NOV-1999; 99WO-US026160.
XX      06-NOV-1998; 98US-0107446P.
XX      (SCHW/) SCHWAB M E.
XX      (CHEN/) CHEN M S.
XX      Schwab ME, Chen MS;
XX      WPI; 2000-400052/34.
XX      P-PSDB; AA71310.
XX      Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX      of the central nervous system and inducing regeneration of neurons.
XX      Claim 26; Fig 2A; 122pp; English.
XX      The present sequence is a cDNA encoding rat Nogo A protein which is a
XX      potent neural cell growth inhibitor and is free of all central nervous
XX      system (CNS) myelin material with which it is natively associated. The
XX      present sequence was generated by fusing R018U37-3, R1-3U21 cDNA
XX      sequences isolated from hexanucleotides-primed rat brain stem/spinal cord
XX      library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte
XX      library. Nogo proteins and fragments displaying neurite growth inhibitory
XX      activity are used in the treatment of neoplastic disease of the CNS e.g.
XX      glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
XX      pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
XX      meningioma, neuroblastoma or retinoblastoma and degenerative nerve
XX      diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
XX      promote Nogo activity can be used to treat or prevent hyperproliferative
XX      or benign dysproliferative disorders e.g. psoriasis and tissue
XX      hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
XX      inhibit production of Nogo protein to induce regeneration of neurons or
XX      to promote structural plasticity of the CNS in disorders where neurite
XX      growth, regeneration or maintenance are deficient or desired. The animal
XX      models can be used in diagnostic and screening methods for predisposition
XX      to disorders and to screen for or test molecules which can treat or
XX      prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
XX      referred in claim 32 and SEQ ID NO: 29 in disclosure of the
XX      specification. However the specification does not include sequences for
XX      these SEQ ID numbers
XX      SQ      Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9,47e-100      Length:      4684
Score:          908.00      Matches:      184
Percent Similarity: 98.94%      Conservative: 3
Best Local Similarity: 97.35%      Mismatches: 2
Query Match:    97.53%      Indels:      0
DB:            3      Gaps:        0

US-09-830-972-29_COPY_990_1178 (1-189) x AAD01173 (1-4684)
QY      1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB      3175 TCAGTTGTGACCTCCTACTGTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3234
QY      21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB      3235 AGCTTATTCTGCTGCTCTCTGAGAGTTCAGAGTTCAGATGTTACAGGCGCTACAT 3294
QY      41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
DB      3295 GCCTTGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGCT 3354
```

```
QY      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB      3355 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA 3414
QY      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB      3415 TCAGAGGAATGGTTCAGAAATACAGTAATCTGCTCTCTGGTCATGTCAGACACAAATA 3474
QY      101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB      3475 AAGAAGCTGAGCGCGCTTTCTTCTAGTGTATTTAGTTGATTCCTCCCTGAAGTTGCAGTG 3534
QY      121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeu 140
DB      3535 TTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCATTTGCTGACACTACTGATTTTAA 3594
QY      141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB      3715 ATCCCTGGATTGAAGCGCAAGACAGAT 3741
XX      ABN86600 standard; DNA; 4684 BP.
XX      ABN86600;
XX      05-NOV-2002 (first entry)
XX      Rat neurotransmitter receptor protein Nogo encoding DNA.
XX      Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
XX      central nervous system; peripheral nervous system; tranquilizer; Nogo;
XX      vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
XX      nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
XX      osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
XX      neurotransmitter receptor; rat; gene; ds.
XX      Rattus norvegicus.
XX      Key      Location/Qualifiers
XX      CDS      253..3744
XX      FT      /*tag= a
XX      FT      /product= "Nogo-A"
XX      US2002072493-A1.
XX      13-JUN-2002.
XX      28-JUN-2001; 2001US-00893348.
XX      19-MAY-1998; 98IL-00124500.
XX      21-JUL-1998; 98WO-US014715.
XX      22-DEC-1998; 98US-00218277.
XX      19-MAY-1999; 99US-00314161.
XX      (YEDA ) YEDA RES & DEV CO LTD.
XX      Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;
XX      Moalem G;
XX      WPI; 2002-607255/65.
XX      P-PSDB; ABB81074, ABB81076, ABB81077.
XX      Promoting nerve regeneration and preventing neuronal degeneration in the
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Db 3280 GTGTTGATGGGTATTACTTACGTTGGTGGCTTTGTTCAATGGTTTGACACTACTGATT 3339
Qy 140 LeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle 159
Db 3340 TTAGCTCTGATCTCACTCTTCAGTATCTCTGTATATATGAACGGCATCAGCGCGAGATA 3399
Qy 160 AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla 179
Db 3400 GATCATTATCTAGGACTTGCAACAAGAGCGTTAAGGATGCCATGGCCAAATCCAGCA 3459
Qy 180 LysIleProGlyLeuLysArgLysAlaGlu 189
Db 3460 AAAATCCCTGGATTGAAGCGCAAGCAGAA 3489

RESULT 44
AAD01175
ID AAD01175 standard; cDNA; 1568 BP.
XX
AC AAD01175;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat neurite growth inhibitor Nogo C cDNA.
XX
KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.
XX
OS Rattus sp.
XX
FH Key
FT Location/Qualifiers
FT 1..1566
FT /*tag= a
FT /product= "Nogo C protein (residues 40-238) flanked by 1-
FT 39 residues at the N-terminal and 239-522 residues at the
FT C-terminal"
FT /transl_except= (pos:7..9, aa:Xaa)
FT /transl_except= (pos:85..87, aa:Xaa)
FT /transl_except= (pos:787..789, aa:Xaa)
FT /transl_except= (pos:826..828, aa:Xaa)
FT /transl_except= (pos:841..843, aa:Xaa)
FT /transl_except= (pos:883..885, aa:Xaa)
FT /transl_except= (pos:889..891, aa:Xaa)
FT /transl_except= (pos:940..942, aa:Xaa)
FT /transl_except= (pos:952..954, aa:Xaa)
FT /transl_except= (pos:1003..1005, aa:Xaa)
FT /transl_except= (pos:1111..1113, aa:Xaa)
FT /transl_except= (pos:1120..1122, aa:Xaa)
FT /transl_except= (pos:1138..1140, aa:Xaa)
FT /transl_except= (pos:1216..1218, aa:Xaa)
FT /transl_except= (pos:1222..1224, aa:Xaa)
FT /transl_except= (pos:1228..1230, aa:Xaa)
FT /transl_except= (pos:1264..1266, aa:Xaa)
FT /transl_except= (pos:1297..1299, aa:Xaa)
FT /transl_except= (pos:1318..1320, aa:Xaa)
FT /transl_except= (pos:1357..1359, aa:Xaa)
FT /transl_except= (pos:1393..1395, aa:Xaa)
FT /transl_except= (pos:1444..1446, aa:Xaa)
FT /transl_except= (pos:1537..1539, aa:Xaa)
FT /note= "Xaa corresponds to in-frame stop codon; the CNS
FT does not end in a stop codon"
FT /partial
FT 118..120
FT misc_feature
FT /*tag= b
FT /note= "Start codon of Nogo C coding region"
FT 715..717
FT misc_feature
FT /*tag= c
FT /note= "Stop codon of Nogo C coding region"
XX

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PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
Schwab ME, Chen MS;
XX
WPI; 2000-400052/34.
DR P-PSDB; AAY71312.
XX
Nogo proteins and nucleic acids useful for treating neoplastic disorders
of the central nervous system and inducing regeneration of neurons.
XX
Claim 23; Fig 14; 122pp; English.
XX
The present sequence is a cDNA encoding rat Nogo C protein which is a
potent neural cell growth inhibitor and is free of all central nervous
system (CNS) myelin material with which it is natively associated. Nogo
proteins and fragments displaying neurite growth inhibitory activity are
used in the treatment of neoplastic disease of the CNS e.g. glioma,
glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
activity can be used to treat or prevent hyperproliferative or benign
dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
Ribozymes or antisense Nogo nucleic acids can be used to inhibit
production of Nogo protein to induce regeneration of neurons or to
promote structural plasticity of the CNS in disorders where neurite
growth, regeneration or maintenance are deficient or desired. The animal
models can be used in diagnostic and screening methods for predisposition
to disorders and to screen for or test molecules which can treat or
prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
referred in claim 32 and SEQ ID NO: 29 in disclosure of the
specification. However the specification does not include sequences for
these SEQ ID numbers
XX
SQ Sequence 1568 BP; 435'A; 274 C; 375 G; 484 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.27e-100 Length: 1568
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.10% Indels: 0
DB: 3 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AAD01175 (1-1568)
Qy 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysTyrGlyValValPheGlyAlaSer 21
Db 151 GTTGTGGACCTCCTCTACTGAGAGACATTAAAGAACTGGAGTGGTGTGGTCCAGC 210
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 211 TTATTCTCTGCTGCTCTCTGACAGTGTTCAGCATTTGTAGTAAACGGCTTACATTGCC 270
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 271 TTGGCCCTGCTCTCGGTGACTATCAGCTTTTAGGATATATAAGGGCGGTGATCCAGGCTATC 330
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 331 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATTTTAGAATCTGAAGTTGCTATATCA 390
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

```

Db 391 GAGGAATTGGTTCAGAAATACAGTAATTCCTGCTCTGGTCATGTGAACAGCAATAA 450  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 451 GAATCAGGCGGCTTTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTGCAGTGTG 510  
Qy 122 MetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 511 ATGTGGGTGTTTACTTATGTGTGGTGCCTTGTTCATATGGTCTGCACACTACTGATTTAGCT 570  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 571 CTGATCTCACTTCTAGTATTCCTGTTATTTATGAACGGCAATCAGTGCAGATAGATCAT 630  
Qy 162 TyrLeuGlyLeuAlaAsnLysAnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 631 TATCTAGGACTTGCACAAAGAGTGTTAAGGATGCCATGGCCAAATCCAAAGCAAAATC 690  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 691 CCTGGATTGAAGCGCAAGCAGAT 714

## RESULT 45

AAV30920

ID AAV30920 standard; cDNA; 2386 BP.

XX

AC AAV30920;

DT 14-SEP-1998 (first entry)

XX

DE Human secreted protein BG160\_1 cDNA.

XX

KW BG160\_1; secreted protein; protein factor; human; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 102..2030

FT /\*tag= a

FT sig\_peptide 1863..1899

FT /\*tag= b

FT /\*note= "putative leader/signal peptide"

FT mat\_peptide 1900..2027

FT /\*tag= c

XX

XX WO9817687-A2.

XX

XX 30-APR-1998.

XX

XX 24-OCT-1997; 97WO-US019590.

XX

XX 25-OCT-1996; 96US-00740274.

XX

XX 24-OCT-1997; 97US-00740274.

XX

XX (GEMY ) GENETICS INST INC.

XX

XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

XX

XX Spaulding V, Agostino MJ;

XX

XX WPI; 1998-261426/23.

XX

XX P-PSDB; AAW58383.

XX

XX Nucleic acid encoding secreted protein from human cells - useful, e.g. as

XX

immuno-modulators, anti-tumour agents, promoters of tissue growth, haemostatic and thrombolytic agents etc.

Claim 20; Page 74-75; 11app; English.

This cDNA clone, designated BG160\_1, codes for a novel human secreted protein (see AAW58383). It was isolated from a human adult brain cDNA library using methods selective for cDNAs that encode secreted proteins. The clone is deposited in composite clone ATCC 98232; an oligonucleotide (see AAT99725) is designed to isolate the clone from the composite. The

XX 21-OCT-2002 (first entry)

XX DNA encoding human NogoC protein.

XX Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;

XX stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;

XX neuroblastoma; hyperproliferative disorder; dysproliferative disorder;

XX cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;

XX tissue hypertrophy; central nervous system; axon regeneration; NogoC;

XX Nogo-associated disease; metastasis; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 215..814

XX /\*tag= a

XX /product= "Human NogoC protein"

XX WO200257483-A2.

XX 25-JUL-2002.

XX 18-JAN-2002; 2002WO-GB0000228.

XX 18-JAN-2001; 2001GB-00001312.

XX (GLAXO) GLAXO GROUP LTD.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX WPI; 2002-599722/64.

XX P-PSDB; ABG30939.

XX Identifying modulators of Nogo or BACE activity for treating acute

XX neuronal injuries, neoplastic or dysproliferative disorders, comprises

XX providing and monitoring interaction between Nogo and BACE polypeptides.

XX Disclosure; Page 62-64; 68pp; English.

XX The present invention relates to a new method of identifying modulators

XX of Nogo function or BACE activity. The method involves providing Nogo and

XX BACE polypeptides capable of binding with each other, monitoring the

XX interaction between these polypeptides, and determining if the test agent

XX is a modulator of Nogo or BACE activity. The method is useful in treating

XX acute neuronal injuries, such as spinal or head injury, stroke,

XX peripheral nerve damage, and in neoplastic (e.g. glioblastomas,

XX neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.

XX cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue

XX hypertrophy) of the central nervous system. The BACE polypeptide is

XX useful in screening methods to identify agents that may act as modulators

XX of BACE activity and in particular agents that may be useful in treating

XX Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,

XX and the polynucleotide encoding the BACE polypeptide are useful in

XX manufacturing a medicament for the treatment or prevention of disorders

XX responsive to the modulation of Nogo activity, in alleviating the

XX symptoms or improving the condition of a patient suffering from this

XX disorder, in axon regeneration, or in preventing metastasis or spreading

XX of a cancer. The polynucleotide may also be an essential component in

XX assays, a probe, in recombinant protein synthesis, and in gene therapy

XX techniques. The present nucleic acid sequence encodes the human NogoC

XX protein of the invention

XX Sequence 1798 BP; 540 A; 314 C; 392 G; 552 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 1,19e-97 Length: 1798

XX Score: 886.00 Matches: 187

XX Percent Similarity: 98.94% Conservative: 0

XX Best Local Similarity: 98.94% Mismatches: 1

XX Query Match: 95.17% Indels: 2

XX DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABK90135 (1-1798)

QY 2 ValValAspLeuLeuTyrTTPArgAspIleIysIysThrGlyValValPheGlyAlaSer 21

DB 248 GTTGTGGACCTCCCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCAGC 307

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

DB 308 CTATTCTGCTGCTTTCATTGACAGTATTGACGATTGTGAGCGTAACAGCCTACATTGCC 367

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleAlaIle 61

DB 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 427

QY 62 GlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

DB 428 CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 487

QY 82 GluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

DB 488 GAGGAGTTGGTTTCAAGAGTACAGTAAATTTCTGCTCTTGGTCAATGGAAGTGCAGATAAG 547

QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

DB 548 GAAGTCAAGGGCCCTCTTCTTAGTTGATTTAGTTAGTTGATTTCTGGAAGTTTGCAGTGTG 607

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141

DB 608 ATGTGGGTATTTACCTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTGGCT 667

QY 142 LeuIleSerLeu-PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161

DB 668 CTCAATTCACCTCTTCAGTGTCTCTGTTATTTA-GAAGCGCATCAGGCACAGATAGATCA 726

QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 727 TTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAAT 786

QY 181 eProGlyLeuLysArgLysAlaGlu 189

DB 787 CCCTGGATTGAAGCGCAAAAGCTGAA 811

RESULT 47

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX AAF98399;

XX 07-JUN-2001 (first entry)

XX Human cDNA clone BG160\_1 sequence SEQ ID 41.

XX Human; secreted protein; nutrient; cytokine modulator; proliferation;

XX differentiation; immune system modulator; tissue growth; chemotactic;

XX haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;

XX haematopoiesis.

XX Homo sapiens.

XX WO200119988-A1.

XX 22-MAR-2001.

XX 14-SEP-2000; 2000WO-US025135.

XX 17-SEP-1999; 99US-00398829.

XX (GEM) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

DR WPI; 2001-244801/25.  
DR P-PSDB; AAB90682.  
XX Isolated nucleic acids encoding polypeptides, useful for modulating e.g.  
PT cytokine and cell proliferation/differentiation activity, the immune  
PT system and hematopoiesis regulating activity.  
XX  
XX  
PS Claim 1; Page 408-409; 557pp; English.  
XX  
XX Human cDNA clones represented in AAF98374 - AAF98489 encode secreted  
CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various  
CC tissue types, and may be used in the prevention, treatment and diagnosis  
CC of diseases associated with inappropriate protein expression. The  
CC polypeptides and nucleic acids may be used as nutrients or to modulate  
CC cytokine and cell proliferation/differentiation activity and may also be  
CC involved in modulation of the immune system. The cDNA sequences,  
CC proteins, their agonists and/or antagonists exhibit hematopoiesis  
CC regulating activity; tissue growth activity; activin/inhibin activity;  
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;  
CC receptor/ligand activity; anti-inflammatory activity; hematopoiesis  
CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition  
CC activity. Included in the invention are probes represented in AAF98490 -  
CC AAF98572 which are specific for the cDNA clones encoding the secreted  
CC proteins  
XX  
SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,04e-97 Length: 2386  
Score: 885.50 Matches: 183  
Percent Similarity: 96.83% Conservative: 0  
Best Local Similarity: 96.83% Mismatches: 1  
Query Match: 95.11% Indels: 5  
DB: Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF98399 (1-2386)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThyGlyValValPheGlyAla 20  
Db 1476 TCAGTTGTTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 1535  
QY 21 SerLeuPheLeuLeuSerLeuThyValPheSerIleValSerValThrAlaTyrIle 40  
Db 1536 AGCCTATTCTGCTGCTTCTATTGACAGTATTGAGCATTTGTGAGCGTAAACGCTACATT 1595  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 1596 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 1655  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 1656 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGG-----GAAGTTGCTATA 1700  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 1701 TCTGAGGAGTGGTTCTGAGAGTACAGTAATTCCTTGGTCATGTGAAGTGCAGATA 1760  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 1761 AAGNACTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTGCAGTG 1820  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 1821 TTGATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGGTGTGACACTACTGATTTTG 1880  
QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 1881 GCCTCATTTTCATCTCTCTGAGTGTGTGTATTATGACAGCGCATCAGGCACAGATAGAT 1940  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1941 CATTATCTAGGACTTCMAATAAGATGTTAAGATGCTATGCCTAAATCCAGCAAAA 2000

QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 2001 ATCCCTGGATTGAAGCGCAAGCTGAA 2027  
RESULT 48  
ABK34580  
ID ABK34580 standard; cDNA; 1514 BP.  
XX  
XX ABK34580;  
AC  
XX 08-MAY-2002 (first entry)  
DT  
XX Human cDNA for novel secreted protein, SEQ ID 349.  
DE  
XX Human; ss; gene; secreted protein; immune deficiency; viral infection;  
KW bacterial infection; fungal infection; autoimmune disorder; burn;  
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;  
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;  
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;  
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;  
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;  
KW lymphoid cell deficiency.  
XX  
OS Homo sapiens.  
XX  
XX WO200177290-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 29-MAR-2001; 2001WO-US010295.  
XX  
XX 06-APR-2000; 2000US-0194941P.  
XX  
XX (GEMY) GENETICS INST INC.  
XX  
XX Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
PI Gulukota K, Graham JR;  
PI  
XX WPI; 2002-179323/23.  
XX  
XX Six hundred and twenty five polynucleotides derived from a variety of  
PT human tissue sources which encode secreted proteins, useful for treating  
PT immune deficiencies and disorders such as autoimmune disorders.  
XX  
XX Claim 1; Page 173; 339pp; English.  
XX  
XX The invention relates to 625 polynucleotides which have been derived from  
CC a variety of human tissue sources and which encode novel secreted  
CC proteins, their complements and sequences that hybridise to them. Also  
CC included are a vector comprising the polynucleotide, a host cell  
CC transformed with the vector, the proteins encoded by the polynucleotides,  
CC antibodies that bind to the proteins and identification of modulators of  
CC the proteins or the expression of the polynucleotide. The polynucleotides  
CC can be used as probes for the identification and isolation of full length  
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used  
CC as nutritional supplements. The protein is useful in the treatment of  
CC various immune deficiencies and disorders such as viral infections,  
CC bacterial infections, fungal infections, autoimmune disorders (e.g.  
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and  
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are  
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's  
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders  
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and  
CC tumours. They are also useful for tissue regeneration, for wound healing  
CC and in the treatment of burns, incisions and ulcers. The proteins are  
CC also useful for regulating haematopoiesis, for treating myeloid or  
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA  
CC sequences encoding a secreted protein  
XX  
SQ Sequence 1514 BP; 455 A; 258 C; 313 G; 488 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.95e-95 Length: 1514

Score: 867.00 Matches: 177  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.13% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABK34580 (1-1514)

QY 13 LysThrGlyValValPheGlyValSerLeuPheLeuLeuSerLeuThrValPheSer 32  
 DB 3 AAGACTGGAGTGGTGGTGGCCAGCTATTCCTGCTGCTTCATTGACAGTATTCAGC 62  
 QY 33 IleValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArg 52  
 DB 63 ATTGTGAGCGTAACAGCTACATTGCCCTGGCTCTCTGTGACCATCAGCTTTAGG 122  
 QY 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72  
 DB 123 ATATCAAGGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 182  
 QY 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92  
 DB 183 TATCTGGAATCTGAAGTTGCTATATCTCAGGAGTTGGTTCAAGATCAGTAATTCCTGCT 242  
 QY 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeu 112  
 DB 243 CTTGTCATGTGAACATGACGATGAAGAACTCAGCGCCCTCTCTAGTTGATGATTTA 302  
 QY 113 ValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeuPhe 132  
 DB 303 GTTGATTTCTGAAGTTTGCAGTGTGATGGGTATTTACCTATGTGGTGGCTTGTGTT 362  
 QY 133 AsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIleTyr 152  
 DB 363 AATGTCCTGACACTACTGATTTGGCTCTCATTTCCACTTTCAGTGTTCCTGTTATTTAT 422  
 QY 153 GluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172  
 DB 423 GAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATTAAGAATGTTAAGAT 482  
 QY 173 AlaMetAlaValIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189  
 DB 483 GCTATGGCTAAATCAAGCAAAAATCCCTGGATTGAAGCGCAAGCTGAA 533

# RESULT 49

ID AAD08386 standard; cDNA; 1683 BP.

AC AAD08386;

DT 09-AUG-2001 (first entry)

DE Human secreted protein-encoding gene 42 cDNA clone HAGFT48, SEQ ID NO:52.

KW Human; secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder;  
 KW endocrine disorder; infection; wound healing; vulnerability; cell culture;  
 KW chemotaxis; food additive; gene therapy; binding partner identification;  
 KW ss.

XX Homo sapiens.

XX Location/Qualifiers  
 FH 830..1192  
 FT /\*tag= a

FT /product= "Human secreted protein precursor"  
 FT /note= "CDS does not include start codon"

FT sig\_peptide /partial  
 FT 830..898 /\*tag= b  
 FT mat\_peptide 899..1189  
 FT /\*tag= c  
 FT /product= "Mature human secreted protein"

PN WO200077022-A1.

XX 21-DEC-2000.

PP 01-JUN-2000; 2000WO-US015136.

PR 11-JUN-1999; 99US-0138629P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;

PI P-PSDB; AAE03939.

DR WPI; 2001-367020/38.

XX Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome.

PS Claim 1; Page 520; 614pp; English.

CC AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03898-AAE03947 represent the proteins they encode. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders; cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention

SQ Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;

## Alignment Scores:

Pred. No.: 1,01e-83 Length: 1683  
 Score: 771.50 Matches: 164  
 Percent Similarity: 87.23% Conservativity: 0  
 Best Local Similarity: 87.23% Mismatches: 1  
 Query Match: 82.87% Indels: 24  
 DB: 4 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAD08386 (1-1683)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

DB 788 GTTGTGACCTCCTGTTACTGAGAGACATTAAAGACTGAGTGGTGTGTTGGTCCAGC 847



QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 848 CTAATTCCTGCTGCTTTTCATGACAGATTACAGCATTTGAGCGTAAACAGCCTACATTCGC 907  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 967  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 968 CAGAAATCAGATGAGGCCACCCATTGAGGCATATCTGGAATCTGGAATCTGATATCT 1027  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 1028 GAGGAGTTGGTTTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCAGATAAG 1087  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1088 GAATCAGGCGCTCTCTTAGTTGATGATTAGTTGATCTCTGAAGCT----- 1137  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
DB 1137 ----- 1137  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 1138 CTCAATTCATCTCTTCAGTGTCTCTGTTATTTATGAAAGCGCATCAGGCACAGATAGATCAT 1197  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1198 TATCTAGGACTTTCGAATTAAGATGTTAAAGATGCTATGGCTAAATTCAGCAAAATC 1257  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 1258 CCTGGATTGAGCGCAAGCTGAA 1281  
RESULT 50  
ID ABX43312  
XX ABX43312 standard; cDNA; 422 BP.  
XX AC ABX43312;  
XX 20-FEB-2003 (first entry)  
XX DE Bovine EST associated with lactation/muscle/fat deposition #8477.  
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
XX KW muscle deposition; fat deposition; genome mapping; gene identification;  
XX KW gene analysis; cattle breeding.  
XX OS Bos Taurus.  
XX PN US2002137139-A1.  
XX PD 26-SEP-2002.  
XX PF 24-SEP-2001; 2001US-00960352.  
XX PR 12-JAN-1999; 99US-0115707P.  
XX PR 11-JAN-2000; 2000US-00480902.  
XX (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
XX Byatt JC, Mathialagan N, Tao N, Warren WC;  
XX WPI; 2003-110599/10.  
XX New nucleic acid associated with lactation, and muscle and fat  
XX deposition, useful for genome mapping, gene identification and analysis,  
PT

PT cattle breeding, or for genetically improving cattle.  
XX Claim 2; SEQ ID NO 8477; 245pp; English.  
XX The invention relates to a purified nucleic acid molecule associated with  
CC lactation or muscle and fat deposition (designated LMFD), derived from  
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second  
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,  
CC appearing as ABX43312-ABX49947, or complements of them. Also included are  
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic  
CC acid linked to a promoter and a 3' non-translated sequence that  
CC functions in the cell to cause termination of transcription and addition  
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
CC (2) determining a level or pattern of a molecule in a bovine cell or  
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
CC of the 15112 nucleic acid sequences or its complement or fragment) with a  
CC complementary nucleic acid molecule obtained from the bovine cell or  
CC tissue, where hybridisation between the marker nucleic acid and the  
CC complementary nucleic acid permits the detection of the molecule; and (b)  
CC detecting the level or pattern of the complementary nucleic acid; where  
CC the detection of the complementary nucleic acid is predictive of the  
CC level or pattern of the molecule. The LMFD nucleic acid is used for  
CC determining a level or pattern of a molecule in a bovine cell or tissue.  
CC It is useful for genome mapping, gene identification and analysis, cattle  
CC breeding, preparation of constructs for use in cattle gene expression, or  
CC for genetically improving cattle. The present sequence is one of the  
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The  
CC present sequence was not shown in the specification but was obtained in  
CC electronic format from the USPTO web site:  
CC seqdata.uspto.gov/sequence.html?DocID=20020137139  
XX  
XX Sequence 422 BP; 109 A; 79 C; 94 G; 140 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3,14e-75 Length: 422  
Score: 695.00 Matches: 140  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 74.65% Indels: 0  
DB: 8 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABX43312 (1-422)

QY 37 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGly 56  
DB 2 ACGGCTACATTCGCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGT 61  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
DB 62 GTGATCCAGGCTATCCAGAAATCTGATGAAGCCACCCATTGAGGCATATTTGGAATCT 121  
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96  
DB 122 GAAGTTGCTATATCTGAGGAGTTGGTTCAAGAGTACAGCAATTCGCTCTGCTCATGTT 181  
QY 97 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeu 116  
DB 182 AACTGCACAATAAAGAACTCAGACGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTG 241  
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThr 136  
DB 242 AAGTTTGCAGTGTGATGTTGGGTATTTACTATGTTGGTCCCTGTTCAATGGTCTGACA 301  
QY 137 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 156  
DB 302 CTACTAATTTTGGCTCTGATTTCACTCTTCAGTTGTTCTCTGTTATTTATGAAGGCATCAG 361  
QY 157 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 176  
DB 362 GCGCAATAGATCATTTATCTGGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAA 421  
RESULT 51  
ADJ56527



ADJ56527 standard; cDNA; 1520 BP.  
ADJ56527;  
06-MAY-2004 (first entry)  
Rat cDNA differentially expressed in MYCN activated cells SeqID 333.  
rat; differential expression; transactivator; proto-oncogene;  
neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;  
MYCN activated cell.  
XX  
XX  
OS Rattus norvegicus.  
XX  
PN US2003119009-A1.  
XX  
XX 26-JUN-2003.  
XX  
XX 25-FEB-2002; 2002US-00084817.  
XX  
XX 23-FEB-2001; 2001US-0270784P.  
XX  
XX (STUA/) STUART S G.  
PA (NUCH/) NUCHTERN J G.  
PA (PLON/) PLON S E.  
PA (SHOH/) SHOHET J M.  
XX  
XX Stuart SG, Nuchtern JG, Plon SE, Shohet JM;  
PI WPI; 2003-635698/60.  
XX  
XX New genes regulated by MYCN activation, useful in gene therapy, other  
PT particularly for treating a subject with e.g. neuroblastoma or other  
PT cancers, or for diagnosing, staging or monitoring the treatment of the  
PT cancer.  
XX  
XX Claim 1; SEQ ID NO 333; 27pp; English.  
XX  
XX This invention relates to novel isolated cDNAs that are differentially  
CC expressed in MYCN activated cells. Specifically, it refers to  
CC polynucleotide sequences that exhibit differential expression patterns in  
CC cells activated by the transactivator MYCN, where MYCN is a proto-  
CC oncogene that is amplified in neuroblastoma cells and is common in small  
CC cell lung cancers. The present invention describes these cDNA molecules  
CC as useful for in hybridisation assays to detect expression of nucleic  
CC acids (or complementary nucleic acids) in a present in a given sample, as  
CC well as for screening assays by identifying molecules or compounds that  
CC specifically bind the cDNA as a ligand and modulate function or activity.  
CC Accordingly, these compositions exhibit cytostatic activity and can also  
CC be used for gene therapy purposes. This polynucleotide sequence is a cDNA  
CC that is differentially expressed in MYCN activated cells, given in an  
CC exemplification of the invention. NOTE: This sequence does not appear in  
CC the printed specification but has been obtained in electronic format from  
CC the US Patent Office at  
CC ftp.usdata.uspto.gov/sequence.html?DocID=20030119009.  
XX  
XX Sequence 1520 BP; 398 A; 354 C; 336 G; 432 T; 0 U; 0 Other  
XX

```

Alignment Scores:
Pred. No.:      7.31e-73          Length:      1520
Score:         682.00           Matches:     128
Percent Similarity:  85.0%       Conservative: 31
Best Local Similarity: 68.45%    Mismatches:  28
Query Match:   73.25%           Indels:      0
DB:            10              Gaps:        0

US-09-830-972-29_COPY_990_1178 (1-189) x ADJ56527 (1-1520)

Qy      3 ValAspLeuLeuThrTrpArgAspIleValSerGlyValValPheGlyAlaSerLeu 22
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      176 AITGACCTGTATATTGGCGGCACATCAAGCAGACGGCATCGTGTITGGAGTTTCCTG 235
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTrpIleAlaLeu 42

```

Db	236	CTGCTGCTCTTCTCCCTGACCAGTTCAGCGTGGTGAGCGTCTGCGCTTACTGCGCCCTG	295
Qy	43	AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln	62
Db	296	GCCGCACTCTCAGCCACCATCAGTTTCGCACTCAACAAGTCGTGTTTACACGACGTGCAG	355
Qy	63	LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu	82
Db	356	AAACCCGACGAAGCCACCCCTTCAAGGCTTCTGGAGCTTGAGATCACCTTCTCTCAG	415
Qy	83	GluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnCysThrIleIysGlu	102
Db	416	GAGCAGATTTCAGAAAGTACACGACTGCTGCAGTTCTACGTGAACGACACACTTAAGGAA	475
Qy	103	LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet	122
Db	476	CTGAGGAGGCTTCTCTGTGTCAGGACCTGTGTGATTTCTTAAATTTTGACATCTCTGATG	535
Qy	123	TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu	142
Db	536	TGGCTCCTGACCTACGTTTGGCGCTCTCTTCAATGGCTTGACCTGCTGCTCATGGCTGTG	595
Qy	143	IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr	162
Db	596	GTTTCAATGTTTACTCTACCTGTAGTGATGTTAAGCACCCAGGCACAGATTGACCAATAT	655
Qy	163	LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaIleGlnAlaLysIlePro	182
Db	656	CTGGACTTTGAGAGACTCACTAAATGCTGTTGTGGCAAGATTGAGCTAAATCCCA	715
Qy	183	GlyLeuLysArgLysAlaGlu	189
Db	716	GGCGCTAAGAGGCAGCTGAG	736
RESULT	52		
AD007887			
ID	AD007887	standard; cDNA; 2331 BP.	
AC	AD007887;		
XX			
DT	01-JUL-2004	(first entry)	
XX			
DE	Human polynucleotide #66.		
XX			
KW	Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;		
KW	anorectic; antidiabetic.		
XX			
OS	Homo sapiens.		
XX			
PN	US2004071700-A1.		
XX			
PD	15-APR-2004.		
XX			
PF	09-OCT-2002; 2002US-00267502.		
XX			
PR	09-OCT-2002; 2002US-00267502.		
XX			
PA	(LIFE-) LIFE SCI DEV CORP.		
XX			
PI	Kim J, Galant R;		
XX			
DR	WPI; 2004-328526/30.		
DR	P-PSDB; AD008104.		
XX			
PT	Identifying compounds that influence fat cell number or size for treating		
PT	or preventing obesity or diabetes by exposing the cell to the agent and		
PT	identifying fat cell number or size relative to cells not exposed to the		
PT	agent.		
XX			
PS	Claim 1; SEQ ID NO 213; 275pp; English.		
XX			
CC	The invention relates to a method of identifying compounds that influence		

CC fat cell number or size comprising providing a cell that expresses a gene  
CC and an agent, exposing the cell to the agent and identifying fat cell  
CC number or size relative to cells not exposed to the agent. The method  
CC also comprises providing an expression vector and an agent, exposing the  
CC vector to the agent, detecting a change in expression of the gene  
CC relative to expression of the gene in an expression vector not exposed to  
CC the agent, treating a subject with the agent and identifying fat cell  
CC number or size in the subject. The agent comprises an antisense  
CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
CC method also comprises providing a polypeptide and an agent, exposing the  
CC polypeptide to the agent, detecting binding of the agent to the  
CC polypeptide or a change in an activity of the polypeptide, treating a  
CC subject with the agent and identifying fat cell number or size in the  
CC subject. The agent comprises an antibody. A method of regulating fat cell  
CC number or size comprises providing a subject containing fat cells and an  
CC agent that changes the expression of a gene, and treating the subject  
CC with the agent under conditions so that fat cell size or number in the  
CC subject is altered. The method is useful for identifying compounds that  
CC influence fat cell number or size, for preparing a composition for  
CC treating or preventing obesity or diabetes. This sequence represents  
CC human cDNA used in the scope of the invention.  
XX  
SQ Sequence 2331 BP; 552 A; 698 C; 649 G; 432 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.33e-72 Length: 2331  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADO07887 (1-2331)

QY 3 ValAspLeuLeuThrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
DB 1768 ATTGACCTGTGTATTGGCGGACATCAAGCAGCGGATCGTGTGGAGTTTCCTG 1827  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
DB 1828 CTGCTGCTCTCTCCCTGACCCAGTTCAGCGTGTGAGCGTCTGCTGACCTGCGCCCTG 1887  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
DB 1888 GCGGCATCTTCACCCACCATCATGTTCCGATCTACAGTCTGTTTACAGCAGTGCAG 1947  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
DB 1948 AAMACCGACGAGCCACCCCTTTCAAGGCTACTTGGAGCTTGAGCTGAGATCCCTTCTCAG 2007  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleTyrGlu 102  
DB 2008 GACGACATTTCAGAGTACAGGACTCCCTGCACTTCTACGTGAACAGCACCTTAAGGAA 2067  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 2068 CTGAGGAGGCTCTCTCTGTCAGGACCTGCTGAGTTCCTTAAATTTGAGTCTCTGATG 2127  
QY 123 TrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142  
DB 2128 TGCTCTGACCTACCTGTGGCGCTCTCTCAATGGCTGACCTGCTGCTGCTGCTGCTG 2187  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
DB 2188 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCAGCCAGCACAGATTGACCAATAT 2247  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 2248 CTGGGACTTGTGAGGACTACATAAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2307  
QY 183 GlyLeuLysArgLysAlaGlu 189  
DB 2308 GCGGCTAAGGACGCTGAG 2328

## RESULT 53

AAAX75770

ID AAX75770 standard; DNA; 3202 BP.

XX AAX75770;

AC AAX75770;

XX 22-JUL-1999 (first entry)

XX Human neuroendocrine-specific protein NSP-A DNA.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
XX frameshift mutation; age-related disease; neurodegenerative disorder;  
XX Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
XX Huntington's disease; multiple sclerosis; alcoholic liver disease;  
XX diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
XX ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
XX neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
XX glial fibrillary acidic protein; GFAP; p33; semaphorin III; HUPF-1;  
XX bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
XX high mobility group protein-C; neuroendocrine specific protein A; ss.

OS Homo sapiens.

XX WO9845322-A2.

XX 15-OCT-1998.

XX 02-APR-1998; 98WO-IB000705.

XX 10-APR-1997; 97US-0043163P.

XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS &amp; SCI.

XX (UYRO-) UNIV ROTTERDAM ERASMUS.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX Van Leeuwen FW, Grosveld FG, Burbach JPH;

XX WPI; 1998-609901/51.

XX Diagnosing disease by detecting frameshift mutations in RNA or  
XX corresponding protein mutations - used to diagnose cancer and  
XX neurological diseases, particularly Alzheimer's disease, and also for  
XX treatment and prevention with specific ribozymes or wild-type RNA.

PS Disclosure; Fig 19; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease  
XX caused by, or associated with, an RNA molecule that has a frameshift  
XX mutation. The method is used to diagnose age-related diseases, especially  
XX cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
XX disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
XX multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
XX and many others listed) or susceptibility to these disorders. The method  
XX allows a definitive diagnosis of Alzheimer's disease in living patients,  
XX at an early stage. It is based on the observation that disease may be  
XX caused by mutations in RNA rather than DNA. The invention describes the  
XX use of neuronal system RNA molecules, specifically microtubule associated  
XX proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
XX associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
XX neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
XX protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
XX 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
XX protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence  
XX encodes the wild type and mutant protein fragments represented in  
XX AAY21434-Y21520

SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.08e-72 Length: 3202

Score: 682.00 Matches: 128

```

Percent Similarity: 85.03% Conservative: 31
Best Local Similarity: 68.45% Mismatches: 28
Query Match: 73.25% Indels: 0
DB: 2 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AAX75770 (1-3202)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db 1890 ATTGACCTGTTGTTATGGCGGACATCAAGCAGCGGCATCGTGTGGGAGTTCCTG 1949
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 1950 CTGCTGCTCTTCCTCCCTACCCAGTTCAGCGGTGAGCGTCTGGCTGCTACCTGCGCCCTG 2009
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 2010 GCGGCACCTTCAGCCACCATCATGTTCCGCATCTCAAGTCTGTTTACAAGCAGTGCAG 2069
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 2070 AAAACCGCAGGAGCCACCTTTCAAGCCTACTTGGAGCTTGAGATCACCTTCTCAG 2129
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
Db 2130 GAGCAGATTCAAGTACAGGACTCCCTGCAGTCTACGTTCAAGTCAAGCAGCAGTAAAGAA 2189
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2190 CTGAGGAGCTCTTCCTTTGTCAGACCTCGGTGGATTCCTTAAATTTGCGAGTCTCGATG 2249
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
Db 2250 TGGCTCTGACCTAGTGGCGCTCTCTCAATGSCCTGACCTGCTGCTCATGCTGTG 2309
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACCTCTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT 2369
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429
QY 183 GlyLeuLysArgLysAlaGlu 189
Db 2430 GCGGCTAAGGACGCTGAG 2450

RESULT 54
ABL64900
XX ABL64900 standard; DNA; 3202 BP.
XX ABL64900;
XX
XX 15-MAY-2002 (first entry)
XX Lung cancer related gene sequence SEQ ID NO:3237.
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX Homo sapiens.
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US010838.
XX
XX 05-JUN-2000; 2000US-0209473P.
XX 05-JUN-2000; 2000US-0209531P.
XX 18-SEP-2000; 2000US-023133P.

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PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Hendress G, Horrigan S;
XX Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, and determining a change
XX in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 3237; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
XX neoplastic agent. The method involves exposing cells to a chemical agent
XX to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening an
XX anti-neoplastic agent, and can be used for producing a product which is
XX the data collected with respect to the anti-neoplastic agent as a result
XX of M1, and the data is sufficient to convey the chemical structure and/or
XX properties of the agent. M1 can be used in the treatment of cancer such
XX as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
XX prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
XX cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
XX cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
XX tumour
XX
XX Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

```



Db 2370 CTGGACCTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLeuValGlyAlaGlu 189  
Db 2430 GCGCTAAGAGGACGCTGAG 2450

## RESULT 56

ADR24525

ID ADR24525 standard; DNA; 3202 BP.

XX ADR24525;

AC ADR24525;

XX 21-OCT-2004 (first entry)

DT 21-OCT-2004 (first entry)

XX Breast cancer prognosis marker #386.

DE ds; breast cancer; prognosis; gene expression; diagnosis.

XX Homo sapiens.

OS WO2004065545-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US001100.

XX 15-JAN-2003; 2003US-00342887.

XX (ROSE-) ROSETTA INPHARMATICS LLC.

XX (NECA-) NETHERLANDS CANCER INST.

XX Van't Veer LJ, He Y;

XX WPI; 2004-593473/57.

XX Classifying a breast cancer patient according to prognosis comprises

XX determining the similarity between the level of expression of each of

XX five genes in a cell sample taken from patient, to control levels.

XX Disclosure; SEQ ID NO 386; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient

XX according to prognosis by determining the similarity between the level of

XX expression of each of five genes for which markers are listed in the

XX specification, in a cell sample taken from the breast cancer patient, to

XX control levels of expression for each respective five genes to obtain a

XX patient similarity value. The methods are useful for classifying a breast

XX cancer patient according to prognosis. Kits and computer program products

XX are useful for data analysis using the diagnostic, prognostic and

XX statistical methods of the invention. This sequence corresponds to a

XX marker used in the method of the invention.

XX SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 2,088-72 Length: 3202

XX Score: 682.00 Matches: 128

XX Percent Similarity: 85.03% Conservatives: 31

XX Best Local Similarity: 68.43% Mismatches: 28

XX Query Match: 73.25% Indels: 0

XX DB: 13 Gaps: 0

XX US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR24525 (1-3202)

XX QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22

XX Db 1890 ATTGACCTGTTGTAATGGCGGACATCAAGCAGCGGCGATCGTGTGGGAGTTTCCTG 1949

XX QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42

XX Db 1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGCGGCGTGGCTACCTGCGCCCTG 2009

XX QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62

Db 2010 GCCGACCTCTCAGCCACCACCATCAGTTTCGCACTCTACAGTCTGTTTACAAGCAGTGCAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGCAGCAAGGCCACCCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCCTTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GAGCAGATTCAAGAGTACACCGACTGCTGCTGAGTTCTACGTGACACGACACTTAAGGAA 2189  
QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTTCTTGTGTCAGGACCTGCTGCTTCTTAAATTTGCGAGTCTCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 2250 TGGCTCTGACCTACGTTGGCGCTCTCTCAATGGCCCTGACCCCTGCTCATGCTGTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
Db 2310 GTTTCATGTTTACTTCTTACCTGTAGTGTATGTTAAGCACACGACGACAGTTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGCTAAGAGGCGCTGAG 2450

## RESULT 57

ADR65814

ID ADR65814 standard; DNA; 3202 BP.

XX ADR65814;

XX 02-DEC-2004 (first entry)

XX Human prostatic carcinoma derived DNA SEQ ID 10 #1.

XX human; cytostatic; diagnosis; prostatic cancer;

XX differential expression analysis; ds.

XX Homo sapiens.

XX WO2004076614-A2.

XX 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.

XX 14-MAY-2003; 2003DE-01022134.

XX (HINZ/) HINZMANN B.

XX (DAHL/) DAHL E.

XX (ROSE/) ROSENTHAL A.

XX (HERM/) HERMANN K.

XX (PILA/) PILARSKY C.

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pillarsky C, Specht T;

XX Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;

XX Xinzhang L, Staub E;

XX WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,

XX useful for diagnosis, treatment and in screening for specific binding

XX agents.

XX Claim 1; Page 160; 1607pp; German.

CC This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.

XX SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2, 08e-72 Length: 3202  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 13 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR65814 (1-3202)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTGTATGGGGGACATCAAGCAGCGGCATCGTGTGGAGTTCCTCG 1949  
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 1950 CTGCTGCTTCTTCTCCCTGACCCAGTTCAGCGGTGCGTGTGCTTACCTTGGCCCTG 2009  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCGGCACTCTACCCACCATCATCTTCGATCTACAGTCTGTTTACAGCAGTGCAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGCAGGAGCCACCCCTTTCAAGGCGCTACTTGGAGCTTGCAGATCCCTTTCTCAG 2129  
QY 83 GluLeuValGlnIleTyrSerAenSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GACGATTCAGAAAGTACAGGAGTTCCTGCGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2189  
QY 103 LeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTTCTTGTCCAGGACCTGGTGGATTCTTAAATTTGAGTTCCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
Db 2250 TGCGTCTGACCTACGTTGGCGCTCTCTTCAATGGCGCTGACCTGCTGCTGCTGCTGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162

Db 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGACCTGTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTGAGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGGCTAAGAGGACGCTGAG 2450  
RESULT 58  
ADR66747  
ID ADR66747 standard; DNA; 3202 BP.  
XX ADR66747;  
XX AC  
XX 02-DEC-2004 (first entry)  
XX Human prostatic carcinoma derived DNA SEQ ID 10 #4.  
XX human; cytostatic; diagnosis; prostatic cancer;  
XX differential expression analysis; ds.  
XX Homo sapiens.  
XX OS  
XX WO2004076614-A2.  
XX PN  
XX 10-SEP-2004.  
XX PD  
XX 22-FEB-2004; 2004WO-DE000433.  
XX PF  
XX 27-FEB-2003; 2003DE-01009985.  
XX PR 14-MAY-2003; 2003DE-01022134.  
XX (HINZ/) HINZMANN B.  
XX (DAHL/) DAHL E.  
XX (ROSE/) ROSENTHAL A.  
XX (HERM/) HERMANN K.  
XX (PILA/) PILARSKY C.  
XX Hinzmann B, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
XX Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
XX Xinzhang L, Staub E;  
XX WPI; 2004-65386/63.  
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
XX useful for diagnosis, treatment and in screening for specific binding  
XX agents.  
XX Claim 1; Page 1329; 1607pp; German.  
XX This invention describes novel cytostatic polynucleotide and polypeptide  
XX sequences which can be used in a method for diagnosing prostatic cancer  
XX or the risk of developing prostatic cancer. Diagnosis is based on  
XX determining over transcription or over expression of the sequences in  
XX prostatic tissue. Screening for inhibitors of the sequences or detection  
XX substances involves a binding assay, any compounds that bind are  
XX selected, optionally after deconvolution of mixtures. Detection of a  
XX predetermined minimum level of the reporter indicates the presence of a  
XX tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
XX short-interfering RNA or ribozymes; an organic molecule of molecular  
XX weight below 5000, preferably 300, that binds to the polypeptide; an  
XX aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
XX polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
XX (monoclonal) antibody directed against Ab or any of the above derivatised  
XX with a reporter group, cell toxin, immunostimulatory molecules and/or  
XX radioisotope. The polynucleotides are identified in human prostatic  
XX cancer by differential expression analysis, using DNA microarrays,  
XX between normal and tumorous tissues, with (over)expression being detected  
XX by quantitative PCR. Analysis of prostatic cancer samples showed that  
XX CD24 was upregulated in many of them. Sections of tissue, isolated from  
XX prostatic cancer patients, or subjects at risk, were incubated





Db 2190 CTGAGGAGGCTCTTCTGTCTCCAGGACCTGGTGGATTCTTAAATTTTCAGTCTCTGATG 2249

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuAlaLeu 142  
 |||:::|||||  
 Db 2250 TGGCTCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTGTG 2309  
 |||:::|||||  
 QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 |||:::|||||  
 Db 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCGCACAGATTGACCAATAT 2369  
 |||:::|||||  
 QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 |||:::|||||  
 Db 2370 CTGGGACTGTGAGGACTACATAATGCTGTGTGGCAAGATTGAGGCTAAATCCCA 2429  
 |||:::|||||  
 QY 183 GlyLeuLysArgLysAlaGlu 189  
 |||:::|||||  
 Db 2430 GGGCTAAGAGGCACGCTGAG 2450  
 |||:::|||||

RESULT 60

AD599925

ID ADS99925 standard; cDNA; 3327 BP.

XX

AC ADS99925;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human reticulon 1 (RTN1), transcript variant 1, cDNA.

XX

KW Human; ss; gene; Bisulphite; metastasis; cancer; cytostatic;

KW DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;

KW electrospray; mass spectrometry; CpG dinucleotide; solid tumour.

XX

OS Homo sapiens.

XX

PN US2003148327-A1.

XX

PD 07-AUG-2003.

XX

PF 21-JAN-2003; 2003US-00240485.

XX

PR 06-APR-2000; 2000DE-01019058.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PR 30-JUN-2000; 2000DE-01032529.

XX

PR 01-SEP-2000; 2000DE-01043826.

XX

PR 06-APR-2001; 2001WO-EP003970.

XX

PA (OLEK/) OLEK A.

PA (PIEP/) PIEPENBROCK C.

PA (BERL/) BERLIN K.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

XX WPI; 2002-010922/01.

DR GENBANK; NM\_021136.

XX

XX New nucleic acid derived from chemically treated metastasis genes, useful

PT for diagnosis of cancers by analysis of cytosine methylation, also for

PT treatment.

XX

XX Claim 2; Page; 9pp; English.

XX

XX The invention relates to a nucleic acid comprising at least 18 bases from

CC a segment of the chemically pretreated DNA of genes associated with

CC metastasis, i.e. any of ADS99709-ADS99906 human genomic sequences or any

CC of the 19 sequences appearing as ADS99911-ADS99929. SEQ ID 2,4,6 etc are

CC the complements of SEQ ID 1,3,5, etc. Also included are an oligomer

CC (particularly an oligonucleotide or peptide nucleic acid) comprising at

CC least one base sequence of at least 9 bases which hybridises to (or is

CC identical with) the sequences referred to above, producing an array of

CC oligomers on a carrier, obtaining genetic and/or epigenetic

CC parameters for diagnosis and/or therapy of diseases (or predisposition to

CC them) by analysis of cytosine methylation and a kit comprising a

CC bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the

CC method of above 5-unmethylated cytosines in a genomic DNA sample are

CC converted chemically to uracil, or another base with hybridisation

CC properties different from those of cytosine, then fragments of the

CC treated DNA amplified (particularly by polymerase chain reaction) using

CC the oligomers and a polymerase (preferably heat stable) to produce

CC labelled amplicons. These are tested for hybridisation to an array of

CC oligomers and any hybridisation detected. The amplicons are labelled with

CC fluorescent or radioactive markers, or with a detachable mass marker to

CC allow their detection by mass spectrometry, specifically using the matrix

CC -assisted laser desorption/ionisation (MALDI) or electrospray techniques.

CC To improve detection in the mass spectrometer, fragments formed in the

CC instrument have only a single net charge (positive or negative). The

CC genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-

CC embedded tissue sample. Oligonucleotides or peptide-nucleic acids that

CC are complementary to (or identical with) parts of the nucleic acids listed

CC above may be used as primers for amplification of the nucleic acids or

CC their complements, and for determining cytosine methylation status and/or

CC single nucleotide polymorphisms in metastasis-related genes. They can be

CC used for analysis of diseases associated with methylation of CpG

CC dinucleotides and to determine (epi)genetic parameters for diagnosis

CC and/or therapy of disease (or predisposition). The genomic DNA sequences

CC are useful for diagnosis and therapy of solid tumours and cancer. The

CC present sequence is human gene fragment or cDNA associated with

CC metastasis. Note: The sequence was not displayed in the specification but

CC was obtained by the indexer from Genbank.

XX

SQ Sequence 3327 BP; 829 A; 907 C; 877 G; 714 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,19e-72 Length: 3327

Score: 682.00 Matches: 128

Percent Similarity: 85.03% Conservative: 31

Best Local Similarity: 68.45% Mismatches: 28

Query Match: 73.25% Indels: 0

DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADS99925 (1-3327)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 |||:::|||||  
 Db 1977 ATTGACCTGTGTATTGGCGGACATCAAGCAGACGGCATCGTGTGGAGTTTCTCTG 2036  
 |||:::|||||

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 |||:::|||||  
 Db 2037 CTGCTGCTCTTCTCCCTGACCAGTTCAGCGGTGGAGCGTCTGCGCTTACCTGCGCCCTG 2096  
 |||:::|||||

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 |||:::|||||  
 Db 2097 GCGGCACCTTCAGCCACCACATCAGTTTCCGCATCTACAAGTCTGTTTACACAGCAGTGCAG 2156  
 |||:::|||||

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 |||:::|||||  
 Db 2157 AAAACCGCAGAGGCGCCCTTTCAAGGCTACTTTGGAGCTTGAGATCACCCCTTCTCAG 2216  
 |||:::|||||

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
 |||:::|||||  
 Db 2217 GAGCAGATTGAGAGTACAGGACTGCGCTGACGATTTCTACGTGACAGACACTTAGGAA 2276  
 |||:::|||||

QY 103 LeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeuMet 122  
 |||:::|||||  
 Db 2277 CTGAGGAGGCTCTTCTTGTCCAGGACCTGGTGGATTCTTAAATTTGACGCTCTGTATG 2336  
 |||:::|||||

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
 |||:::|||||  
 Db 2337 TGGCTCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTGTG 2396  
 |||:::|||||

QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 |||:::|||||  
 Db 2397 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCGCACAGATTGACCAATAT 2456  
 |||:::|||||

QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 |||:::|||||  
 Db 2457 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2516  
 |||:::|||||

QY 183 GlyLeuLysArgLysAlaGlu 189  
 DB 2517 GCGGCTAGAGGACGCTGAG 2537

RESULT 61  
 ID ADB79854  
 AC ADB79854 standard; DNA; 1502 BP.  
 AC ADB79854;  
 DT 04-DEC-2003 (first entry)  
 DE Rat rs-Rex-s human NSP C homolog coding sequence, SEQ ID 94.  
 DE Analgesic; pain; streptozocin-induced diabetes; rat; gene; de.  
 DE Rattus norvegicus.  
 OS EP1279744-A2.  
 PN 29-JAN-2003.  
 PD 26-JUL-2002; 2002EP-00255249.  
 PR 27-JUL-2001; 2001GB-00018354.  
 PR 07-FEB-2002; 2002GB-00002910.  
 XX (WARN ) WARNER LAMBERT CO.  
 PA Brooksbank RA, Dixon AK, Lee K, Pincock RD;  
 PI WPI: 2003-395407/38.  
 DR P-PSDB; ADB79853.  
 XX Use of isolated gene sequences and encoded polypeptides that are  
 PT upregulated in the spinal cord in response to streptozocin-induced  
 PT diabetes for screening compounds for the treatment of pain, or for  
 PT diagnosing pain.  
 XX Claim 1; Page 171; 334pp; English.  
 PS The present invention relates to nucleotide sequences which are useful in  
 CC the screening of compounds for the treatment of pain, or for the  
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the  
 CC spinal cord in response to streptozocin-induced diabetes. The present  
 CC sequence is one such nucleotide sequence.

Alignment Scores:  
 Pred. No.: 9,528-73 Length: 1502  
 Score: 681.00 Matches: 127  
 Percent Similarity: 85.03% Conservative: 32  
 Best Local Similarity: 67.91% Mismatches: 28  
 Query Match: 73.15% Indels: 0  
 DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADB79854 (1-1502)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 DB 179 ATTGACCTTCTGTACTGGGGGACATCAAGCAGCGGGGATGTGTTCCGGAGCTTCTG 238

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 DB 239 CTGCTGCTTCTCTCCCTGACCCAGTTCAGCGTGTGTGAGCGTGTGCTGCTGCTGCTG 298

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 DB 299 GCTGCCCTCTCTGCCACCATCATGCTCCGCACTCAAGTCCGTTCTCAAGCTGTGAG 358

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82

DB 359 AAAACAGATGAGGTACCCCTTCAAGSCCTACCTGGAGCTGGAGATCACCCCTGTCCAG 418  
 QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
 DB 419 GAGCAGATCCAGAGATACACAGACTGCTGAGCTATACGTGAAACAGACACTCTGAAGAG 478  
 QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 DB 479 CTACGGAGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
 DB 539 TGGCTCTGACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598  
 QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 DB 599 GTTTCGATGTTTACTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 658  
 QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 DB 659 CTGGGACTTGTGAGGACTCATATAACACCCGTTGTGGCAAGATCCAGGCTAAATCC 718  
 QY 183 GlyLeuLysArgLysAlaGlu 189  
 DB 719 GCGGCTAGAGGACGCTGAG 739

RESULT 62  
 ID ADO07889  
 AC ADO07889 standard; cDNA; 2343 BP.  
 AC ADO07889;  
 DT 01-JUL-2004 (first entry)  
 DE Mouse polynucleotide #58.  
 DE Mouse; Gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 DE anorectic; antidiabetic.  
 OS Mus sp.  
 XX US2004071700-A1.  
 XX 15-APR-2004.  
 XX 09-OCT-2002; 2002US-00267502.  
 XX 09-OCT-2002; 2002US-00267502.  
 XX (LIFE-) LIFE SCI DEV CORP.  
 XX Kim J, Galant R;  
 XX WPI: 2004-328526/30;  
 XX P-PSDB; ADO08106.  
 XX Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX Claim 1; SEQ ID NO 215; 275pp; English.  
 XX The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antiseize

CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC polypeptide or a change in an activity of the polypeptide, treating a  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC mouse cDNA used in the scope of the invention.

XX Sequence 2343 BP; 536 A; 710 C; 646 G; 451 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1.78e-72	Length:	2343
Score:	681.00	Matches:	127
Percent Similarity:	85.03%	Conservative:	32
Best Local Similarity:	67.91%	Mismatches:	28
Query Match:	73.15%	Indels:	0
DB:	12	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADO07889 (1-2343)

QY	3	ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
DB	1780	ATTGACCTCTGTACTGGCGGACATCAAGCAGACTGGGATGTGTTCGGAGCTTCCTG 1839
QY	23	PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB	1840	CTGCTGCTCTCTCCCTCCACCCATTTAGCGTTTGGAGCGTCTGCTACCTGGCCCTG 1899
QY	43	AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
DB	1900	GCGCCCTCTCTGCCACATCAGCTTCGGCACTACAGTCGCTTCTCAGCTGTGCAG 1959
QY	63	LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
DB	1960	AAACAGATGAGGCTCACCTTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTCCAG 2019
QY	83	GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
DB	2020	GAGCAGATCAGAAAGTACACAGACTGCTGCTGCTGATGTGAACAGACTCTGAAGGAG 2079
QY	103	LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
DB	2080	CTACGAGGCTTTCTCTGTCAGGACCTGGTGGATTCCTTAAATTTGAGTCTCATG 2139
QY	123	TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142
DB	2140	TGCTCTGACCTACCTGTGGCGGCTTCTCAATGGCTGACCTGCTGTGTATGGCTGTG 2199
QY	143	IleSerLeuPheSerValProValIleTyrGluArgHisGlnIleAspHisTyr 162
DB	2200	GTTTCGATGTTTACTCTACCTGTGTGTAGCTTTAAGCAGCAGGACCAAGTTGACCAAT 2259
QY	163	LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
DB	2260	CTGGGACTTGTGAGGACTCATATAACACCGTCTGGCAAGATCCAGGCTAATATCCC 2319
QY	183	GlyLeuLysArgLysAlaGlu 189
DB	2320	GGCGCAAGAGGACCGCTGAG 2340

RESULT 63  
 ABX46402  
 ID ABX46402 standard; cDNA; 422 BP.  
 XX  
 AC ABX46402;  
 XX  
 DT 21-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #11567.  
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
 KW muscle deposition; fat deposition; genome mapping; gene identification;  
 KW gene analysis; cattle breeding.  
 XX Bos Taurus.  
 XX US2002137139-A1.  
 XX 26-SEP-2002.  
 PD 24-SEP-2001; 2001US-00960352.  
 PF 12-JAN-1999; 99US-0115707P.  
 PR 11-JAN-2000; 2000US-00480902.  
 XX (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;  
 XX WPI; 2003-110599/10.  
 DR New nucleic acid associated with lactation, and muscle and fat  
 PT deposition, useful for genome mapping, gene identification and analysis,  
 PT cattle breeding, or for genetically improving cattle.  
 XX Claim 2; SEQ ID NO 11567; 245pp; English.  
 PS The invention relates to a purified nucleic acid molecule associated with  
 CC lactation or muscle and fat deposition (designated LMFD), derived from  
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second  
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,  
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are  
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic  
 CC acid linked to a promoter and a 3' non-translated sequence that  
 CC functions in the cell to cause termination of transcription and addition  
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
 CC (2) determining a level or pattern of a molecule in a bovine cell or  
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a  
 CC complementary nucleic acid molecule obtained from the bovine cell or  
 CC tissue, where hybridisation between the marker nucleic acid and the  
 CC complementary nucleic acid permits the detection of the molecule; and (b)  
 CC detecting the level or pattern of the complementary nucleic acid, where  
 CC the detection of the complementary nucleic acid is predictive of the  
 CC level or pattern of the molecule. The LMFD nucleic acid is used for  
 CC determining a level or pattern of a molecule in a bovine cell or tissue.  
 CC It is useful for genome mapping, gene identification and analysis, cattle  
 CC breeding, preparation of constructs for use in cattle gene expression, or  
 CC for genetically improving cattle. The present sequence is one of the  
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The  
 CC present sequence was not shown in the specification but was obtained in  
 CC electronic format from the USPTO web site:  
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139  
 XX Sequence 422 BP; 99 A; 85 C; 96 G; 142 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	2.01e-72	Length:	422
Score:	672.00	Matches:	138
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.28%	Mismatches:	0
Query Match:	72.18%	Indels:	0
DB:	8	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABX46402 (1-422)

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

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Db 4 AACTTGTTCCTGCTCTCGTCAGACGATTTACGATTTGAGTGTAAACGGCCTACATT 63
Qy 41 AlaleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 64 GCCTTGGCCCTGCTCTGTGACTATCATCAGCTTTAGGATATATAAGGGTGTGATCCAGCT 123
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 124 ATCCAGAAATCTGATGAAGGCCACCCATTAGGGCATATTTGGATCTGAAGTTGCTATA 183
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 184 TCTGAGGAGTTGGTTTCAGAGTACAGCAATCTGCTCTGTGTCATGTTAACTGCACAATA 243
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 244 AAAGAACTCAGACGCCCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 303
Qy 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 304 TTGATGTGGGATTTACCTATGTTGGTGCCCTGTGTTCAAAGTCTGACACTACTAATTTTG 363
Qy 141 AlaleuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle 159
Db 364 GCTCTGATTTCACTCTTCAGTGTTCTCTGTTATTTATGAACGCATCAGGCCCAATA 420

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## RESULT 64

ADB85247

ID ADB85247 standard; DNA; 1473 BP.

XX AC ADB85247;

XX DT 04-DEC-2003 (first entry)

XX DE Rat C1-13 protein neuronal-specific gene SEQ ID NO:128.

XX KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;

XX KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;

XX KW protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.

XX OS Rattus norvegicus.

XX PN EP1284297-A2.

XX PD 19-FEB-2003.

XX PF 26-JUL-2002; 2002EP-00255228.

XX PR 27-JUL-2001; 2001GB-00018354.

XX PS 07-FEB-2002; 2002GB-00002880.

XX PA (WARN ) WARNER LAMBERT CO.

XX PI Brookebank RA, Dixon AK, Lee K, Pincock RD;

XX DR WPI; 2003-364994/35.

XX DR P-PSDB; ADB85246.

XX PT Use of gene sequence that is down-regulated in response to streptozocin-

XX PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in

XX PT screening of compounds for treating or diagnosing pain.

XX PS Claim 1; Page 197; 256pp; English.

XX CC The invention relates to a novel isolated gene sequence that is down-

XX CC regulated in the spinal cord in response to streptozocin-induced

XX CC diabetes, or comprising, hybridising or having at least 80% sequence

XX CC identity to a sequence whose expression products are kinases,

XX CC phosphatases, ion channel proteins, receptors, transporters, G-protein

XX CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,

XX CC given in the specification. A gene of the invention has analgesic

XX CC activity, and may have a use in gene therapy. The gene sequences, vector,

CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a gene of the invention.

XX SQ Sequence 1473 BP; 357 A; 373 C; 343 G; 400 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8.29e-71 Length: 1473  
 Score: 665.00 Matches: 127  
 Percent Similarity: 85.03% Conservative: 32  
 Best Local Similarity: 67.91% Mismatches: 28  
 Query Match: 71.43% Indels: 1  
 DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADB85247 (1-1473)

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Qy 3 ValAspLeuLeuTyrTyrArgAspIleLeValysThrGlyValValPheGlyAlaSerIleu 22
Db 146 ATTGACCTTCTGTACTGCGGGACATCAGCAGACGGGGATTGTTCGGGAGCTTCCTG 205
Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 206 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTTGTGAGCGTTCGTCGCTACTGCGCCTG 265
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 266 GCTGCCCTCTCTGCCACCATCAGCTTCGGCATCTACAAGTCCGTTCTACAGCTGTGCAG 325
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 326 AAAACAGATGAGGCTCACCTTTCAAGGCTTACCTGAGCTGGAGATCACCTGTGCCAG 385
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
Db 386 GAGCAGATCCAGAGTACACAGACTGCTGCAGCTATACGTGACAGACACTCTCGAGGAG 445
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 446 CTACGGAGGCTCTTCTCTGTCCAAAGACCTAGTGGATTCTTAAATTTTGCAGTCTCATG 505
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
Db 506 TGGCTCTGACCTACGTTGGCGCACTCTTCAATGGCCTGACCCCTGCTGTATGGCTGTG 565
Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Db 566 GTTTCGATGTTTACTCTACTCTGTGGTATATGTTAAGCACCAGGCACAGGTTGACCAATAT 625
Qy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 626 CTGGGACTTGTGAGGACTCACATAAACACCCGTTGTGGCAAGATCCAGGCTTAAATCCCC 685
Qy 183 GlyLeuLysArgLysAlaGlu 189
Db 686 GGCAGC-AAGAGGCATGCTGAG 705

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## RESULT 65

AAH57558

ID AAH57558 standard; cDNA; 3279 BP.

XX AC AAH57558;

XX DT 10-SEP-2001 (first entry)

XX DE Human brain cell specific cDNA sequence SEQ ID NO:398.

XX KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;

XX KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;

XX KW metabolic disease; developmental disease; cytostatic; immunomodulatory;



CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,  
CC cytotactic and tranquiliser activities. This polynucleotide is a full  
CC length human cDNA sequence of the invention. NOTE: This sequence is not  
CC given in the sequence listing of the specification but can be obtained on  
CC CD-ROM from the European Patent Office, Vienna Sub-office.  
XX

SQ Sequence 4607 BP; 1428 A; 944 C; 945 G; 1290 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,54e-65 Length: 4607  
Score: 627.50 Matches: 116  
Percent Similarity: 81.05% Conservative: 38  
Best Local Similarity: 61.05% Mismatches: 35  
Query Match: 67.40% Indels: 1  
DB: 13 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR06965 (1-4607)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleTyrLysThrGlyValValPheGlyAla 20  
Db 2353 TCAGTGCAGCATCTGATTTCCTGGAGAGATGGAAGAAGCTGGTGTCTTGGCACC 2412  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2413 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTATCATGCTGGTTCCTTACCTC 2472  
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 2473 ATCCCTGGCTCTCTCTGTACCATCATGCTTTCAGGATCTACAACTCGTCATCAAGCT 2532  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 2533 GTACAGAGTCAGAGAGAGCCATCTCAAGCTACCTGGAGTAGACATCTCTG 2592  
Qy 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 2593 TCCTCAGAAGCTTTCATTAATACATGAATGCTGCATGTCGATCAATCAAGCGCCCTG 2652  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 2653 AACTCATATTTCGTCTCTCTGTGAGAAGATCTGGTGTACTCTTGAAGCTGCTGTC 2712  
Qy 121 LeuMetTrpValPheTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuIleLeu 140  
Db 2713 TTCATGTGCTGATGACCTATGTTGCTGTCTTTTAAAGCAATCACCTCTTAATCTT 2772  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 2773 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAGACCCAGATTGAT 2832  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 2833 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGAAAGATCAAGCAAAA 2892  
Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db 2893 CTCCTCGAATCGCCCAAAAAGAGCAGAA 2922

RESULT 67

AAZ38318

ID AAZ38318 standard; cDNA; 708 BP.

XX

XX

AC AAZ38318;

XX

DT 09-FEB-2000 (first entry)

XX

DE Human transmembrane protein cDNA clone HP02061 coding sequence.

XX

KW HP02061; transmembrane domain; Saos-2; homology;

KW neuroendocrine-specific protein C; antibody; assay reagent;

KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

KW antagonist; ligand; therapeutic; ds.

XX

OS Homo sapiens.

XX Key

FT CDS

FT Location/Qualifiers

FT 1..708

FT /\*tag= a

FT /product= "Human transmembrane protein HP02061"

FT /note= "No stop codon given in the specification"

XX

PN WO9955862-A2.

XX

PD 04-NOV-1999.

XX

PF 27-APR-1999; 99WO-JP002226.

XX

PR 28-APR-1998; 98JP-00119395.

XX

PA (SAGA ) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

XX

PI Kato S, Kimura T;

XX

XX WPI; 2000-023358/02.

DR P-PSDB; AAY52387.

XX

PT Human proteins with transmembrane domains, involved in control of cell

PT proliferation and differentiation, useful for treating e.g. cancer or

PT inflammation.

XX

XX Claim 3; Page 85; 114pp; English.

PS

CC This sequence represents the coding sequence of human cDNA clone HP02061

CC which encodes a 26 kD protein with two putative transmembrane domains.

CC The cDNA was isolated from a Saos-2 (human osteosarcoma cell line) cDNA

CC library. The protein has homology with the human neuroendocrine-specific

CC protein C (PIR Accession No. I60904), and may have a similar function.

CC The protein may be used to raise specific antibodies, as assay reagents,

CC as diagnostic tissue markers, for the isolation of cognate receptors,

CC ligands and binding proteins, and as biologically active agents.

CC Nucleotides encoding the protein may be used as primers and probes or

CC antisense molecules, and in gene therapy. Cells transformed with these

CC nucleotides may be used to screen for agonists and antagonists which are

CC potentially useful therapeutically

XX

SQ Sequence 708 BP; 158 A; 195 C; 169 G; 186 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,59e-66 Length: 708

Score: 624.50 Matches: 115

Percent Similarity: 81.05% Conservative: 39

Best Local Similarity: 60.53% Mismatches: 35

Query Match: 67.08% Indels: 1

DB: 3 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ38318 (1-708)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleTyrLysThrGlyValValPheGlyAla 20

Db 139 CGGTGCAGCATCTGATTTCCTGGAGAGATGGAAGAAGCTGGTGTCTTGGCACC 198

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 199 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTATCATGCTGGTTCCTTACCTC 258

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 259 ATCTGGCTCTCTCTCTGTCCACCATCAGCTTCAGGATCTACAACTCGTCATCAAGCT 318

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 319 GTACAGAGTCAGAGAGAGCCATCTCAAGCTACCTGGAGTAGACATCTCTG 378

Qy 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100

XX

Db 379 TCCTCAGAGCTTTCATTAATACATGATGCTGCCATCAACAGGCGCCCTG 438  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAATCATTAATTCGCTCTCTCTGTTGAGAGATCTGTTGACTCTTGAAGCTGGCTGC 498  
 QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCAACCTTCTAATTC 558  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 559 GCTGAACCTCTCATTTTCAGTGTCCGATGCTATGAGAAGTACAGACCCAGATTGAT 618  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGMAAAGATCCAAGCAAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 679 CTCCTTGAATCGCCCAAAAAAAGGCAGAA 708

## RESULT 68

ADK67496

ID ADK67496 standard; cDNA; 711 BP.

XX

AC ADK67496;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human RTN-3 cDNA sequence.

XX

KW ds; neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3;

KW amyloidosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..711

FT FT /\*tag= a

FT FT /product= "RTN-3 protein"

XX

PN WO2003088926-A2.

XX

PD 30-OCT-2003.

XX

PF 08-APR-2003; 2003WO-US008829.

XX

PR 17-APR-2002; 2002US-0373284P.

XX

PA (PHAA ) PHARMACIA &amp; UPJOHN CO.

XX

PI Yan R, Lu Y;

XX

DR WPI; 2003-854033/79.

XX

DR P-PSDB; ADK67497.

XX

PT New polypeptide having BACE1 activity, useful in preparing a composition

PT for treating amyloidosis or Alzheimer's disease.

XX

PS Claim 2; SEQ ID NO 1; 42pp; English.

XX

CC The invention relates to an isolated polypeptide having BACE1 activity.

CC The protein is RTN4 or RTN3 protein. The polypeptide is useful in

CC preparing a composition for treating amyloidosis or Alzheimer's disease.

XX

SQ Sequence 711 BP; 161 A; 196 C; 168 G; 186 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,61e-66 Length: 711

Score: 624.50 Matches: 115

Percent Similarity: 81.05% Conservative: 39

Best Local Similarity: 60.53% Mismatches: 35  
 Query Match: 67.08% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADK67496 (1-711)

QY 1 SerValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 139 GCGGTGCACGATCTCATTTCTTGGAGAGATGTGAAGAAGACTGGGTGTCTTTGGCACC 198  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 199 AGCTGATCATGCTGCTTTCCTGCGACGCTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 258  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 259 ATCTCGGCTCTTCTCTGTCCATCAGCTTTCAGGATCTACAGTCCGCTCATCCAAGCT 318  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 319 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGAGTAGACATTACTCTG 378  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 379 TCCTCAGAAGCTTTCATAATTACATGAATGCTGCATGGTGCACATCAACAGGCGCCCTG 438  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAATCATTAATTCGCTCTCTTCTGTGTAAGATCTGTTGATCTCTTGAAGCTGGCTGC 498  
 QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTTCTAATTC 558  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 559 GCTGAACCTCTCATTTTCAGTGTCCGATGCTATGAGAAGTACAAGACCCAGATTGAT 618  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGMAAAGATCCAAGCAAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 679 CTCCTTGAATCGCCCAAAAAAAGGCAGAA 708

## RESULT 69

AAH34853

ID AAH34853 standard; cDNA; 1330 BP.

XX

AC AAH34853;

XX

DT 03-SEP-2001 (first entry)

XX

DE Human colon cancer antigen encoding cDNA SEQ ID NO:1935.

XX

KW Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW colorectal carcinoma; chromosome 11; ss.

XX

OS Homo sapiens.

XX

PN WO200122920-A2.

XX

PD 05-APR-2001.

XX

PF 28-SEP-2000; 2000WO-US026524.

XX

PR 29-SEP-1999; 99US-0157137P.

XX

PR 03-NOV-1999; 99US-0163280P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Barash SC, Birse CE, Rosen CA;





```
DB: 2 Gaps: 1
US-09-830-972-29_COPY_990_1178 (1-189) x AAX60810 (1-1656)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysValThrGlyValValPheGlyAla 20
Db 165 GCGGTGCAGACTGATTTCTGGAGAGATGAGAGAGACTGGTTGCTTTGGCACC 224
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 225 ACGCTGATCATGCTCTTCCCTGGCAGCTTTTCAGTGTCTCATGCTGGTGTCTTACCTC 284
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 285 ATCTGGCTCTTCTCTGTCCACCATCAGTTCAGGATCTACAGTCCGCTCATCCAGCT 344
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 345 GTACAGAGTCAGAGAGGCCATCCATTCAGAGCTTACCTGGACGTAGACATTACTCTG 404
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 405 TCCTCAGAGCTTTCCATAATTACATGAATGCTGCCATGTCACATCAACAGGGCCCTG 464
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 465 AAACATCATTTATGCTCTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTC 524
QY 121 LeuMetTrpValPheTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 525 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAAGGATCACTTCTAATCTT 584
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 585 GCTGAATGCTCATTTTCAGTGTCCGATTTGTCTATGAGAGTACAAAGCCAGATTGAT 644
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 645 CACTATGTGGTATGCCCGCAGATCAGCAAGTCAATTTGTTGAAAGATCCAAAGCAAAA 704
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 705 CTCCTCGAATGCCCAAAAAGGCGAGAA 734
RESULT 71
ID AAS59216 standard; cDNA; 1656 BP.
AC AAS59216;
XX
XX 16-JAN-2002 (first entry)
DE Human cDNA encoding a secreted protein yb8_1.
XX
KW Human; secreted protein; ss; antiinflammatory; immunosuppressive;
KW neurotropic; neuroprotective; antiarthritic; antimicrobial; veterinary;
KW cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant;
KW vasotropic; antiparkinsonian; immunostimulant; dermatological;
KW antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser;
KW cerebroprotective; cytokine; cell proliferation; cell differentiation;
KW immune deficiency; severe combined immunodeficiency; SCID; tumour;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW graft-versus-host disease; myeloid deficiency; wound healing; ulcer;
KW periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; infection; cardiac disease;
KW stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
KW food supplement.
XX
OS Homo sapiens.
XX
XX WO200175068-A2.
XX
XX 11-OCT-2001.
XX
PF 22-MAR-2001; 2001WO-US009369.
XX
XX 30-MAR-2000; 2000US-00539330.
XX
XX 04-DEC-2000; 2000US-00729674.
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Jacobs K, Mccoy JM, Lavallie E, Collins-Racie LA, Evans C;
XX Treacy M, Agostino MJ, Steininger RJ, Spaulding V, Wong GG, Clark H;
XX Fechtel K, Merberg D;
XX
XX WPI: 2001-639363/73.
XX
XX P-PSDB; AAU38998.
XX
XX Secreted human proteins, useful as vaccine for treating various diseases
XX such as autoimmune disorders (e.g. multiple sclerosis), and nervous
XX system disorders (e.g. stroke).
XX
XX Claim 13; Page 471; 619pp; English.
XX
XX The invention relates to novel human secreted proteins, the nucleic acids
XX encoding them. The protein may exhibit cytokine, cell proliferation or
XX cell differentiation activity or may induce production of other cytokines
XX in certain cell populations and may exhibit immune stimulating or immune
XX suppressing activity, which is useful for the treatment of various immune
XX deficiencies and disorders e.g. severe combined immunodeficiency (SCID),
XX autoimmune disorders e.g. multiple sclerosis, systemic lupus
XX erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation.
XX The proteins are also useful in the treatment of diseases and disorders
XX including tissue, skin and organ transplantation and in graft-versus-host
XX diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid
XX cell deficiencies, wound healing and tissue repair, in the treatment of
XX burns, incisions and ulcers; as well as in treatment of periodontal
XX disease, osteoporosis or osteoarthritis, mediated by inflammatory
XX processes, diseases of the peripheral nervous system, Alzheimer's,
XX Parkinson's disease, Huntington's disease, amyotrophic lateral
XX sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and
XX central nervous system vessel e.g. stroke, sepsis, inflammatory bowel
XX disease, ulcers, bone regeneration. The protein, having activin- or
XX inhibin-related activities is useful as a contraceptive based on the
XX ability of inhibins to decrease fertility in female mammals and decrease
XX spermatogenesis in male mammals. The proteins and nucleic acids are also
XX useful as food supplements. The present sequence encodes a secreted
XX protein of the invention
XX
XX SQ Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other;
```



QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrile 100  
DB 405 TCTCAGAAAGCTTTCATTAATACATGAATGCTGCATCAACAGGGCCCTG 464  
QY 101 LysGluLeuArgPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 465 AAACATTAATTCGCTCTCTTCTGGTAGAAGATCTGGTTCCTTGAAGCTGGCTGC 524  
QY 121 LeuMetTyrPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
DB 525 TTCAATGCTGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTTCTAATCTT 584  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 585 GCTGAACCTGCTCATTTTCAGTGTCCGATGTCTATGAGAAGTCAACAGCCAGATTGAT 644  
QY 161 HisTyrLeuGlyAlaAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 645 CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATTTGTAAGAAAGATCCAGCAAAA 704  
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
DB 705 CTCCTCGGAATCGCCAAAAGGAGGAGAA 734

## RESULT 73

AAZ36240

ID AAZ36240 standard; cDNA; 1668 BP.

AC AAZ36240;

XX 22-FEB-2000 (first entry)

DE cDNA encoding a bone marrow secreted protein designated BMS240.

KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;  
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;  
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;  
KW erythroid progenitor cell; colony stimulating factor; granulocyte;  
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;  
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;  
KW stem cell disorder; aplastic anaemia; bone differentiation;  
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;  
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;  
KW bone fracture; cartilage damage; artificial joint; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 99..809

FT /\*tag= a

FT /product= "bone marrow secreted protein"

FT poly\_a\_signal 1626..1631

FT /\*tag= b

XX WO9933979-A2.

XX 08-JUL-1999.

XX 18-DEC-1998; 98WO-US027008.

XX 30-DEC-1997; 97US-0068958P.

XX 24-SEP-1998; 98US-0101603P.

XX 30-SEP-1998; 98US-0102540P.

XX (CHIR ) CHIRON CORP.

XX Lin H, Cao L;

XX WPI; 2000-038344/03.

XX P-PSDB; AAY53634.

XX New isolated human polynucleotide and secreted proteins can induce

PT production of other cytokines in certain cell populations.

XX Claim 11; Page 98-100; 120pp; English.

CC AAZ36228-49 encode bone marrow secreted proteins of human bone marrow  
CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or  
CC cell differentiation activity (either inducing or inhibiting). They can  
CC be used to support colony forming cells or factor-dependent cell lines,  
CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell  
CC deficiencies. In addition, they may be used to support the growth and  
CC proliferation of erythroid progenitor cells, and to treat various  
CC anaemias. They can have colony stimulating factor (CSF) activity and can  
CC be used to support the growth and proliferation of myeloid cells such as  
CC granulocytes, monocytes or macrophages, to prevent or treat myelo-  
CC suppression, to support the growth and proliferation of megakaryocytes  
CC and platelets, thereby allowing prevention or treatment of platelet  
CC disorders such as thrombocytopenia, to support the growth and  
CC proliferation of hematopoietic stem cells, either in place of or in  
CC conjunction with platelet transfusions, to treat stem cell disorders,  
CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to  
CC repopulate the stem cell compartment after irradiation or chemotherapy.  
CC They can be used for growth or differentiation of bone, cartilage,  
CC tendon, ligament, or nerve tissue, as well as for wound healing and  
CC tissue repair and replacement, and in the treatment of burns, incisions  
CC and ulcers, to induce cartilage and/or bone growth in circumstances where  
CC bone is not normally formed and thus have an application in healing bone  
CC fractures and cartilage damage or defects, prophylactic use in fracture  
CC reduction and also in the improved fixation of artificial joints  
XX SQ Sequence 1668 BP; 435 A; 414 C; 349 G; 470 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8.63e-66 Length: 1668  
Score: 624.50 Matches: 115  
Percent Similarity: 81.05% Conservative: 39  
Best Local Similarity: 60.53% Mismatches: 35  
Query Match: 67.08% Indels: 1  
DB: 3 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ36240 (1-1668)

QY 1 SerValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 237 GCGGTGACGATCTGATTTCTGGAGAGATGTGAGAGAGACTGGGTTGTCTTTGGCACC 296  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 297 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGTTCTTACCTC 356  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 357 ATCTCTGGCTCTTCTCTCTGTCCATCAGCTTCAGGATCTCAAGTCCGTTCATCAAGCT 416  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 417 GTACAGAAAGTCAAGAAAGGCCATCCATTCAAGGCTACCTGGAGCTAGACATTACTCTG 476  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 477 TCCTCAGAAGCTTTCATAAATTACATGAATGCTGCATGTCATCAACAGGGCCCTG 536  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 537 AAACCTCATTTATTCGCTCTCTTCTGTGAAGATCTGGTGTGACTCTCTGAAGCTGGCTGC 596  
QY 121 LeuMetTyrPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
DB 597 TTCAATGCTGCTGATCCTCTGTTGGTGTCTGTTTAAACGGAATCACCTTCTAATCTT 656  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 657 GCTGAAGCTGCTCATTTTCAGTGTCCGATGTCTATGAGAAGTACAAGACCAGATTGAT 716

QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 776

QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 777 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 806

## RESULT 74

AAZ38319  
 ID AAZ38319 standard; cDNA; 1759 BP.

XX AC AAZ38319;

XX DT 09-FEB-2000 (first entry)

XX DE Human transmembrane protein cDNA clone HP02061.

XX KW HP02061; transmembrane domain; Saos-2; homology;

XX KW neuroendocrine-specific protein C; antibody; assay reagent;

XX KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

XX KW antagonist; ligand; therapeutic; ds.

XX OS Homo sapiens.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 142..852

XX FT /\*tag= a

XX FT /product= "Human transmembrane protein HP02061"

XX FT

XX FT

XX FT

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XX FT

DB: 3 Gaps: 1  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ38319 (1-1759)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 280 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGATGGGTTGTCTTTGGCACC 339

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLafTyle 40  
 Db 340 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTGCATCAGTGTGTTCTTACCTC 399

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 400 ATCTGGCTCTTCTCTCTGTCCATCAGCTTCAGGATCTACAGTCCGTTCATCCAGCT 459

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 460 GTACAGAAGTCAGAGAAGGCCATCCATTCAAGGCTACCTGGACGTAGACATTACTCTG 519

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 520 TCCTCAGAAGCTTTCCATTAATTACATGAATGCTGCCATGTCATCAACAGGCGCCCTG 579

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 580 AAATCTATTATTCCTCTCTCTGTGGTGAAGATCTGGTTCCTCTTGAAGCTGGCTGTC 639

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 640 TTCAATGGCTGATGACCTATGTTGGTCTGCTTTTAAACGGAATCACCTCTTAATCTT 699

QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 700 GCTGAACCTGCTCAATTTTCAGTGTCCGATGCTATGAGAAGATCAAGACCCAGATTGAT 759

QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 760 CACTATGTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 819

QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 820 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 849

RESULT 75  
 AAV59748  
 ID AAV59748 standard; DNA; 1766 BP.

XX AC AAV59748;  
 DT 19-JAN-1999 (first entry)

XX DE Human secreted protein gene 92 clone HAUBL57.

XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; ischaemic lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX OS Homo sapiens.

XX PN WO9839448-A2.

XX PD 11-SEP-1998.

XX PF 06-MAR-1998; 98WO-US004493.

XX PR 07-MAR-1997; 97US-0038621P.

XX PR 07-MAR-1997; 97US-0040161P.

XX PR

XX PR

XX PR

XX PR

QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 776

QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 777 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 806

## RESULT 74

AAZ38319  
 ID AAZ38319 standard; cDNA; 1759 BP.

XX AC AAZ38319;

XX DT 09-FEB-2000 (first entry)

XX DE Human transmembrane protein cDNA clone HP02061.

XX KW HP02061; transmembrane domain; Saos-2; homology;

XX KW neuroendocrine-specific protein C; antibody; assay reagent;

XX KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

XX KW antagonist; ligand; therapeutic; ds.

XX OS Homo sapiens.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 142..852

XX FT /\*tag= a

XX FT /product= "Human transmembrane protein HP02061"

XX FT

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QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 776

QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 777 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 806

## RESULT 74

AAZ38319  
 ID AAZ38319 standard; cDNA; 1759 BP.

XX AC AAZ38319;

XX DT 09-FEB-2000 (first entry)

XX DE Human transmembrane protein cDNA clone HP02061.

XX KW HP02061; transmembrane domain; Saos-2; homology;

XX KW neuroendocrine-specific protein C; antibody; assay reagent;

XX KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

XX KW antagonist; ligand; therapeutic; ds.

XX OS Homo sapiens.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 142..852

XX FT /\*tag= a

XX FT /product= "Human transmembrane protein HP02061"

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QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 776

QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 777 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 806

## RESULT 74

AAZ38319  
 ID AAZ38319 standard; cDNA; 1759 BP.

XX AC AAZ38319;

XX DT 09-FEB-2000 (first entry)

XX DE Human transmembrane protein cDNA clone HP02061.

XX KW HP02061; transmembrane domain; Saos-2; homology;

XX KW neuroendocrine-specific protein C; antibody; assay reagent;

XX KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

XX KW antagonist; ligand; therapeutic; ds.

XX OS Homo sapiens.

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PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
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PR 11-APR-1997; 97US-0043313P.
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PR 23-MAY-1997; 97US-0047500P.
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PR 23-MAY-1997; 97US-0047502P.
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PR 23-MAY-1997; 97US-0047583P.
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PR 23-MAY-1997; 97US-0047593P.
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PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
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PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048664P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 16-JUL-1997; 97US-0051926P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.

PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
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PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
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PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.

XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 1998-506364/43.
DR P-PSDB; AAW74963.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX Claim 1; Page 473-474; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 92 from
CC the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W5026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)
XX
XX Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;
SQ
Alignment Scores:
Pred. No.: 9,348-66 Length: 1766
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 2 Gaps: 1
US-09-830-972-29_COPY_990_1178 (1-189) x AAV59748 (1-1766)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 287 GCGGTGCACGATCTGATTTCTTGGAGAGATGTGAAGAGACTGGTTTCTTTGGACC 346
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PR 22-AUG-1997; 97US-0056884P.  
 PR 22-AUG-1997; 97US-0056886P.  
 PR 22-AUG-1997; 97US-0056887P.  
 PR 22-AUG-1997; 97US-0056888P.  
 PR 22-AUG-1997; 97US-0056889P.  
 PR 22-AUG-1997; 97US-0056892P.  
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 PR 22-AUG-1997; 97US-0056894P.  
 PR 22-AUG-1997; 97US-0056903P.  
 PR 22-AUG-1997; 97US-0056908P.  
 PR 22-AUG-1997; 97US-0056909P.  
 PR 22-AUG-1997; 97US-0056910P.  
 PR 22-AUG-1997; 97US-0056911P.  
 PR 05-SEP-1997; 97US-0057669P.  
 PR 05-SEP-1997; 97US-0057761P.  
 PR 12-SEP-1997; 97US-0058785P.  
 PR 02-OCT-1997; 97US-0061060P.  
 PR 06-MAR-1998; 98WO-US004493.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;  
 PI Bednariuk DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;  
 PI Ferrite AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX  
 DR WPI; 2002-634796/68.  
 DR P-PSDB; ABG95423.  
 XX  
 PT New isolated human secreted protein for diagnosing, preventing, treating  
 PT or ameliorating medical conditions and used as a food additive or  
 PT preservative.  
 XX  
 PS Example 1; SEQ ID NO 254; 129pp; English.  
 XX  
 CC The invention relates to an isolated protein that is one of 186 human  
 CC secreted proteins, given in the specification, encoded by one of 309 cDNA  
 CC sequences also given in the specification. The protein is used in a  
 CC pharmaceutical composition used to prevent, treat or ameliorate a medical  
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. The present sequence represents a cDNA derived from a gene  
 CC encoding one of the novel human secreted proteins of the invention. Note:  
 CC This sequence did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6420526B1  
 XX  
 SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;  
 Alignment Scores: Length: 1766  
 Pred. No.: 9,34e-66  
 Score: 624.50  
 Matches: 115  
 Percent Similarity: 81.05%  
 Best Local Similarity: 60.53%  
 Query Match: 67.08%  
 DB: 1  
 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABS73741 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

Db 287 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTGTTCTTTGGCACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 347 AGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 407 ATCTTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAAGTCCGCTCATCCAAGCT 466  
 QY 61 IleGlnLysSerAspGluLysHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 527 TCTTCAGAAGCTTTCATTAATTTACATGATGTCGATGTCACATCAACAGGCGCTG 586  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAATCAATTATTTCGCTCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 647 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAATCACCTTCTTAATCTT 706  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 707 GCTGAACGTCTCATTTTCAGTGTCCCGATTGCTATGAGAGCTACAAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGTTAAAGAGATCCAAGCAAA 826  
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 Db 827 CTCCTGGAAATCGCCAAAAAAGGCAGAA 856  
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 ACD82884  
 ID ACD82884 standard; cDNA; 1766 BP.  
 XX ACD82884;  
 AC ACD82884;  
 XX  
 DT 22-SEP-2003 (first entry)  
 DE  
 DE cDNA sequence #244 containing coding region of a human secreted protein.  
 KW Human; secreted protein; hyperproliferative disorder; leukaemia;  
 KW breast cancer; wound; reproductive disorder; blood-related disorder;  
 KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;  
 KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;  
 KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;  
 KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;  
 KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;  
 KW angina pectoris; cerebral ischaemia; congenital heart defect;  
 KW respiratory disorder; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;  
 KW immunosuppressive; antibacterial; haemostatic; thrombolytic;  
 KW anticoagulant; neuroprotective; thyromimetic; antiallergic;  
 KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;  
 KW cerebroprotective; cardiant; nootropic; antiparkinsonian;  
 KW antiinflammatory; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX US2003049618-Al.  
 PN  
 XX 13-MAR-2003.  
 PD  
 XX 16-MAR-2001; 2001US-00809391.  
 XX

PR 07-MAR-1997; 97US-0038621P.  
PR 07-MAR-1997; 97US-0040162P.  
PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040626P.  
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PR 23-MAY-1997; 97US-0047590P.  
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PR 06-JUN-1997; 97US-0048964P.  
PR 06-JUN-1997; 97US-0048974P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 08-JUL-1997; 97US-0051926P.  
PR 16-JUL-1997; 97US-0052874P.  
PR 18-AUG-1997; 97US-0055724P.  
PR 22-AUG-1997; 97US-0056630P.  
PR 22-AUG-1997; 97US-0056631P.  
PR 22-AUG-1997; 97US-0056632P.  
PR 22-AUG-1997; 97US-0056637P.  
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PR 22-AUG-1997; 97US-0056864P.  
PR 22-AUG-1997; 97US-0056872P.  
PR 22-AUG-1997; 97US-0056874P.  
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PR 22-AUG-1997; 97US-0056877P.  
PR 22-AUG-1997; 97US-0056878P.  
PR 22-AUG-1997; 97US-0056879P.  
PR 22-AUG-1997; 97US-0056880P.  
PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
PR 22-AUG-1997; 97US-0056886P.  
PR 22-AUG-1997; 97US-0056887P.  
PR 22-AUG-1997; 97US-0056888P.  
PR 22-AUG-1997; 97US-0056889P.  
PR 22-AUG-1997; 97US-0056892P.  
PR 22-AUG-1997; 97US-0056893P.  
PR 22-AUG-1997; 97US-0056894P.  
PR 22-AUG-1997; 97US-0056903P.  
PR 22-AUG-1997; 97US-0056908P.  
PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 22-AUG-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057659P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 09-OCT-1997; 97US-0058785P.  
PR 06-MAR-1998; 97US-0061660P.  
PR 08-SEP-1998; 98WO-US004493.  
PR 17-MAR-2000; 2000US-0190068P.  
XX  
PA (RUBE//) RUBEN S M.  
PA (ROSE//) ROSEN C A.  
PA (SOPP//) SOPPET D R.  
PA (CART//) CARTER K C.  
PA (BEDN//) BEDNARIK D P.  
PA (ENDR//) ENDRESS G A.  
PA (YUGG//) YU G.  
PA (NIJJ//) NI J.  
PA (FENG//) FENG P.  
PA (YOUN//) YOUNG P E.  
PA (GREE//) GREENE J M.  
PA (FERR//) FERRIE A M.  
PA (DUAN//) DUAN D R.  
PA (HUJJ//) HU J.  
PA (FLOR//) FLORENCE K A.  
PA (OLSE//) OLSEN H S.  
PA (FISC//) FISCHER C L.  
PA (EBNE//) EBNER R.  
PA (BREW//) BREWER L A.  
PA (MOOR//) MOORE P A.  
PA (SHIY//) SHI Y.  
PA (LAPL//) LAFLEUR D W.  
PA (LIYY//) LI Y.  
PA (ZENG//) ZENG Z.  
PA (KYAW//) KYAW H.  
XX  
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Greene JM, Ferrie AM;  
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX  
DR WPI; 2003-521800/49.  
DR P-FSDB; ABO34617.  
XX  
PT New genes and its encoded prostate cancer antigen proteins, useful for  
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
PT ischemia.  
XX  
PS Claim 4; SEQ ID NO 254; 260pp; English.  
XX  
CC The present invention relates to the isolation of novel human secreted  
CC proteins and the polynucleotide sequences encoding them. The invention

CC also discloses vectors, host cells, antibodies, and recombinant methods  
CC for producing human secreted proteins. The polypeptide and polynucleotide  
CC sequences for the secreted proteins are useful for preventing, treating,  
CC ameliorating or diagnosing medical conditions such as hyperproliferative  
CC disorders (e.g. leukemia or breast cancers), wounds, reproductive  
CC disorders, blood-related disorders (e.g. haemophilia or  
CC thrombocytopenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,  
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),  
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
CC disorders, neurological disorders (e.g. Alzheimer's disease or  
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/paipdIDEntry.html](http://seqdata.uspto.gov/paipdIDEntry.html)

XX SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

Alignment Scores:  
Pred. No.: 9,34e-66 Length: 1766  
Score: 624.50 Matches: 115  
Percent Similarity: 81.05% Conservative: 39  
Best Local Similarity: 60.53% Mismatches: 35  
Query Match: 67.08% Indels: 1  
DB: Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ACD82884 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAla 20  
Db 287 GCGGTGCACGATCTGATTTCTCGAGAGATGTGAAGACGTCGGTGTCTTTGGCACC 346  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 347 ACCTGATCATGTGCTGCTTCCCTGGCAGCTTTTCAGTGTATCATGCTGTGTTCTTACCTC 406  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 407 ATCTGCTGCTTCTCTCTGTCCACATCAGCTTCAGATCTACAGTCCGTCATCCAGCT 466  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
Db 467 GTACAGAAGTCAGAGAAGGCCATCCATCAAGCCCTACCTGACCTAGACATTAATCTTG 526  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 527 TCCTCAGAAGCTTTCCATTAATACATGAATGCTGCCATGTGCACATCAACAGGCCCTTG 586  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 587 AACTCATTAATTCGCTCTCTCTGTGAGAGATCTGGTTGACTTCCTTGAAGCTGGCTGC 646  
QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 647 TTCATGTGGCTGATGACCTATGTTGGTGTGCTGTTTAAACGGAATCAACCTTCTAATCTT 706  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 707 GCTGAATGCTCATTTTTCAGTGTCCCGATTGCTATGAGAGATGACCAAGCCAGATTGAT 766  
QY 161 HisTyrIleGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 767 CATATGTTGGCATGCCCGCAGATCGACCAATCAATGCTTGAAGAAGTCCAGCAAA 826  
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db 827 CTCCTTGAATCGCAAAAAAAGGAGAG 856

RESULT 78

ADI22969  
ID ADI22969 standard; cDNA; 1766 BP.  
XX ADI22969;  
XX ADI22969;  
DT 22-APR-2004 (first entry)  
XX cDNA encoding novel human secreted protein seq id 254.  
KW cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.  
XX Homo sapiens.  
XX US2003175858-A1.

PD 18-SEP-2003.  
XX 18-JUN-2001; 2001US-00882171.

XX 07-MAR-1997; 97US-0038621P.  
PR 07-MAR-1997; 97US-0040162P.  
PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040626P.  
PR 11-APR-1997; 97US-0043311P.  
PR 11-APR-1997; 97US-0043312P.  
PR 11-APR-1997; 97US-0043313P.  
PR 11-APR-1997; 97US-0043314P.  
PR 11-APR-1997; 97US-0043315P.  
PR 11-APR-1997; 97US-0043568P.  
PR 11-APR-1997; 97US-0043569P.  
PR 11-APR-1997; 97US-0043576P.  
PR 11-APR-1997; 97US-0043578P.  
PR 11-APR-1997; 97US-0043580P.  
PR 11-APR-1997; 97US-0043669P.  
PR 11-APR-1997; 97US-0043670P.  
PR 11-APR-1997; 97US-0043671P.  
PR 11-APR-1997; 97US-0043672P.  
PR 11-APR-1997; 97US-0043674P.  
PR 23-MAY-1997; 97US-0047492P.  
PR 23-MAY-1997; 97US-0047500P.  
PR 23-MAY-1997; 97US-0047501P.  
PR 23-MAY-1997; 97US-0047502P.  
PR 23-MAY-1997; 97US-0047503P.  
PR 23-MAY-1997; 97US-0047581P.  
PR 23-MAY-1997; 97US-0047582P.  
PR 23-MAY-1997; 97US-0047583P.  
PR 23-MAY-1997; 97US-0047584P.  
PR 23-MAY-1997; 97US-0047585P.  
PR 23-MAY-1997; 97US-0047586P.  
PR 23-MAY-1997; 97US-0047587P.  
PR 23-MAY-1997; 97US-0047588P.  
PR 23-MAY-1997; 97US-0047589P.  
PR 23-MAY-1997; 97US-0047590P.  
PR 23-MAY-1997; 97US-0047592P.  
PR 23-MAY-1997; 97US-0047593P.  
PR 23-MAY-1997; 97US-0047594P.  
PR 23-MAY-1997; 97US-0047595P.  
PR 23-MAY-1997; 97US-0047596P.  
PR 23-MAY-1997; 97US-0047597P.  
PR 23-MAY-1997; 97US-0047598P.  
PR 23-MAY-1997; 97US-0047599P.  
PR 23-MAY-1997; 97US-0047600P.  
PR 23-MAY-1997; 97US-0047601P.  
PR 23-MAY-1997; 97US-0047612P.  
PR 23-MAY-1997; 97US-0047613P.  
PR 23-MAY-1997; 97US-0047614P.  
PR 23-MAY-1997; 97US-0047615P.  
PR 23-MAY-1997; 97US-0047617P.  
PR 23-MAY-1997; 97US-0047618P.  
PR 23-MAY-1997; 97US-0047632P.





PS Claim 3; SEQ ID NO 254; 142pp; English.

XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and its complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)). The present sequence  
CC represents a human secreted protein cDNA.

XX SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

#### Alignment Scores:

Pred. No.:	9,346-66	Length:	1766
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADH73971 (1-1766)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	287	CGCGTGCAGCATCTGATTTCTTGGAGATGTGAAGAAGACTGGGTTTGTCTTGGCACC	346
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	347	ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCACTACAGTGTGTTCTTACCTC	406
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	407	ATCTGGCTCTCTCTGTCCATCATCAGTTCAGGATCTACAGTCCGTATCCAGCT	466
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	467	GTACAGAAGTCAGAGAAGGCCATCCATTAAAGCTTACCTGGACGTAGACATTACTCTG	526
Qy	81	SerGluGluLeuValGlnLysTyrSerHsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	527	TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGACATCAACAGGGCCCTG	586
Qy	101	LysGluLeuLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	597	AAACTCATATTCTGCTCTTCTGTGTAGAGATCTGGTTGACTCTTGAAGCTGGCTGTC	646
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	647	TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTTCTAATCTT	706
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	707	GCTGAACATGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAACCCAGATTGAT	766
Qy	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	767	CACATATGTGGCATGCCCGGAGATCAGACCAGTCAATTGTTGAAAAGATCCAGCAAAA	826
Qy	181	IleProGlyLeu---LysArgLysAlaGlu	189
Db	827	CTCCCTGGAATCGCCCAAAAAAAGGCAGAA	856

#### RESULT 80

ADM36177  
ID ADM36177 standard; DNA; 1911 BP.  
AC ADM36177;  
XX 03-JUN-2004 (first entry)  
XX Human RTN3 isoform VI coding sequence, SEQ ID 60.  
XX Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;  
XX amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 124..834  
XX FT /\*tag= a  
XX FT /product= "RTN3 isoform VI"  
XX WO2004001069-A2.  
XX 31-DEC-2003.  
XX 20-JUN-2003; 2003WO-FR001910.  
XX 25-JUN-2002; 2002FR-00007846.  
XX (UYPA-) UNIV PASTEUR LOUIS.  
XX Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
XX Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX WPI; 2004-071743/07.  
XX P-ESDB; ADM36178.  
XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
XX amyotrophic lateral sclerosis, comprises detecting modulation of the  
XX reticulon 3 gene.  
XX Claim 17; SEQ ID NO 60; 116pp; French.

The present invention relates to a method for diagnosing, or evaluating  
progression of, a neuromuscular disease. The method comprises detecting  
modulation of the expression of a product (I) of the RTN (reticulon)3  
gene. Differential expression of RTN3 is a specific marker of  
neuromuscular disease, allowing early diagnosis from readily available  
muscle biopsies. The method is also useful for determining the efficacy  
of treatment. The method is used to diagnose (also to evaluate  
progression or therapy of) neuromuscular disorders, specifically  
amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
small interfering RNA) that can block/reduce expression of these isoforms  
are useful for treating neuromuscular diseases and (ii) cells that  
express RTN3 are useful in screening for therapeutic agents. The present  
sequence is a RTN3 DNA sequence used to illustrate the invention.

SQ Sequence 1911 BP; 488 A; 463 C; 406 G; 554 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1,046-65	Length:	1911
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36177 (1-1911)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	262	CGCGTGCAGCATCTGATTTCTTGGAGATGTGAAGAAGACTGGGTTTGTCTTGGCACC	321

QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 322 ACGCTGATCGTGTCTTCCCTGGCAGCTTTTCAGTGTGCTGTTTCTACCTC 381  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 382 ATCTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 441  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 442 GTACAGAAGTCAGAGAAGAGCCCATTCATTCAAGGCCCTACCTGGACGTAGACATTACTCTG 501  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 502 TCTTCAGAACCTTTCATTAATACATGAATGCTGCCATGTCACATCAACAGGGCCCTG 561  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaVal 120  
 DB 562 AACTCATTTATTCGCTCTTCTGTGGTAGAAGATCTGGTTGATCTCTTGAAGCTGGCTGTC 621  
 QY 121 LeuMetTrpValPheTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 622 TTCATGTGCTGATGACCTATGTTGTGTCTTTTAAACGGAATCACCCCTCTCAATCTT 681  
 QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 682 GCTGAACCTGCTCATTTTCAGTGTCCGATTTGTCTATGAGAAGTACAAGACCCAGATTGAT 741  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 742 CACTATGTTGGATCCGCCGAGATCAGACCAAGTCAATGTTGTAAGAAGATCCAGCAAAA 801  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 DB 802 CTCCTCGGAATCGCCAAAAGGAGGAGAA 831  
 RESULT 81  
 ID ABA09204 standard; cDNA; 1915 BP.  
 XX ABA09204;  
 XX  
 DT 11-JAN-2002 (first entry)  
 XX  
 DE Human neuroendocrine-specific protein-like homologue cDNA, SEQ ID NO:980.  
 KW Human; cytokine; cell proliferation; tissue growth; immunomodulator; growth factor;  
 KW haematopoiesis regulation; tumour; tumour; tumour; tumour; tumour; tumour;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; tumour; tumour; tumour; tumour;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; anti-inflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157188-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US003800.  
 XX  
 PR 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 XX  
 PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;  
 XX WPI; 2001-457740/49.  
 DR P-PSDB; ABB11960.  
 XX Human proteins and DNA encoding sequences useful for preventing, treating  
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 PT and cancer.  
 XX Claim 1; Page 838; 1963pp; English.  
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention  
 XX Sequence 1915 BP; 492 A; 463 C; 411 G; 549 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: Length: 1915  
 Score: 624.50 Matches: 115  
 Percent Similarity: 81.05% Conservative: 39  
 Best Local Similarity: 60.53% Mismatches: 35  
 Query Match: 67.08% Indels: 1  
 DB: 4 Gaps: 1  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABA09204 (1-1915)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 287 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTCTTTGGCACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 347 ACGCTGATCATGCTCTTCTTCCCTGGCAGCTTTCAGTGTGCTGTTGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 407 ATCTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 466



QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 467 GTACAGAGTCAAGAGAGCCATTCATTCAAGGCTACCTGGAGCTAGACATTAATCTG 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 527 TCCTCAGAAGCTTTCATTAATACATGAATGTCGTCATGTCACATCAACAGGCGCTG 586  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 587 AAATCATATTTCGCTCTCTCTGTAAGAGATCGGTGACTCTTGAAGCTGCTGTC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 647 TTCATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGATCACCTCTTAATCTT 706  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 707 GCTGAATGCTCATTTTCAGTGTCCGATTTGCTATGAGAGTACAAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 767 CACTATGTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 826  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 DB 827 CTCCTCGAATCGCCCAAAAAGGAGCA 856

RESULT 82  
 ID AAF93902 standard; cDNA; 2530 BP.  
 XX AAF93902;  
 AC AAF93902;  
 DT 23-MAY-2001 (first entry)  
 XX Human cDNA encoding a membrane or secretory protein clone PSEC0103.  
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; ss.  
 XX Homo sapiens.  
 XX EP1067182-A2.  
 XX 10-JAN-2001.  
 XX 07-JUL-2000; 2000EP-00114090.  
 XX 08-JUL-1999; 98JP-00194179.  
 PR 11-JAN-2000; 2000JP-00118775.  
 PR 02-MAY-2000; 2000JP-00183766.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 WPI; 2001-093989/11.  
 DR P-PSDB; AAB88475.  
 XX Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.  
 XX Claim 1; SEQ ID NO 317; 609pp + Sequence Listing; English.  
 XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene

CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes  
 XX

SQ Sequence 2530 BP; 665 A; 577 C; 534 G; 754 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.55e-65 Length: 2530  
 Score: 624.50 Matches: 115  
 Percent Similarity: 81.05% Conservative: 39  
 Best Local Similarity: 60.53% Mismatches: 35  
 Query Match: 67.08% Indels: 1  
 DB: 5 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF93902 (1-2530)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 276 GCGGTGCACGATCTGATTTCTCGAGAGATGCTGAAGAAGACTGGGTTTGTCTTTGGCACC 335  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 336 ACGTGTATCATGTGCTTCTCCCTGGCAGCTTTCAGTGTGCATCAGTGTGTTCTTACCTC 395  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 396 ATCTGGCTCTCTCTCTGTCACCATCAGCTTCAGATCTACAGCTCGTATCCAGCT 455  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 456 GTACAGAAGTCAGAAGAAGGCCATCCATTTCAAGGCTACCTGGAGCTAGACATTAATCTG 515  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 516 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGTCACATCAACAGGCGCTG 575  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 576 AAATCATATTTCGCTCTCTCTGTAAGAGATCTGGTGTGACTCTTGAAGCTGCTGTC 635  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 636 TTCATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAAATCACCTTCTTAATCTT 695  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 696 GCTGAATGCTCATTTTCAGTGTCCGATTTCTATGAGAAGTACAAGACCCAGATTGAT 755  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 756 CACTATGTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 815  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 DB 816 CTCCTCGAATCGCCCAAAAAGGAGCA 845

RESULT 83  
 ID ADL02184 standard; cDNA; 2559 BP.  
 XX



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PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
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PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.

PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 1998-506364/43.
DR P-PSDB; AAW74964.
XX New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX Claim 1; Page 475-476; 721pp; English.
XX This sequence represents a nucleic acid molecule designated Gene 92 from
CC the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused to
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W75026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)
XX SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

Alignment Scores:
Pred. No.: 1.66e-65 Length: 2664
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 2 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x AAV59749 (1-2664)

Qy 1 SerValValAspLeuLeuTyrTTPArgAspIleValysThrGlyValValpHeGlyAla 20
Db 262 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 321
Qy 21 SerLeuPheLeuLeuLeuSerSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCTCATCTGTTGTTTCTTACCTC 381
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleAla 60
Db 382 ATCCTGGCTTCTCTCTGTCCATCAGTTCAGGATCTACAAAGTCGTCATCAAGCT 441
Qy 61 IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 442 GTACAGAAGTCAGAAGAAGGCATCCATTCAAGCCTACCTGGACGTAGACATTACTCTG 501
Qy 81 SerGluGluLeuValGlnIleLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 502 TCCTCAGAAGCTTTCATATTAATGATGCTGCCATGGTGACATCAACAGGCCCTG 561
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaVal 120
Db 562 AAACCTATTTCGTCCTCTTCTGAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 621
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QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
      |||||:::
Db 622 TTCATGCTGCTGATGACCTATGTTGCTGCTGTTTAAACGGAATCACCTCTTAATTCCT 681
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
      |||:::
Db 682 GTGAACCTGCTCATTTTCAGTGCCGATGTTCTATGAGAAGTACAAAGACCCAGATTGAT 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
      |||||:::
Db 742 CACTATGTTGGCATCCGCCAGATCAGACCAAGTCAATTGTTCAAAAGATCCAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
      ::|||:::
Db 802 CTCCTCGGAATCGCAAAAAAAGGCAGAA 831

RESULT 85
ABS73742
ID ABS73742 standard; cDNA; 2664 BP.
XX
AC ABS73742;
XX
DT 15-JAN-2003 (first entry)
XX
DE Human cDNA #3 for novel secreted protein gene 92.
XX
KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
OS Homo sapiens.
XX
PN US6420526-B1.
XX
PD 16-JUL-2002.
XX
PF 08-SEP-1998; 98US-00149476.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
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PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
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PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
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PR 23-MAY-1997; 97US-0047617P.
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PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051928P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
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PR 22-AUG-1997; 97US-0056632P.
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PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
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PR 22-AUG-1997; 97US-0056872P.
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PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
PR 06-MAR-1998; 98WO-US004493.
XX
```

(HUMA-) HUMAN GENOME SCI. INC.

PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;  
PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;  
PI Ferlie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
xx  
WPI: 2002-634796/68.  
DR P-PSDB: ABG95424.  
DR

New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or preservative.

Example 1; SEQ ID NO 255; 129pp; English.

The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at [seqdata.uspto.gov/sequence.html?docID=642052691](http://seqdata.uspto.gov/sequence.html?docID=642052691)

Sequence 2664 BP: 707 A: 605 C: 566 G: 779 T: 0 U: 7 Other: .

Alignment Scores:		
Pred. No.:	1.66e-65	Length:
Score:	624.50	Matches:
Percent Similarity:	81.05%	Conservative:
Best Local Similarity:	60.53%	Mismatches:
Query Match:	67.08%	Indels:
DB:	6	Gaps:
		1
		1
		2664

US-09-830-972-29 COPY 990 1178 (1-189) X ABS73742 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleIysIysThrGlyValValPheGlyAla	20
Db	262	GGCGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTGCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATGCTGTTTCCTGGCAGCTTTCAGTGTCACTAGTGTGGTTTCTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla	60
Db	382	ATTCCTGGCTTCTCTCTGTCAACATCATGTTCAAGATCTACAAGTCCGTCATCCAAGCT	441
Qy	61	IleGlnIysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle	80
Db	442	GTACAGAAGTCAGAAGAGGCCATCCATTCAAGCCTACCTGGACGTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	502	TCTTCAGAAGCTTTCATAATTACATGATGATCTGCCCATCTGCACATCAACACAGGGCCGTG	561
Qy	101	LysGluLeuArgArcLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120

[illegible]

## RESULT 86

ACD82885  
ID ACD82885 standard; cDNA: 2664 BP.

AC ACD82885:

XX  
DT 22-SEP-20XX  
DE CUNA SERVICE #245 CONTACT[illegible]

KW breast cancer; wound; reproductive disorder; blood-related disorder;  
KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;  
KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;  
KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;  
KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;  
KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;  
KW angina pectoris; cerebral ischaemia; congenital heart defect;  
KW respiratory disorder; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; inflammation; Crohn's disease; vulvarny;  
KW immunosuppressive; antibacterial; haemostatic; thrombolytic;  
KW anticoagulant; neuroprotective; thymomimetic; antiallergic;  
KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotoxic; antianginal;  
KW cerebroprotective; cardiant; nootropic; antiparkinsonian;  
KW antiinflammatory; gene; ss.

xx  
os  
Homo sapiens.

XX PN US2003049618-A1.

XX  
PD  
13-MAR-2003XX  
PF 16-MAR-2001. 2001US-00809391XX  
07-MAR-1997. 07118-0039621D

PR 07-MAR-1997; 97US-0040162P.

PR 07-MAR-1997; 97US-0040333P.

PR 07-MAR-1997; 97US-0040336P.

PR 11-APR-1997; 97US-0043311P.

PR 11-APR-1997; 97US-0043313P.

PR 11-APR-1997; 97US-004331SP.

PR 11-APR-1997; 97US-0043569P.

PR 11-APR-1997; 97US-0043578F;  
PR 11-APR-1997; 97US-0043578P;

PR 11-APR-1997; 97US-0043580E;  
PR 11-APR-1997; 97US-0043669P;

PR 11-APR-1997; 97US-0043670P.  
PR 11-APR-1997. 97US-0043671P

PR 11-APR-1997; 97US-0043672P.  
PR 11-APR-1997; 97US-0043674P.  
PR 23-MAY-1997; 97US-0047492P.  
PR 23-MAY-1997; 97US-0047500P.  
PR 23-MAY-1997; 97US-0047501P.  
PR 23-MAY-1997; 97US-0047502P.  
PR 23-MAY-1997; 97US-0047503P.  
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PR 23-MAY-1997; 97US-0047594P.  
PR 23-MAY-1997; 97US-0047595P.  
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PR 23-MAY-1997; 97US-0047597P.  
PR 23-MAY-1997; 97US-0047598P.  
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PR 23-MAY-1997; 97US-0047618P.  
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PR 06-JUN-1997; 97US-0048964P.  
PR 06-JUN-1997; 97US-0048974P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 08-JUL-1997; 97US-0051926P.  
PR 16-JUL-1997; 97US-0052874P.  
PR 18-AUG-1997; 97US-0055724P.  
PR 22-AUG-1997; 97US-0056630P.  
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PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
PR 22-AUG-1997; 97US-0056886P.  
PR 22-AUG-1997; 97US-0056887P.  
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PR 22-AUG-1997; 97US-0056903P.  
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PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 22-AUG-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057669P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 09-OCT-1997; 97US-0061660P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
PR 17-MAR-2000; 2000US-0190068P.  
XX (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (VUGG/) YU G.  
PA (NIJU/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJU/) HU J.  
PA (FLOK/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFLE/) LAFLEUR D W.  
PA (LIYV/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX WPI: 2003-521800/49.  
DR P-PSDB; ABO34618.  
DR  
XX  
XX  
PT New genes and its encoded prostate cancer antigen proteins, useful for  
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
PT ischemia.  
XX  
PS Claim 4; SEQ ID NO 255; 260pp; English.  
XX  
XX The present invention relates to the isolation of novel human secreted  
CC proteins and the polynucleotide sequences encoding them. The invention  
CC also discloses vectors, host cells, antibodies, and recombinant methods  
CC for producing human secreted proteins. The polypeptide and polynucleotide  
CC sequences for the secreted proteins are useful for preventing, treating,  
CC ameliorating or diagnosing medical conditions such as hyperproliferative  
CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive  
CC disorders, blood-related disorders (e.g. haemophilia or  
CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,  
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),  
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
CC disorders, neurological disorders (e.g. Alzheimer's disease or  
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/psipdb/entry.html](http://seqdata.uspto.gov/psipdb/entry.html)  
XX

SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

Alignment Scores:	1.66e-65	Length:	2684
Pred. No.:	Score:	Matches:	115
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Best Local Similarity:	60.53%	Indels:	1
Query Match:	67.08%	Gaps:	1
DB:	9		

US-09-830-972-29 COPY 990 1178 (1-189) x ACD82885 (1-2664)

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Db	262	CGG	GTGCACGATCTCATTTTCTGGAGAGATGTGAAGAAGACTCGGTGTGTCTTTGGCACC	321
Qy	40	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACG	CTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTCCTTCACTC	381
Qy	60	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATC	TGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCGGTCATCCAAAGCT	441
Qy	80	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTAC	AGAAGTCAGAAGAAGCCATCCATTCAAAGCTTACCTGGACGTAGTAAACATTTACTCTG	501
Qy	100	81	SerGluGluLeuValGlnLysTyrSerIleSerAlaLeuGlyHisValAenCysThrIle	100
Db	502	TCCT	CAGAAGCTTTCATTAATTACATGAATGCTGCCATGGTGCACTCAACAGGGCCCTG	561
Qy	120	101	LysGluLeuArgGluLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	562	AAAC	TATATTTCGTCCTCTTCTGCTGAGAGATCTGGTTGACTCCTTGAAGCTGGCTGTC	621
Qy	140	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	622	TTCA	TGTGCTGATGACCTTATGTTGGTGCTGTGTTTTAACGGAAATCACCCCTTCTAAATCTTT	681
Qy	160	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	741	682	GCTGAACCTGCTCATTTTTCAGTGTCCCGATGTCTATGTAGAAGATGACAAGCCAGATTGAT	741
Qy	180	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	801	742	CACATGTTGGCATCCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGCAAA	801
Qy	189	181	IleProGlyLeu---LysArgLysAlaGlu	189
Db	831	802	CTCCCTGGAAATCGCCAAAATAAAGGCAGAA	831

RESULT 87

ADI22970

ID ADI22970 standard; cDNA; 2664 BP.

XX  
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XX

AC ADI22970;

XX  
DT 22-APR-2004 (first entry)

XX  
DE  
DE

cDNA encoding novel human secreted protein seq id 255.

XX  
XX  
KW

XX  
OS Homo sapiens.

XX  
PN US2003175858-A1.

XX  
PD 18-SEP-2003.

XX  
PF 18-JUN-2001; 2001US-00882171.

XX	07-MAR-1997;	97US-0038621P.
PR		

PR	07-MAR-1997	97US-00401622
PR	07-MAR-1997	97US-00401633
PR	07-MAR-1997	97US-00403339
PR	07-MAR-1997	97US-00403344
PR	07-MAR-1997	97US-00403363
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PR	06-JUN-1997	97US-0048974P
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PR	08-AUG-1997	97US-0051926P
PR	16-JUL-1997	97US-0052874P
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PR	22-AUG-1997	97US-0056872P
PR	22-AUG-1997	97US-0056874P
PR	22-AUG-1997	97US-006875P





XX OS Homo sapiens.  
XX PN US2003225248-A1.  
XX PD 04-DEC-2003.  
XX PF 10-JUN-2002; 2002US-00164861.  
XX PR 07-MAR-1997; 97US-0038621P.  
XX PR 07-MAR-1997; 97US-0040161P.  
XX PR 07-MAR-1997; 97US-0040162P.  
XX PR 07-MAR-1997; 97US-0040163P.  
XX PR 07-MAR-1997; 97US-0040333P.  
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XX PR 07-MAR-1997; 97US-0040336P.  
XX PR 07-MAR-1997; 97US-0040626P.  
XX PR 11-APR-1997; 97US-0043311P.  
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XX PR 11-APR-1997; 97US-0043674P.  
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XX PR 23-MAY-1997; 97US-0047612P.  
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XX PR 23-MAY-1997; 97US-0047617P.  
XX PR 23-MAY-1997; 97US-0047618P.  
XX PR 23-MAY-1997; 97US-0047632P.  
XX PR 23-MAY-1997; 97US-0047633P.  
XX PR 06-JUN-1997; 97US-0048964P.  
XX PR 06-JUN-1997; 97US-0048974P.  
XX PR 13-JUN-1997; 97US-0049610P.  
XX PR 08-JUL-1997; 97US-0051926P.  
XX PR 16-JUL-1997; 97US-0052874P.  
XX PR 18-AUG-1997; 97US-0055724P.  
XX PR 22-AUG-1997; 97US-0056630P.  
XX PR 22-AUG-1997; 97US-0056631P.  
PR 22-AUG-1997; 97US-0056632P.  
PR 22-AUG-1997; 97US-0056636P.  
PR 22-AUG-1997; 97US-0056637P.  
PR 22-AUG-1997; 97US-0056638P.  
PR 22-AUG-1997; 97US-0056644P.  
PR 22-AUG-1997; 97US-0056845P.  
PR 22-AUG-1997; 97US-0056862P.  
PR 22-AUG-1997; 97US-0056864P.  
PR 22-AUG-1997; 97US-0056872P.  
PR 22-AUG-1997; 97US-0056874P.  
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PR 22-AUG-1997; 97US-0056876P.  
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PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
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PR 22-AUG-1997; 97US-0056887P.  
PR 22-AUG-1997; 97US-0056888P.  
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PR 22-AUG-1997; 97US-0056892P.  
PR 22-AUG-1997; 97US-0056893P.  
PR 22-AUG-1997; 97US-0056894P.  
PR 22-AUG-1997; 97US-0056903P.  
PR 22-AUG-1997; 97US-0056908P.  
PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 05-SEP-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057669P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 02-OCT-1997; 97US-0061060P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bedharik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX WPI; 2004-131264/13.  
DR P-PSDB; ADH74281.  
XX Isolated nucleic acid molecules encoding human secreted proteins, useful  
PT for preventing, diagnosing and treating disorders associated with  
PT aberrant expression and activity.  
XX Claim 3; SEQ ID NO 255; 142pp; English.  
XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and it's complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbant assay (ELISA)). The present sequence

```
CC represents a human secreted protein cDNA.
XX
SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

Alignment Scores:
Pred. No.: 1,66e-65 Length: 2664
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservatives: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 12 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x ADH73972 (1-2664)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
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DB 262 GCGGTGCAGACTGATTTCTCGAGAGATGTGACAGAGACTGGGTTCTTGGCACC 321

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
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DB 322 ACCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCTCATCAGTGTGTTCTTACCTC 381

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 382 ATCTGGCTCTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTGTATCCAGCT 441

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 442 GTACAGAGTCAGAGAGGCCATCCATTCMAAGCCCTCTGGACGTACACATTACTCTG 501

QY 81 SerGluGluLeuValGlnIlySerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 502 TCCTCAGAGCTTCCCAATATACATGAATGCTGCCATGTGCACATCAACAGGGCCCTG 561

QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 562 AAACATCATTTCTCTCTCTGGTAGAGATCTGTTGACCTCTTGAAGCTGGCTGTC 621

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 622 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGAATCACCTTCTAATCTT 681

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 682 GCTGAACGTGCTCATTTTCTAGTGTCCCGATTGCTATCAGAGATACAGACCCAGATTGAT 741

QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 742 CACTATGTTGGCATCCCGAGATCAGACCAATGCTAATTGTTGAAAAGATCCAGCAAA 801

QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 802 CTCCTCGGAATGCCCAAAAAGAGGAGAA 831

RESULT 89
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XX
AC ADQ24047;
XX
XX 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6867.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW db.
XX
OS Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
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Db 740 GCTGAACGCTCTCATTTTCAGTGTCCGATGTCTATGAGAGTACAGACCCAGATTGAT 799  
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Db 860 CTCCTCGAATCGCCCAAAAAAAGGCAGAA 889

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XX 03-JUN-2004 (first entry)  
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XX Human RTN3 isoform III coding sequence, SEQ ID 54.  
XX  
XX Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;  
KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 124..891  
FT /\*tag= a  
FT /product= "RTN3 isoform III"  
XX  
XX WO2004001069-A2.  
XX  
XX 31-DEC-2003.  
XX  
XX 20-JUN-2003; 2003WO-FR001910.  
XX  
XX 25-JUN-2002; 2002FR-00007846.  
XX  
XX (UYPA-) UNIV PASTEUR LOUIS.  
XX  
XX Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX  
XX WPI; 2004-071743/07.  
XX  
XX P-PSDB; ADM36172.  
XX  
XX  
XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX  
XX  
XX Claim 35; SEQ ID NO 54; 116pp; French.  
XX  
XX The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
XX Sequence 1968 BP; 496 A; 482 C; 411 G; 579 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 1.44e-65 Length: 1968  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservative: 38

Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 12 Gaps: 1  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36171 (1-1968)

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Db 322 GTGCACGATCTGATTTCTCGAGAGATGTGAAGAACTGGGTTGTCTTGGCACCCAGC 381  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 382 CTGATCATGTGCTTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTTCTTACCTCATC 441  
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 442 CTGGCTCTTCTCTGTGCACCATCAGCTTCAAGATCTACAAGTCGTTCATCAAGCTGTA 501  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 502 CAGAAGTCAGAAAGGCCATCCATTCAAGGCCTCACTGGACGTAGACATTACTCTGTCC 561  
Qy 82 GluGlnLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 562 TCAGAAGCTTTCCATAAATTACATGATCTGCCATGTGTGCACATCAACAGGGCCCTGAAA 621  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 622 CTCATTATTCTCTCTTCTGTGTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTCTTC 681  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
Db 682 ATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTTCTTAATCTTGT 741  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 742 GAACCTGCTCATTTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCAGATTGATCAC 801  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 802 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTGTGAAGAGATCCAAGCAAACTC 861  
Qy 182 ProGlyLeu---LysArgLysAlaGlu 189  
Db 862 CCTGGAATCGCCAAAAAAGGCAGAA 888

RESULT 91  
ID ADQ84465  
XX ADQ84465 standard; cDNA; 2250 BP.  
XX  
XX AC ADQ84465;  
XX  
XX DT 07-OCT-2004 (first entry)  
XX  
XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #1279.  
XX  
XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
XX cancer; cell proliferative disorder; gene; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO2004060270-A2.  
XX  
XX PD 22-JUL-2004.  
XX  
XX PF 15-OCT-2003; 2003WO-US029126.  
XX  
XX PR 18-OCT-2002; 2002US-0418988P.  
XX  
XX XX (GETH ) GENENTECH INC.  
XX PA (WUTD/) WU T D.  
XX PA (ZHOU/) ZHOU Y.  
XX

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PI Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 1279; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.74e-65 Length: 2250
Score: 623.50 Matches: 115
Percent Similarity: 80.95% Conservative: 38
Best Local Similarity: 60.85% Mismatches: 35
Query Match: 66.97% Indels: 1
DB: 12 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x ADQ84465 (1-2250)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 1 GTGCAGATCTGATTCTTGGAGAGATGTGAAGACATGGGTGTCTTGGCACCAGC 60
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerIleValThrAlaTyrIleAla 41
Db 61 CTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCTCATGCTGTGTTCTTACTCTATC 120
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 121 CTGGCTCTTCTCTCTCACCATCATCAGTCTCAGATCTACAGTCCGCTCATCAAGCTGTA 180
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

PI Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 1279; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.74e-65 Length: 2250
Score: 623.50 Matches: 115
Percent Similarity: 80.95% Conservative: 38
Best Local Similarity: 60.85% Mismatches: 35
Query Match: 66.97% Indels: 1
DB: 12 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x ADQ84465 (1-2250)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 1 GTGCAGATCTGATTCTTGGAGAGATGTGAAGACATGGGTGTCTTGGCACCAGC 60
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerIleValThrAlaTyrIleAla 41
Db 61 CTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCTCATGCTGTGTTCTTACTCTATC 120
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 121 CTGGCTCTTCTCTCTCACCATCATCAGTCTCAGATCTACAGTCCGCTCATCAAGCTGTA 180
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

XX Sequence 2250 BP; 629 A; 469 G; 456 C; 696 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1,74e-65 Length: 2250  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservative: 38  
Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADQ86409 (1-2250)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 1 GTGCACGATCTGATTTCTCGAGAGATGTAAGAAGACTGGGTTGTCTTTGGCCACACG 60  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrIleAla 41  
Db 61 CTGATCATGCTGCTTCCCTGCGAGCTTTCAGTGTCTCATGCTGGTTCCTTACTCATC 120  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaTle 61  
Db 121 CTGGCTCTCTCTCTGTCACATCATGCTTCAGATCTCAAGTCTCAAGTCTCAAGTCTGA 180  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 181 CAGAAGTCAGAAGAGGCCATCCATTTCAAGCTTACCTGGAGCTAGACATTAATCTGTCC 240  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLys 101  
Db 241 TCAGAAGCTTCTCCATAATATACATGAATGCTGCCATGCTGGTCATCAACAGGGCCCTGAAA 300  
Qy 102 GluLeuArgLysLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 301 CTCATTATTCGTCTCTTTCTGTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTCTTC 360  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 361 ATGTGGCTGATCACCATTATGTTGGTCTGCTTTTAAAGGAATCACCCTCTTAATCTTGTCT 420  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 421 GAACTGCTCAITTTTCAGTGTCCGATTTCTATGAGAAGTCAACAGCCAGATGATCATC 480

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 481 TATGTTGGCATCGCCGAGATCAGACCAAGTCATTGTTGAAGATCCAGCAAACTC 540  
Qy 182 ProGlyLeu---LysArgLysAlaGlu 189  
Db 541 CCTGGAATCGCAAAAAAAGGCAGAA 567  
RESULT 93  
ADQ85262  
ID ADQ85262 standard; cDNA; 2250 BP.  
XX AC ADQ85262;  
XX 07-OCT-2004 (first entry)  
XX Human tumour-associated antigenic target (TAT) cDNA sequence #2076.  
DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
KW cancer; cell proliferative disorder; gene; ss.  
XX Homo sapiens.  
XX WO2004060270-A2.  
XX 22-JUL-2004.  
XX 15-OCT-2003; 2003WO-US029126.  
XX 18-OCT-2002; 2002US-0418988P.  
XX (GETH ) GENENTECH INC.  
XX (WUTD/) WU T D.  
XX (ZHOU/) ZHOU Y.  
XX Wu TD, Zhou Y;  
XX WPI; 2004-534300/51.  
XX New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.

Claim 1; SEQ ID NO 2076; 5504pp; English.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative

CC disorder associated with increased expression or activity of the above  
CC protein; and (17) a method of binding an antibody, oligopeptide or  
CC organic molecule to a cell that expresses the protein described above.  
CC The TAT sequences have cytostatic activities, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing,  
CC preventing or treating cancer. The composition is also used for preparing  
CC a medicament for the therapeutic treatment or diagnostic detection of a  
CC cell proliferative disorder or cancer. The present sequence represents a  
CC human TAT cDNA sequence from the present invention.  
XX  
SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.74e-65 Length: 2250  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservatives: 38  
Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 13 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADQ85262 (1-2250)

QY 2 ValValAspLeuLeuThrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 1 GTGCAGCATCTGATTTCTGGAGAGATGTGAAGACATGGTTGTCTTTGGCACCAG 60  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTrpIleAla 41  
DB 61 CTGATCATGCTGTTTCCCTGGCAGCTTTTCAGTGTCTCATGAGTGGTTCTTACCTCATC 120  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 121 CTGGCTCTTCTCTCTGTCACCATCAGTTCAGATTCAGATTCAGATTCAGATTCAGATTC 180  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 181 CAGAGTCAGAGAGGCGCATCTCAATTCAGAGCTTCTGAGCTAGACATTAATCTGTCTC 240  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 241 TCAGAGAGCTTCCATTAATACATGAATGCTGCATGTCATCAACAGGCGCTGMAA 300  
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuVal 121  
DB 301 CTCATTAATTCGCTCTCTTCTGGTAGAGATCTGGTGAATCTTGAAGCTGCTGCTTC 360  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 361 ATGTGCTGATGACCTATGTTGGTGTCTGTTTAAAGGAATCACTCTTAATCTTGTCT 420  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 421 GAATGCTCATTTTCAGTGTCCGATGTCTATGAGAGTACAGAGCCAGATTCATCAC 480  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 481 TATGTTGGATGCCCGCAGATCAGACCAAGTCAATTTGTTGAAAAGATCCAGCAAACTC 540  
QY 182 ProGlyLeu---LysArgLysAlaGlu 189  
DB 541 CCTGGAAATGCCAAAAGAGGAGAA 567

RESULT 94

ID ADQ83313

XX ADQ83313 standard; cDNA; 2250 BP.

AC ADQ83313;

XX 07-OCT-2004 (first entry)

DT Human tumour-associated antigenic target (TAT) cDNA sequence #127.

XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;

KW cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (GETH) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,

XX preventing or treating cell proliferative disorders such as cancer.

XX Claim 1; SEQ ID NO 127; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic

XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide

XX sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of

XX (a); (c) the complement of (a) or (b); (d) a sequence that has 80%

XX sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-

XX (c). Also described: (1) an expression vector comprising the above

XX nucleic acid; (2) a host cell comprising the above expression vector; (3)

XX a process for producing a polypeptide; (4) an isolated polypeptide

XX comprising: (a) an amino acid sequence encoded by any of the above

XX nucleotide sequences; (b) an amino acid sequence encoded by the full-

XX length coding region of the above nucleotide sequences; or (c) a sequence

XX having at least 80% identical to (a) or (b); (5) a chimeric polypeptide

XX comprising the above polypeptide fused to a heterologous polypeptide; (6)

XX an isolated antibody that binds to the above polypeptide; (7) a process

XX for producing the antibody; (8) an isolated oligopeptide that binds to

XX the above polypeptide; (9) a tumour-associated antigenic target (TAT)

XX binding organic molecule that binds to the above polypeptide; (10) a

XX composition of matter comprising the above (chimeric) polypeptide,

XX antibody, oligopeptide or TAT binding organic molecule, in combination

XX with a carrier; (11) an article of manufacture comprising a container and

XX inhibiting the growth of a cell that expresses the above protein, where

XX the growth of the cell is at least in part dependent upon a growth

XX potentiating effect of the above protein; (13) a method of

XX therapeutically treating a mammal having a cancerous tumour comprising

XX cells that express the above protein; (14) a method of determining the

XX presence of a protein in a sample suspected of containing the protein

XX described above; (15) methods of diagnosing the presence of a tumour in a

XX mammal; (16) a method for treating or preventing a cell proliferative

XX disorder associated with increased expression or activity of the above

XX protein; and (17) a method of binding an antibody, oligopeptide or

XX organic molecule to a cell that expresses the protein described above.

XX The TAT sequences have cytostatic activities, and can be used in gene

XX therapy. The composition and methods are useful for diagnosing,

XX preventing or treating cancer. The composition is also used for preparing

XX a medicament for the therapeutic treatment or diagnostic detection of a

XX cell proliferative disorder or cancer. The present sequence represents a

XX human TAT cDNA sequence from the present invention.

XX SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.74e-65 Length: 2250

Score: 623.50 Matches: 115

Percent Similarity: 80.95% Conservatives: 38

Best Local Similarity: 60.85% Mismatches: 35

Query Match: 66.97% Indels: 1

DB: 13 Gaps: 1





Db 747 CACTATGTTGGGATTCGCCGGGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAG 806

Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189

Db 807 CTTCTGGAATCGCCAAAGAAAGGCGAGAA 836

# RESULT 96

ADM36175  
ID ADM36175 standard; DNA; 3231 BP.

XX AC ADM36175;

XX DT 03-JUN-2004 (first entry)

XX Human RTN3 isoform V coding sequence, SEQ ID 58.

XX Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;

XX amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 124..2154

XX FT /\*tag= a

XX FT /product= "RTN3 isoform V"

XX WO2004001069-A2.

XX PD 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX XX (UYPA-) UNIV PASTEUR LOUIS.

XX Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

XX Gonzalez De Aguilar J, Boutillier AL, Gaiddon C, Rene F;

XX WPI; 2004-071743/07.

XX P-PSDB; ADM36176.

XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.

XX PS Claim 35; SEQ ID NO 58; 116pp; French.

XX The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.

XX SQ Sequence 3231 BP; 947 A; 717 C; 690 G; 877 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2.89e-65 Length: 3231  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservative: 38  
Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-29\_copy\_990\_1178 (1-189) x ADM36175 (1-3231)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
1585 GTGCACGATCTGATTTCCTGGAGAGAGTGTGAAGAAGACTGGCGTTGTCTTTGGCACCACG 1644

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
1645 CTGATCATGCTGCTTTCCCTGGCAGCTTCAGTGTGCATCAGTGTGGTTCTTACCTCATC 1704

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
1705 CTGGCTCTTCTCTCTGTCCACATCAGCTTCAGATCTACAGTCCGTCATCCAGCTGTA 1764

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
1765 CAGAAGTCAGAAAGAGGCCATCAATTCAGGCTACCTGGAGCTAGACATTACTCTGTCC 1824

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
1825 TCAGAAGCTTTCCATAATTACATGAATGCTGCATGGTGCAATCAACAGGCGCCCTGAAA 1884

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
1885 CTCATTATTCGTCCTCTTCTGTGTAGAGATCTGGTTGACTCTTGAAGCTGGCTGCTTC 1944

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
1945 ATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTCTTAATTCTTGCT 2004

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIlePheHis 161  
2005 GAACTGCTCATTTTCAGTGTCCGATGTCTATAGAAAGTACAAAGCCAGATGATCAC 2064

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
2065 TATGTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGACCAAACTC 2124

Qy 182 ProGlyLeu---LysArgLysAlaGlu 189

Db 2125 CCTGGAATCGCCAAAAGAAAGGCGAGAA 2151

## RESULT 97

ADM36169  
ID ADM36169 standard; DNA; 3288 BP.

XX AC ADM36169;

XX DT 03-JUN-2004 (first entry)

XX Human RTN3 isoform II coding sequence, SEQ ID 52.

XX Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 124..2211

XX FT /\*tag= a

XX FT /product= "RTN3 isoform II"

XX WO2004001069-A2.

XX PD 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX PA (UYPA-) UNIV PASTEUR LOUIS.

XX Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

[illegible]



Qy 182 ProGlyLeu---LysArgLysAlaGlu 189  
 Db 3133 CCTGGATCGCCAAAGGAGGAGAA 3159

## RESULT 100

ADM36167  
 ID ADM36167 standard; DNA; 4296 BP.

XX AC ADM36167;

XX DT 03-JUN-2004 (first entry)

XX DE Human RTN3 isoform I coding sequence, SEQ ID 50.

XX KW Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
 KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 124..3219

XX FT /\*tag= a

XX FT /product= "RTN3 isoform I"

XX WO2004001069-A2.

XX PN 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX PA (UYPA-) UNIV PASTEUR LOUIS.

XX FI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

XX FI Gonzales De Aguilar J, Bouillier AL, Gaidon C, Rene F;

XX DR WPI; 2004-071743/07.

XX DR P-PSDB; ADM36168.

XX PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
 PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
 PT reticulon 3 gene.

XX PS Claim 35; SEQ ID NO 50; 116pp; French.

XX CC The present invention relates to a method for diagnosing, or evaluating  
 CC progression of, a neuromuscular disease. The method comprises detecting  
 CC modulation of the expression of a product (I) of the RTN (reticulon)3  
 CC gene. Differential expression of RTN3 is a specific marker of  
 CC neuromuscular disease, allowing early diagnosis from readily available  
 CC muscle biopsies. The method is also useful for determining the efficacy  
 CC of treatment. The method is used to diagnose (also to evaluate  
 CC progression or therapy of) neuromuscular disorders, specifically  
 CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
 CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
 CC small interfering RNA) that can block/reduce expression of these isoforms  
 CC are useful for treating neuromuscular diseases and (ii) cells that  
 CC express RTN3 are useful in screening for therapeutic agents. The present  
 CC sequence is a RTN3 DNA sequence used to illustrate the invention.

SQ Sequence 4296 BP; 1290 A; 944 C; 895 G; 1167 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4.31e-65	Length:	4296
Score:	623.50	Matches:	115
Percent Similarity:	80.95%	Conservative:	38
Best Local Similarity:	60.85%	Mismatches:	35
Query Match:	66.97%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36167 (1-4296)

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 Db 2650 GTGCACCATCTGATTTCTCGAGAGATGTGAGAAGACTGGGTTTGTCTTTGGCACACG 2709  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 2710 CTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCTCATCTAGTGTGGTTCTTACTCTATC 2769  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 2770 CTGGCTCTTCTCTCTGTACCATCAGCTTCAGGATCTACAGTCCGTCATCAAGCTGTA 2829  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 2830 CAGAAGTCAGAAGAAGGCCATCCATTCAAGGCCCTACCTGGACGTAGACATTACTCTGTCC 2889  
 Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 2890 TCAGAAGCTTTCCATATAATTACATGAATGCTGCCATGTGTGCACATCAACAGGGCCCTGAAA 2949  
 Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 2950 CTCATTATTCGTCTCTTCTGTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTCTTC 3009  
 Qy 122 MetTyrValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 3010 ATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTTCTAATTTCTTGTCT 3069  
 Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 3070 GAACGTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTACAAAGACCCAGATTGATCAC 3129  
 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 3130 TATGTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAACTC 3189  
 Qy 182 ProGlyLeu---LysArgLysAlaGlu 189  
 Db 3190 CCTGGAATCGCCAAAAAAGGAGGAGAA 3216

Search completed: June 19, 2005, 07:21:13

Job time : 412 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 18, 2005, 20:51:35 ; Search time 125.5 Seconds  
(without alignments)  
2464.194 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SWVDLLYWRDIKKTGWVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
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- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	931	100.0	4822	3	US-09-484-970B-106
2	927	99.6	799	2	US-08-700-607-2
3	927	99.6	1669	4	US-09-949-016-117588
4	914	98.2	2610	4	US-09-023-655-382
5	682	73.3	3209	4	US-09-949-016-117589
6	682	73.3	3202	4	US-09-949-016-1127
7	627.5	67.4	4262	4	US-09-949-016-1127
8	624.5	67.1	1766	3	US-09-149-476-254
9	624.5	67.1	2664	3	US-09-149-476-255
10	543	58.3	3517	4	US-09-799-451-111
11	526.5	56.6	1095	2	US-08-700-607-4
12	518	55.6	2014	4	US-09-270-767-13561

13	508.5	54.6	794	3	US-09-149-476-102	Sequence 102, App
14	473.5	50.9	2181	4	US-09-949-016-1419	Sequence 1419, Ap
c 15	341	36.6	601	4	US-09-949-016-117588	Sequence 117588,
c 16	341	36.6	601	4	US-09-949-016-117589	Sequence 117589,
17	341	36.6	42075	4	US-09-949-016-14995	Sequence 14995, A
18	286	30.7	443	4	US-09-513-999C-3784	Sequence 3784, Ap
19	279.5	30.0	135667	4	US-09-949-016-15051	Sequence 15051, A
20	279.5	30.0	152486	4	US-09-949-016-12869	Sequence 12869, A
c 21	276.5	29.7	601	4	US-09-949-016-40169	Sequence 40169, A
c 22	276.5	29.7	601	4	US-09-949-016-119335	Sequence 119335,
23	276	29.6	261	2	US-08-700-607-9	Sequence 9, Appli
24	271	29.1	13906	4	US-09-949-016-14730	Sequence 14730, A
25	256	27.5	200	4	US-09-513-999C-11198	Sequence 11198, A
26	236.5	25.4	15661	4	US-09-949-016-13161	Sequence 13161, A
27	144	15.5	1125	4	US-09-248-796A-1905	Sequence 1905, Ap
c 28	141	15.1	601	4	US-09-949-016-40170	Sequence 40170, A
c 29	141	15.1	601	4	US-09-949-016-119336	Sequence 119336,
c 30	122	13.1	601	4	US-09-949-016-117609	Sequence 117609,
31	111	11.9	266	4	US-09-313-294A-703	Sequence 703, App
c 32	102	11.0	601	4	US-09-949-016-48087	Sequence 48087, A
33	100	10.7	425	3	US-08-905-223-178	Sequence 178, App
c 34	95	10.2	1722	4	US-08-956-171E-407	Sequence 407, App
c 35	95	10.2	1722	4	US-08-781-986A-407	Sequence 407, App
36	89	9.6	1828	3	US-08-487-596-7	Sequence 7, Appli
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38	88.5	9.5	4550	3	US-09-462-136-1	Sequence 4281, Ap
39	88.5	9.5	4661	4	US-09-949-016-4281	Sequence 100, App
40	88.5	9.5	4673	4	US-09-814-915A-100	Sequence 100, App
41	88	9.5	1273	4	US-09-949-016-5725	Sequence 5725, Ap
42	87.5	9.4	1779	4	US-09-134-000C-2072	Sequence 2072, Ap
43	87.5	9.4	3156	3	US-09-134-001C-2168	Sequence 2168, Ap
44	86	9.2	296	4	US-09-313-294A-81	Sequence 81, Appl
45	85	9.1	1302	4	US-08-956-171E-322	Sequence 322, App

ALIGNMENTS

RESULT 1

US-09-484-970B-106  
; Sequence 106, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmut, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: EP-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 106  
; LENGTH: 4822  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 44857.15CB1  
; NAME/KEY: unsure  
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-106

Alignment Scores:  
Pred. No.: 2.36e-119 Length: 4822  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-484-970B-106 (1-4822)



Qy	1	SerValValAspLeuLeuThrTrpArgAspIleLysThrGlyValValPheGlyAla	20
Db	3265	TCAGTTGTCACCTCTCTGTACTGAGAGACATTAAGAAGACTCGAGTGGTGTGGTGCC	3324
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle	40
Db	3325	AGCCTATTCTCTGCTCTTCATTGACAGTATTGAGCATTTGAGCGTAAACAGCTACATT	3384
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAla	60
Db	3385	GCCTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT	3444
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIle	80
Db	3445	ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA	3504
Qy	81	SerGluGluLeuValGlnLysTyrlSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	3505	TCGTAGAGATTGGTTTCAGAAGTACAGTAATTCCTGCTCTGGTCATGTGAACCTGCAGATA	3564
Qy	101	LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	3565	AAGAACTCAGGCGCCTCTTCATTGTGATGATTAGTTGATTCCTCTGAGATTGCAGTG	3624
Qy	121	LeuMetTrpValPheThrTyrlValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	3625	TTGATGTGGGTATTATCATGTGTGGTGCCTTGTTTTAATGGCTGCACACTACTGATTTTG	3684
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrlGluArgHisGlnAlaGlnIleAsp	160
Db	3685	GCCTCTCAATTCACCTTCCTCAGTGTTCCTGTTATTATTGAACGGCATCAGGCACAGATAGAT	3744
Qy	161	HisTyrlLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	3745	CATTATCTAGGACTTGCAAATAAGAAATGTTAAGATGCTATGGCTAAAAATCCAGCAAAA	3804
Qy	181	IleProGlyLeuLysArgLysAlaGlu	189
Db	3805	ATCCCTGGATTGAAGCGCAAGCTGAA	3831

## RESULT 2

US-08-700-607-2  
; Sequence 2, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME:- Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-2

Alignment Scores:
Pred. No.: 4,77e-120 Length: 799
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 2 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-700-607-2 (1-799)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleIysIysThrGlyValValPheGlyAlaSer 21
Db 108 GTTGTGACCTCTCTGTACGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCAG 167
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 168 CTAATTCCTGCTGCTTTCATTGACAGTATTTCAGCATTTGAGCGTACAGGCTACATTGCC 227
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
Db 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287
Qy 62 GlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGlnSerGluValAlaIleSer 81
Db 288 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 347
Qy 82 GluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 348 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTCTCTTGGTCATGTGAATCTGACGATTAAG 407
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuIysPheAlaValLeu 121
Db 408 GAACCTCAGCGGCTCTCTCTAGTTAGTATTAGTTAGTCTCTGGAAGTTTGCAGTGTTC 467
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 528 CTCATTTCACTCTCAGTGTTCCTGTTATTATTAAGCGGCATCAGGCACAGATAGATCAT 587
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaIysIleGlnAlaLysIle 181
Db 588 TATCTAGGACTTGCAAAATAGAAATGTTAAAGATCTATGGCTAAATCCAGCAAAAATC 647
Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 648 CTGGATTGAAGCGCAAGCTGAA 671

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### RESULT 3

US-09-949-016-3253  
 ; Sequence 3253, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949.016  
 ; CURRENT FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3253  
;; LENGTH: 1669  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-3253

Alignment Scores:  
Pred. No.: 1 56e-119 Length: 1669  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 4 Gaps: 0

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Db 308 CTATTCTCTGCTCTTTCATTCAGCATTTAGCATTTGTGAGCGTTAACAGCCTACATTGCC 367  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 427  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 428 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTGAAGTTGCTATATCT 487  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 488 GAGGAGTTGGTTTCAGAAGTACAGTAATTCGTCTTTGGTTCATGTGAACCTGCACGATAAG 547  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 548 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 607  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 608 ATGTGGGTATTTACCTATGTTGGTGCTTGTATATGCTGACACTACTGATTTTGGCT 667  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 668 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATTCAGGCGACAGATGATCAT 727  
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 728 TATCTAGGACTTGCAAATTAAGAATGTTAAAGATGCTATGGCTAAATTCAGCAAAATC 787  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 788 CTGGATTGAAGCGCAAGCTGAA 811

## RESULT 4

US-09-023-655-382  
; Sequence 382, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

;; TITLE OF INVENTION: EXPRESSION  
;; NUMBER OF SEQUENCES: 1508  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;; STREET: 3174 PORTER DRIVE  
;; CITY: PALO ALTO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/023,655  
;; FILING DATE: HEREWITH  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Zeller, Karen J.  
;; REGISTRATION NUMBER: 37,071  
;; REFERENCE/DOCKET NUMBER: PA-0001 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (650) 855-0555  
;; TELEFAX: (650) 845-4166  
;; INFORMATION FOR SEQ ID NO: 382:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2610 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: LUNGNOT14  
;; CLONE: 1508778  
US-09-023-655-382

Alignment Scores:  
Pred. No.: 2 14e-117 Length: 2610  
Score: 914.00 Matches: 188  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 0  
Query Match: 98.17% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-023-655-382 (1-2610)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 1311 GTTGTGACCTCTCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 1370  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41  
Db 1371 CTATTCTGCTGCTTTCATTCAGCATTTAGCATTTGTGAGCGTTAACAGCCTACAAATTC 1430  
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCTAT 1490  
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 1491 CCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATATC 1550  
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleL 101  
Db 1551 TGAGGAGTTGGTTCAGAAGTACAGTAATTCCTGCTCTGGTTCATGTGAACTGCACGATAA 1610  
Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 121  
Db 1611 GGAACCTCAGGCGCCTCTCTTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 1670



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QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2190 CTGAGAGGCTCTCTCTGTCAGACCTGGTGGATTCCTTAAATTTGCAGTCTGATG 2249
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142
Db 2250 TGGCTCTGACCTACCTGTTGGCGCTCTCTTCAATGGCTGACCTGCTCATGCTG 2309
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACCTCTAGTGTATGTTAAGCACCGACACAGATTGACCAATAT 2369
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysAlaValGlnAlaLysIlePro 182
Db 2370 CTGGGACTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTTAAATCCCA 2429
QY 183 GlyLeuLysArgLysAlaGlu 189
Db 2430 GCGGCTAAGAGGACGCTGAG 2450

RESULT 7
US-09-949-016-2988
; Sequence 2988, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 2988
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2988

Alignment Scores:
Pred. No.: 2,6e-77 Length: 2262
Score: 627.50 Matches: 116
Percent Similarity: 81.05% Conservative: 38
Best Local Similarity: 61.05% Mismatches: 35
Query Match: 67.40% Indels: 1
DB: 4 Gaps: 1

US-09-830-972-29_copy_990_1178 (1-189) x US-09-949-016-2988 (1-2262)
QY 1 SerValValAspLeuLysTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 7 TCAGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC 66
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 67 AGCTGATCATGCTCTTCCCTGCGACGCTTTCAGTGTTCATGCTGCTGTTCTTACCTC 126
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 127 ATCTCGGCTCTCTCTCTGTCACCATCAGTTCAGGATCTCAAGTCGCTCATCCAGCT 186
QY 61 IleGlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 187 GTACAGAAGTCAGAAGAGGCGCATCCATTCAAAGCCTACCTGGACGTAGACATCTACTG 246
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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Db 247 TCCTCAGAGCTTTCATATAATTCATGATCTGCCATGCTGCATCAACAGGSCCTCG 306
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 307 AAATCATATTATTCGTTCTCTTCTGTAGAGATCTGTTGACTCTCTTGAAGCTGCTGTC 366
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 367 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTTTAACGGAATCACCTTCTTAATCTT 426
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 427 GCTGAACATGCTCATTTTTCAGTGTCCGATTTCTATGAGAAGTAGTCAACAGCCAGATTGAT 486
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 487 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAAGCAAA 546
QY 181 IleProGlyLeu--LysArgLysAlaGlu 189
Db 547 CTCCTGGATGCGCAAAAAAAGGCAGAA 576

RESULT 8
US-09-149-476-254
; Sequence 254, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
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1	EARLIER FILING DATE: 1997-08-22	2	EARLIER APPLICATION NUMBER: 60/056,894
3	EARLIER FILING DATE: 1997-08-22	4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/056,911	6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,636	8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/056,874	10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,910	12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,864	14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,631	16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/056,845	18	EARLIER FILING DATE: 1997-08-22
19	EARLIER APPLICATION NUMBER: 60/056,892	20	EARLIER FILING DATE: 1997-08-22
21	EARLIER APPLICATION NUMBER: 60/057,761	22	EARLIER FILING DATE: 1997-08-22
23	EARLIER APPLICATION NUMBER: 60/047,595	24	EARLIER FILING DATE: 1997-05-23
25	EARLIER APPLICATION NUMBER: 60/047,599	26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/047,588	28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/047,585	30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/047,586	32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/047,590	34	EARLIER FILING DATE: 1997-05-23
35	EARLIER APPLICATION NUMBER: 60/047,594	36	EARLIER FILING DATE: 1997-05-23
37	EARLIER APPLICATION NUMBER: 60/047,589	38	EARLIER FILING DATE: 1997-05-23
39	EARLIER APPLICATION NUMBER: 60/047,593	40	EARLIER FILING DATE: 1997-05-23
41	EARLIER APPLICATION NUMBER: 60/047,614	42	EARLIER FILING DATE: 1997-05-23
43	EARLIER APPLICATION NUMBER: 60/043,578	44	EARLIER FILING DATE: 1997-04-11
45	EARLIER APPLICATION NUMBER: 60/043,576	46	EARLIER FILING DATE: 1997-04-11
47	EARLIER APPLICATION NUMBER: 60/047,501	48	EARLIER FILING DATE: 1997-05-23
49	EARLIER APPLICATION NUMBER: 60/043,670	50	EARLIER FILING DATE: 1997-04-11
51	EARLIER APPLICATION NUMBER: 60/056,632	52	EARLIER FILING DATE: 1997-08-22
53	EARLIER APPLICATION NUMBER: 60/056,664	54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056,876	56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056,881	58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/056,909	60	EARLIER FILING DATE: 1997-08-22
61	EARLIER APPLICATION NUMBER: 60/056,875	62	EARLIER FILING DATE: 1997-08-22
63	EARLIER APPLICATION NUMBER: 60/056,862	64	EARLIER FILING DATE: 1997-08-22
65	EARLIER APPLICATION NUMBER: 60/056,887	66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/056,908	68	EARLIER FILING DATE: 1997-08-22
69	EARLIER APPLICATION NUMBER: 60/048,964	70	EARLIER FILING DATE: 1997-06-06
71	EARLIER APPLICATION NUMBER: 60/057,650	72	EARLIER FILING DATE: 1997-09-05
73	EARLIER APPLICATION NUMBER: 60/056,884	74	EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Alignment Scores:
Pred. No.:      4 6e-77      Length:      1766
Score:          624.50      Matches:      115
Percent Similarity: 81.0%      Conservative: 39
Best Local Similarity: 60.5%      Mismatches: 35
Query Match:      67.0%      Indels:      1
DB:              3          Gaps:      1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-149-476-254 (1-1766)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAla 20
Db 287 GCGGTGCACGATCTCATTTCTGGAGAGATGGAAGAGACGTGGTGTCTTTGGCACC 346
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 347 ACGCTGATCATGCTCTTCCCTGGCAGCTTTTCAGTGTCTCATCGTGTGTTTCTTACCTC 406
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 407 ATCTGGCTCTTCTCTGTACCATCAGTTTCAGATCTACATCCGTATCCGTATCCAGCT 466
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 467 GTACAGAAGTCAGAAAGAGGCCATCCATTCAAAGCTTACCTGGAGGTAGACATTACTCTG 526
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 527 TCCTCAGAAAGCTTCCATAATTTACATGAATGCTGCATGTCATCAACAGAGGCCCTG 586
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 587 AAACATATATTCGTCTCTTCTGTGTAGAGATCTGGTGTACTCTCTGAAGCTGGCTGTC 646
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140
Db 647 TTCATGTGGCTGATCAGCTATGTTGCTGTGTTTAAACGGAATCACCTTCTTAATCTT 706
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 707 GCTGAAGTCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAGACCCAGATTGAT 766
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaValIleGlnAlaLys 180
Db 767 CACTATGTGGATCGCCGAGATCAGACCAAGTCAATTTGAAAGATCAAGCAAAA 826
Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 827 CTCCTCGAATCGCCAAAAAAGGCAGAA 856

RESULT 9
US-09-149-476-255
; Sequence 255, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
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; EARLIER APPLICATION NUMBER: 60/047,582
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; EARLIER APPLICATION NUMBER: 60/047,596
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
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EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
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EARLIER APPLICATION NUMBER: 60/056,889  
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EARLIER APPLICATION NUMBER: 60/056,911  
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EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
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EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
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EARLIER APPLICATION NUMBER: 60/056,892  
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EARLIER APPLICATION NUMBER: 60/047,585  
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EARLIER APPLICATION NUMBER: 60/047,586  
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EARLIER APPLICATION NUMBER: 60/047,589  
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EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,614  
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EARLIER APPLICATION NUMBER: 60/043,578  
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EARLIER APPLICATION NUMBER: 60/043,576  
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EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

## Alignment Scores:

Pred. No.:	8,91e-77	Length:	2664
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	3	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-149-476-255 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	262	GGGTTGCACGATCTGATTTCTGGAGAGATGTGAAGACACTGGGTTTCTCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTATCAGTGTGTTTCTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCCTGGCTCTTCTCTGTCCACCATCAGTTCAGGATCTACAAGTCCTGATCCAAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAAGTCAGAAGAGGCCATTCATTCAAAGCCTACCTGGACGCTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	502	TCCTCAGAAGCTTTTCATTAATTACATGAATGCTGCCATGTGTCACATCAACAGGCGCTG	561
Qy	101	LysGluLeuArgAlaLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120





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;
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPLNOB01
; CLONE: 31870
;
US-08-700-607-4

Alignment Scores:
Pred. No.: 1,19e-63 Length: 1095
Score: 526.50 Matches: 104
Percent Similarity: 72.77% Conservative: 35
Best Local Similarity: 54.45% Mismatches: 30
Query Match: 56.55% Indels: 22
DB: Gaps: 2

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-700-607-4 (1-1095)

Qy 1 SerValValAspLeuLeuTyTrrArgAspIleIysThrGlyValValPheGlyAla 20
Db 329 GCGGTGCACGATCTGATTMTTGGAGAGATGTGAAGAAGACTGGTGTTCCTTGGCACC 388
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 389 AGCTGATCATCTGCTTCCTTCCTGGCAGCTTCAGTGTTCATCATCTACAAAGTCGTCATCAAGCT 448
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
Db 449 ATCTGGCTTCCTCTCTGTCAACATCATCACTTCAGGATCTACAGATCCGTCATCCAAAGCT 508
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 509 GTACAGAGTCAGAAGAAGGCCATCCATTCAAGCTTACTCTGACGTAGACATTACTCTG 568
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 569 TCTCAGAAAGCTTTCATAAATTACATGAATGCTGCATGTGTGCACATCAACAGGCGCCTG 628
Qy 101 LysGluLeuArgArGLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaVal 120
Db 629 AAACATCAATTTCCTGTCCTCTCTGTAAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTG 688
Qy 121 LeuMetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 689 TTCATGTGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCCCTCTTAATCTT 748
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 749 GCTGAACCTGCTCAATTTNAGTGTCCCGATTCTGTTATNAGAAGTAC----- 793
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaVal 180
Db 794 -----AAGGTTCCACAGCAA 808

Qy 180 sleProGlyLeu---LysArgLysAlaGlu 189
Db 809 ACTCCCTGGAATCGCCAAAAAAGGCAGAA 839

RESULT 12
US-09-270-767-13561
; Sequence 13561, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13561

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1	EARLIER FILING DATE: 1997-04-11	60/043,315
2	EARLIER APPLICATION NUMBER: 60/043,315	
3	EARLIER FILING DATE: 1997-04-11	60/048,974
4	EARLIER APPLICATION NUMBER: 60/048,974	
5	EARLIER FILING DATE: 1997-06-06	60/056,886
6	EARLIER APPLICATION NUMBER: 60/056,886	
7	EARLIER FILING DATE: 1997-08-22	60/056,877
8	EARLIER APPLICATION NUMBER: 60/056,877	
9	EARLIER FILING DATE: 1997-08-22	60/056,889
10	EARLIER APPLICATION NUMBER: 60/056,889	
11	EARLIER FILING DATE: 1997-08-22	60/056,893
12	EARLIER APPLICATION NUMBER: 60/056,893	
13	EARLIER FILING DATE: 1997-08-22	60/056,630
14	EARLIER APPLICATION NUMBER: 60/056,630	
15	EARLIER FILING DATE: 1997-08-22	60/056,878
16	EARLIER APPLICATION NUMBER: 60/056,878	
17	EARLIER FILING DATE: 1997-08-22	60/056,662
18	EARLIER APPLICATION NUMBER: 60/056,662	
19	EARLIER FILING DATE: 1997-08-22	60/056,872
20	EARLIER APPLICATION NUMBER: 60/056,872	
21	EARLIER FILING DATE: 1997-08-22	60/056,882
22	EARLIER APPLICATION NUMBER: 60/056,882	
23	EARLIER FILING DATE: 1997-08-22	60/056,888
24	EARLIER APPLICATION NUMBER: 60/056,888	
25	EARLIER FILING DATE: 1997-08-22	60/056,879
26	EARLIER APPLICATION NUMBER: 60/056,879	
27	EARLIER FILING DATE: 1997-08-22	60/056,880
28	EARLIER APPLICATION NUMBER: 60/056,880	
29	EARLIER FILING DATE: 1997-08-22	60/056,894
30	EARLIER APPLICATION NUMBER: 60/056,894	
31	EARLIER FILING DATE: 1997-08-22	60/056,911
32	EARLIER APPLICATION NUMBER: 60/056,911	
33	EARLIER FILING DATE: 1997-08-22	60/056,636
34	EARLIER APPLICATION NUMBER: 60/056,636	
35	EARLIER FILING DATE: 1997-08-22	60/056,874
36	EARLIER APPLICATION NUMBER: 60/056,874	
37	EARLIER FILING DATE: 1997-08-22	60/056,910
38	EARLIER APPLICATION NUMBER: 60/056,910	
39	EARLIER FILING DATE: 1997-08-22	60/056,864
40	EARLIER APPLICATION NUMBER: 60/056,864	
41	EARLIER FILING DATE: 1997-08-22	60/056,631
42	EARLIER APPLICATION NUMBER: 60/056,631	
43	EARLIER FILING DATE: 1997-08-22	60/056,845
44	EARLIER APPLICATION NUMBER: 60/056,845	
45	EARLIER FILING DATE: 1997-08-22	60/056,892
46	EARLIER APPLICATION NUMBER: 60/056,892	
47	EARLIER FILING DATE: 1997-08-22	60/057,761
48	EARLIER APPLICATION NUMBER: 60/057,761	
49	EARLIER FILING DATE: 1997-08-22	60/047,595
50	EARLIER APPLICATION NUMBER: 60/047,595	
51	EARLIER FILING DATE: 1997-05-23	60/047,599
52	EARLIER APPLICATION NUMBER: 60/047,599	
53	EARLIER FILING DATE: 1997-05-23	60/047,588
54	EARLIER APPLICATION NUMBER: 60/047,588	
55	EARLIER FILING DATE: 1997-05-23	60/047,585
56	EARLIER APPLICATION NUMBER: 60/047,585	
57	EARLIER FILING DATE: 1997-05-23	60/047,586
58	EARLIER APPLICATION NUMBER: 60/047,586	
59	EARLIER FILING DATE: 1997-05-23	60/047,590
60	EARLIER APPLICATION NUMBER: 60/047,590	
61	EARLIER FILING DATE: 1997-05-23	60/047,594
62	EARLIER APPLICATION NUMBER: 60/047,594	
63	EARLIER FILING DATE: 1997-05-23	60/047,589
64	EARLIER APPLICATION NUMBER: 60/047,589	
65	EARLIER FILING DATE: 1997-05-23	60/047,593
66	EARLIER APPLICATION NUMBER: 60/047,593	
67	EARLIER FILING DATE: 1997-05-23	60/047,614
68	EARLIER APPLICATION NUMBER: 60/047,614	
69	EARLIER FILING DATE: 1997-05-23	
70	EARLIER APPLICATION NUMBER: 1997-05-23	

EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

## Alignment Scores:

Pred. No.: 2,37e-61 Length: 794  
Score: 508.50 Matches: 102  
Percent Similarity: 76.37% Conservative: 37  
Best Local Similarity: 56.04% Mismatches: 41  
Query Match: 54.62% Indels: 3  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-149-476-102 (1-794)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 254 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTCCTTGGAC-- 311  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle 40  
Db 312 AGCGTGATCATGCTGCTTCCCTGGCAGCTTCAGTGTCATCARTGTGGGTTCCTTAMCT 371  
QY 40 eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
Db 372 CATCTGGTCTCTCTCTGTCCACCATCARTTCAGGATCTACAGTCGTCATCCAGC 431  
QY 60 alleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80  
Db 432 TGTWAGAAARTCAGAAGGGCCATCCAWTCCAAAGCCCTACCTGGACGTAGACATTACTC 491  
QY 80 leSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI 100  
Db 492 TGTCTTCAGAGCTTTCATTAATTACATGAATGCTGCCATGTGTGCATCAACAGGCC 551  
QY 100 leLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaV 120  
Db 552 TGAACATCTATTATTCCTCTCTTCGTGTAGAGATCTGTTGATCTCTCTTGAAGCTGGCTG 611

QY 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140  
Db 612 TCTTCATGTGGCTGATGACCTATGTGTGGTCTGTTTAAACGAATCACCTTCTAATTC 671  
QY 140 euaAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA 160  
Db 672 TTGCTGAACCTGCTCAITTTTCAGTGCCGATTTGTCTATGAGAAGTACAGACCCAGATTG 731  
QY 160 spHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla 180  
Db 732 ATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCCAAGCA 791  
QY 180 ys 180  
Db 792 AA 793

## RESULT 14

US-09-949-016-1419  
Sequence 1419, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1419  
LENGTH: 2181  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1419

Alignment Scores:  
Pred. No.: 9,77e-56 Length: 2181  
Score: 473.50 Matches: 95  
Percent Similarity: 65.67% Conservative: 37  
Best Local Similarity: 47.26% Mismatches: 56  
Query Match: 50.86% Indels: 13  
DB: 4 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-1419 (1-2181)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 1162 GTGGCGGACCTGCTCTACTTGAAGGACACGAGGAGTCTCAGGAGTGTCTTTCACAGCCCTG 1221  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 1222 ATGTGTCCTCCTCTGCTCTGCTGTCATCTAGCATCTGTCGTGGCGGCGCACTTGGCT 1281  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 1282 CTGTGTGCTCTGCGGCACCATCTCTCTCAGGGTTTACCGCAAGTGTCTGAGGCCGTG 1341  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 1342 CACCGGGGGATGGAGCCCAACCCCTTTCAGGCTTACCTGGATGTGGACCTCACCTGACT 1401  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 1402 CGGGAGCAGACGGAACGTTGTGTCACCATGATCACCTCCCGCGTGTCTTCGCGGCCACG 1461  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 1462 CAGCTGGCGCACTTCTCTGGTAGAGACCTCGTGGATTCCTCAAGCTGGCCCTCCTC 1521  
Qy 122 MetTtpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1522 TTCTACATCTTGACCTTCTGGTGCCATCTTCAATGGTTTGACTCTCTCATCTGGGA 1581  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1582 GTGATTGGTCTATTCAACATCCCTGCTGTACCGGAGCAGCCAGGCTCAGATCGACCA 1641  
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1642 TATGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1701  
Qy 182 ProGlyLeu- - - - - LysArgLysAla 188  
Db 1702 CCAGGACGGAGCCCTGCTCTGCAGCGCGGAGTCTCGGATCCAAAGCCAAAGCC 1761  
Qy 189 Glu 189  
Db 1762 GAA 1764  
RESULT 15  
US-09-949-016-117588/c  
; Sequence 117588, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 117588  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-117588  
Alignment Scores:  
Pred. No.: 4,72e-38 Length: 601  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
Gaps: 0  
DB: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-117588 (1-601)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 224 GTTGTGACCTCTCTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGTGGCAGC 165  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 164 CTATTCCTGCTCTTTCATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 105  
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 104 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCTATC 45  
Qy 62 GlnLysSerAspGluGlyHisProPheArg 71  
Db 44 CAGAAATCAGATGAAGGCCACCCATTCAGG 15  
Alignment Scores:  
Pred. No.: 4,72e-38 Length: 601  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
Gaps: 0  
DB: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-117588 (1-601)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 224 GTTGTGACCTCTCTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGTGGCAGC 165  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 164 CTATTCCTGCTCTTTCATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 105  
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 104 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCTATC 45  
Qy 62 GlnLysSerAspGluGlyHisProPheArg 71  
Db 44 CAGAAATCAGATGAAGGCCACCCATTCAGG 15

RESULT 16  
US-09-949-016-117589/c  
; Sequence 117589, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 117589  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-117589  
Alignment Scores:  
Pred. No.: 4,72e-38 Length: 601  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
Gaps: 0  
DB: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-117589 (1-601)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 518 GTTGTGACCTCTCTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGTGGCAGC 459  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 458 CTATTCCTGCTCTTTCATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 399  
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 398 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCTATC 339  
Qy 62 GlnLysSerAspGluGlyHisProPheArg 71  
Db 338 CAGAAATCAGATGAAGGCCACCCATTCAGG 309  
RESULT 17  
US-09-949-016-14995  
; Sequence 14995, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14995  
; LENGTH: 42075  
; TYPE: DNA



```
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-12869 (1-135667)
QY 1 SerValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 122176 GCAGCTATTGACCTGTTGATGGCGGACATCAAGCAGACGGGCATCGTGTGGAGT 122235
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 122236 TTCCTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGGAGCGTGGCTACCTG 122295
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 122296 GCCCTGGCGGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTGTGTTTACAAGCA 122355
QY 61 IleGlnLysSerAspGluGlyHisProPheArg 71
Db 122356 GTGCAGAAACCGACGAGGCCACCCCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 122415
QY 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 122416 CCACGTACACGGGCTTTTACCTCAGCTGATTTTTCAGCTCAGCATGCTGATCAT 122475
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThr 99
Db 122476 -----GTTTCTCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTG 122529
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 122530 AATATCTAACATTTCTGCTGAATTTCTGAAACAACTCGATTTATTTTCCAAATACTT 122589
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 122590 ATTGCTTTGTTGAGTTTTCATATGAT 122616
QY 133 AsnGlyLeuThrLeuLeuAlaLeuLeuSerLeuPheSer-ValProValIleTyr 152
Db 122617 -----TTACTATTAAACAGTAATATAATCCAACTACTTAATCTCTCAGCAATATC 122670
QY 152 rGluArgHisGlnAlaGlnIleAspHisTyrLeu 163
Db 122671 AGAAAGGCACAGCAGGCATTTTGTCCCTATTATA 122704

RESULT 20
US-09-949-016-12869
; Sequence 12869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12869
; LENGTH: 152486
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12869

Alignment Scores: 1.47e-25 Length: 152486
Pred. No.: 279.50 Matches: 73
Percent Similarity: 50.00% Conservative: 23
Best Local Similarity: 38.02% Mismatches: 52

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-12869 (1-152486)
QY 1 SerValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 90995 GCAGCTATTGACCTGTTGATGGCGGACATCAAGCAGACGGGCATCGTGTGGAGT 91054
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 91055 TTCCTGCTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGGAGCGTGGCTACCTG 91114
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 91115 GCCCTGGCGGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTGTGTTTACAAGCA 91174
QY 61 IleGlnLysSerAspGluGlyHisProPheArg 71
Db 91175 GTGCAGAAACCGACGAGGCCACCCCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 91234
QY 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 91235 CCACGTACACGGGCTTTTACCTCAGCTGATTTTTCAGCTCAGCATGCTGATCAT 91294
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThr 99
Db 91295 -----GTTTCTCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTG 91348
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 91349 AATATCTAACATTTCTGCTGAATTTCTGAAACAACTCGATTTATTTTCCAAATACTT 91408
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 91409 ATTGCTTTGTTGAGTTTTCATATGAT 91435
QY 133 AsnGlyLeuThrLeuLeuAlaLeuLeuSerLeuPheSer-ValProValIleTyr 152
Db 91436 -----TTACTATTAAACAGTAATATAATCCAACTACTTAATCTCTCAGCAATATC 91489
QY 152 rGluArgHisGlnAlaGlnIleAspHisTyrLeu 163
Db 91490 AGAAAGGCACAGCAGGCATTTTGTCCCTATTATA 91523

RESULT 21
US-09-949-016-40169/c
; Sequence 40169, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40169
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40169

Alignment Scores: 5.26e-29 Length: 601
Pred. No.: 276.50 Matches: 72
Score: 72
```



```
Percent Similarity: 50.00% Conservative: 23
Best Local Similarity: 37.89% Mismatches: 55
Query Match: 29.70% Indels: 40
DB: 4 Gaps: 4

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-40169 (1-601)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 580 GCAGCTATTGACCTGTTGTTGGCGGACATCAAGCAGACGGGCATCGTTGTTGGAGT 521
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 520 TTCCCTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCGCTACCTG 461
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 460 GCCTGGCGCGCACTCTCAGCCACCATCAGTTTCCGCACTTACAAGTCTGTTTACAAGCA 401
QY 61 IleGlnLysSerAspGluGlyHisProPheArg-----AlaTyrLeuGluSerGluVal 78
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 400 GTGCAGAAAACCGCAGGAGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341
QY 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla-----LeuGlyHis 95
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 340 CCAGTACAGCAGGGGCTTTTACCTCAGCTGATTTTTCAGTCACAGATGACATTTGATCAT 281
QY 96 ValAsnCysThr-----99
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 280 GTTTCCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTGAATATC 221
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspLeuValAsp 114
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 220 TAACATTTCTGGTGAATTTCTGAAACAACTCGAATTTCTTATTCCTCAATCTATTGCT 161
QY 115 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGly 134
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 160 TTGTTGAGTTTTCATATGAT-----140
QY 135 LeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSer-ValProValIleTyrGluAr 154
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 139 TTACTATTACAGTAATCAATCAACAACTACTTAATCTCTCAGCAATATCAGAAAG 80
QY 154 gHisGlnAlaGlnIleAspHisTyrLeu 163
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 79 GCACAGCAGGCATTTTGTGCTCTATTATTA 52

RESULT 22
US-09-949-016-119335/c
; Sequence 119335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119335
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-119335
Alignment Scores:
```

```
Pred. No.: 5,26e-29 Length: 601
Score: 276.50 Matches: 72
Percent Similarity: 50.00% Conservative: 23
Best Local Similarity: 37.89% Mismatches: 55
Query Match: 29.70% Indels: 40
DB: 4 Gaps: 4

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-119335 (1-601)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 580 GCAGCTATTGACCTGTTGTTGGCGGACATCAAGCAGACGGGCATCGTTGTTGGAGT 521
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 520 TTCCCTGCTGCTCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCGCTACCTG 461
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 460 GCCTGGCGCGCACTCTCAGCCACCATCAGTTTCCGCACTTACAAGTCTGTTTACAAGCA 401
QY 61 IleGlnLysSerAspGluGlyHisProPheArg-----AlaTyrLeuGluSerGluVal 78
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 400 GTGCAGAAAACCGCAGGAGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341
QY 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla-----LeuGlyHis 95
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 340 CCAGTACAGCAGGGGCTTTTACCTCAGCTGATTTTTCAGTCACAGATGACATTTGATCAT 281
QY 96 ValAsnCysThr-----99
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 280 GTTTCCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTGAATATC 221
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspLeuValAsp 114
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 220 TAACATTTCTGGTGAATTTCTGAAACAACTCGAATTTCTTATTCCTCAATCTATTGCT 161
QY 115 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGly 134
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 160 TTGTTGAGTTTTCATATGAT-----140
QY 135 LeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSer-ValProValIleTyrGluAr 154
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 139 TTACTATTACAGTAATCAATCAACAACTACTTAATCTCTCAGCAATATCAGAAAG 80
QY 154 gHisGlnAlaGlnIleAspHisTyrLeu 163
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 79 GCACAGCAGGCATTTTGTGCTCTATTATTA 52

RESULT 23
US-08-700-607-9
; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: SPINPET01  
CLONE: 28742  
US-08-700-607-9

Alignment Scores:  
Pred. No.: 1,62e-29 Length: 261  
Score: 276.00 Matches: 59  
Percent Similarity: 89.71% Conservativeness: 2  
Best Local Similarity: 86.76% Mismatches: 7  
Query Match: 29.65% Indels: 0  
DB: Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-700-607-9 (1-261)

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAla 41  
DB 2 CTATNCNGCTGCTTCATTGACATATTCAGCATGTGAGGTGACGCTACATTGCC 61  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 62 TTNGCCCTGCNCTCTGTGACCATCAGTNTAGGCTATACAGGGTGTGATCCAGCTATC 121  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 122 CAGAAATCAGATGAAGGNCACCATTCAGGGCATATCTGGANTCTGAAGTTGCTATATCT 181  
QY 82 GluGluLeuValGlnLysTyrSer 89  
DB 182 GAGGAGTTGNTTCAGAGTACAG 205

RESULT 24  
US-09-949-016-14730  
; Sequence 14730, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14730  
; LENGTH: 13906  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14730  
Alignment Scores:  
Pred. No.: 1.62e-29 Length: 261  
Score: 276.00 Matches: 59  
Percent Similarity: 89.71% Conservativeness: 2  
Best Local Similarity: 86.76% Mismatches: 7  
Query Match: 29.65% Indels: 0  
DB: Gaps: 0

Pred. No.: 4.87e-26 Length: 13906  
Score: 271.00 Matches: 50  
Percent Similarity: 87.32% Conservativeness: 12  
Best Local Similarity: 70.42% Mismatches: 9  
Query Match: 29.11% Indels: 0  
DB: Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-14730 (1-13906)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 2007 TCAGTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACGTGGGTTGTCTTTGGCACC 2066  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIle 40  
DB 2067 AGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATGTCAGTGTGGTTCTTACCTC 2126  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 2127 ATCTGGCTCTTCTCTGTCCATCATCAGTTCAGGATCTACAAGTCCGTCATCAAGCT 2186  
QY 61 IleGlnLysSerAspGluGlyHisProPheArg 71  
DB 2187 GTACAGAAGTCAGAAGAAGGCCATCCATTCAG 2219  
RESULT 25  
US-09-513-999C-11198  
; Sequence 11198, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 11198  
; LENGTH: 200  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-11198  
Alignment Scores:  
Pred. No.: 6.72e-27 Length: 200  
Score: 256.00 Matches: 52  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 27.50% Indels: 0  
DB: Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-513-999C-11198 (1-200)  
QY 138 LeuLeuAlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAla 157  
DB 2 CTGATTTGGCTCTCAATTCATCTTCACTTCTGTTCTGTTATTTATGAACGGCATCAGGCA 61  
QY 158 GlnIleAspHisTyrLeuGlyLeuAlaAsnLysEnValLysAspAlaMetAlaLysIle 177  
DB 62 CAGATAGATCATATTATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATC 121  
QY 178 GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189  
DB 122 CAGCAAAATCTCTGGATTGAAGCGCAAGCTGNA 157  
RESULT 26  
US-09-949-016-13161  
; Sequence 13161, Application US/09949016



Db 247 CTGTTTGGTTGATGCTCTGAAACAGTCAATTTATTCAATATCTTTTCCATTTA 306  
Qy 38 AlaTyrIleAlaLeu-----Ala-LeuLeuSerValThrIleSerPheArgIleTy 54  
Db 307 GCTTACATTGGTTATTGATCTCTGCTGCTGATATTCGGTAATTTGATTACTGT 366  
Qy 54 rlySGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAlaTyrIle 74  
Db 367 AAAGGCT----- 373  
Qy 74 uGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGl 94  
Db 374 -----TCCTTGCTAATTCAACCAACTG----- 397  
Qy 94 yHisValAsnCysThrIleLysGlu----- 402  
Db 398 -----GTAATTGCTGAAGATTCAATGATGAAGTATTCAGAAATTCGCCAACTTT 453  
Qy 103 -----LeuArgLeuPheLeuValAspLeuValAspSe 115  
Db 454 AATGTGCATTTCGAAGAAAGTTTAAATAAATTTCTATTCA-CATGACATTGAAACCCAC 512  
Qy 115 rleuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLe 135  
Db 513 TTGAAAGCTGCTGCTGTTATTTATATTTATATAAATTGACTTCATGCTTTTCATTGTA 572  
Qy 135 uThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHi 155  
Db 573 CACTTIGATTTCATTTTCGTTGTGTTGATTTTCACCGTTCCTGTCATTTACAAACTTA 632  
Qy 155 sGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAl 175  
Db 633 CAAGAAGAAATTTGATGCTGCTGCTGCGGATATTACCAAGACCATTAACCAACTGTC 692  
Qy 175 alySleGlnAlaLys 180  
Db 693 TGAATTTACTGAAAG 708

RESULT 28  
US-09-949-016-40170/c  
; Sequence 40170, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40170  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-40170  
Alignment Scores:  
Pred. No.: 5,33e-10 Length: 601  
Score: 141.00 Matches: 28  
Percent Similarity: 80.00% Conservative: 8  
Best Local Similarity: 62.22% Mismatches: 9  
Query Match: 15.15% Indels: 0  
Gaps: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-40170 (1-601)

Qy 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90  
Db 136 AGGGCTACTTGGAGCTTGAGATCACCTTTCTCAGGAGCAGATTACAGAGTACACGGAC 77  
Qy 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 76 TGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAAGCTCAGGAGGCTCTTCTCTGTCCAG 17  
Qy 111 AspLeuValAspSer 115  
Db 16 GACCTGGTGGATTCC 2  
RESULT 29  
US-09-949-016-119336/c  
; Sequence 119336, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119336  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-119336  
Alignment Scores:  
Pred. No.: 5,33e-10 Length: 601  
Score: 141.00 Matches: 28  
Percent Similarity: 80.00% Conservative: 8  
Best Local Similarity: 62.22% Mismatches: 9  
Query Match: 15.15% Indels: 0  
Gaps: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-119336 (1-601)  
Qy 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90  
Db 136 AGGGCTACTTGGAGCTTGAGATCACCTTTCTCAGGAGCAGATTACAGAGTACACGGAC 77  
Qy 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 76 TGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAAGCTCAGGAGGCTCTTCTCTGTCCAG 17  
Qy 111 AspLeuValAspSer 115  
Db 16 GACCTGGTGGATTCC 2  
RESULT 30  
US-09-949-016-117609/c  
; Sequence 117609, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 117609
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-117609

Alignment Scores:
Pred. No.: 2,46e-07 Length: 601
Score: 122.00 Matches: 38
Percent Similarity: 35.19% Conservative: 0
Best Local Similarity: 35.19% Mismatches: 3
Query Match: 13.10% Indels: 67
DB: 4 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-117609 (1-601)
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHis-----155
DB 505 GCTCTCATTTCACTCTCTAGTGTCTCTGTATTATGAACGGCATCAGGTAATTTCTTAA 446
QY 155 -----155
DB 445 CTAAGTCTGCTACTTCAGAAATAGACACTCACTCTATTACATGGGATTACGGGATGATTA 386
QY 155 -----155
DB 385 GTGCCCATTTTCAATGCTTACAAAATGAGAAGTGTGATGGTTTCTTAAGCCTTTAGCT 326
QY 155 -----155
DB 325 TGACACATAGTAGTGGTTAATAAGMTCTTTAGCAACGGGTAATAATCTTTTATACCTCT 266
QY 156 ----GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysValIleAspAlaMe 174
DB 265 CTTTCAGGCACAGATAGATCATTTATCTAGGACTTGCAAAATGAAGAATGTTAAAGATGCTAT 206
QY 174 tAlaIleGlnAlaIleValIle 181
DB 205 GGCTAAGTAGTATTATTAATC 184

RESULT 31
US-09-313-294A-703
; Sequence 703, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 703
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549677H1
US-09-313-294A-703

Alignment Scores:
Pred. No.: 2.32e-06 Length: 266
Score: 111.00 Matches: 22
Percent Similarity: 65.08% Conservative: 19
Best Local Similarity: 34.92% Mismatches: 20

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 117609
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-117609

Alignment Scores:
Pred. No.: 2,46e-07 Length: 601
Score: 122.00 Matches: 38
Percent Similarity: 35.19% Conservative: 0
Best Local Similarity: 35.19% Mismatches: 3
Query Match: 13.10% Indels: 67
DB: 4 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-117609 (1-601)
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHis-----155
DB 505 GCTCTCATTTCACTCTCTAGTGTCTCTGTATTATGAACGGCATCAGGTAATTTCTTAA 446
QY 155 -----155
DB 445 CTAAGTCTGCTACTTCAGAAATAGACACTCACTCTATTACATGGGATTACGGGATGATTA 386
QY 155 -----155
DB 385 GTGCCCATTTTCAATGCTTACAAAATGAGAAGTGTGATGGTTTCTTAAGCCTTTAGCT 326
QY 155 -----155
DB 325 TGACACATAGTAGTGGTTAATAAGMTCTTTAGCAACGGGTAATAATCTTTTATACCTCT 266
QY 156 ----GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysValIleAspAlaMe 174
DB 265 CTTTCAGGCACAGATAGATCATTTATCTAGGACTTGCAAAATGAAGAATGTTAAAGATGCTAT 206
QY 174 tAlaIleGlnAlaIleValIle 181
DB 205 GGCTAAGTAGTATTATTAATC 184

RESULT 32
US-09-949-016-48087/c
; Sequence 48087, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 48087
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-48087

Alignment Scores:
Pred. No.: 0.000157 Length: 601
Score: 102.00 Matches: 21
Percent Similarity: 70.00% Conservative: 7
Best Local Similarity: 52.50% Mismatches: 12
Query Match: 10.96% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-48087 (1-601)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 120 ACAGTGGCGGACCTGCTGCTACTGGAGGACACAGGACGCTGAGGAGTGGTCTTCACAGGC 61
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 60 CTGATGGTCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 33
US-08-905-223-178
; Sequence 178, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
```







QY 112 LeuValAapSerLeuLysPheAlaValLeuMetTrpValPheThrTyValGlyAlaLeu 131  
Db 779 GTTGTACCTAAC-----GCAATAACAATTATCGTCAGCTTA 744  
QY 132 PheAnGlyLeuThrLeuLeuLeuLeuLeuLeuSer 144  
Db 743 ATCAGTGGTCTTGTAAATGTTGATTGTTATTTGTCAGTCAAT 705

RESULT 35  
US-08-781-986A-407/c  
; Sequence 407, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781.986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 407:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1722 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-781-986A-407

Alignment Scores:  
Pred. No.: 0.00821 Length: 1722  
Score: 95.00 Matches: 36  
Percent Similarity: 48.87% Conservative: 29  
Best Local Similarity: 27.07% Mismatches: 42  
Query Match: 10.20% Indels: 26  
DB: 4 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-781-986A-407 (1-1722)

QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyIle----- 40  
Db 1067 TTGATTAAATGTAATATATATCTATCTATGTTAGTAGTCACGGGTTTGTCTTT 1008

QY 41 -----AlaLeuAlaLeuSerValThr-----IleSerPhe 51  
Db 1007 AACTCTGCAGCTGTAAAGCCGATGCTAATAACAATATGACAGATATTATCGTTCTTTA 948

QY 52 ArgIleTyLysGlyValIleGlnAlaLeuGlnLysSerAspGluGlyHisPropheArg 71  
Db 947 GCTGTTATTATTTGATTGAAATTTCAATTAACCTGCCGATCGAAATCATCCTTAT--- 891

QY 72 AlaTyLysGluSerGluValAlaIleSerGluGluLeuValGlnLysTySerAsnSer 91

Db 890 GGCCATTGGAAGTCTGAAATAATTCTTCA-----TTATTGGTGTCAATTTGTCATTATG 837  
QY 92 AlaLeuGlyHisValAsnCyThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111  
Db 836 TTTGTAGGT---ATCCAAGTAGTTATTCAAATGCACCTCGTTTCTTCAAAGAAGATGAC 780  
QY 112 LeuValAapSerLeuLysPheAlaValLeuMetTrpValPheThrTyValGlyAlaLeu 131  
Db 779 GTTGTACCTAAC-----GCAATAACAATTATCGTCAGCTTA 744  
QY 132 PheAnGlyLeuThrLeuLeuLeuLeuLeuLeuSer 144  
Db 743 ATCAGTGGTCTTGTAAATGTTGATTGTTATTTGTCAGTCAAT 705

RESULT 36  
US-08-487-596-7  
; Sequence 7, Application US/08487596  
; Patent No. 6440681  
; GENERAL INFORMATION:  
; APPLICANT: Elliot, Kathryn J.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND  
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL  
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487.596  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO US94/02447  
; FILING DATE: 08-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,503  
; FILING DATE: 08-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/028,031  
; FILING DATE: 08-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,154  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/504,455  
; FILING DATE: 03-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-9951  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1828 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
; FEATURE:

```
; NAME/KEY: CDS
; LOCATION: 155...1561
; OTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"
US-08-487-596-7

Alignment Scores:
Pred. No.: 0.0627 Length: 1828
Score: 89.00 Matches: 42
Percent Similarity: 38.54% Conservative: 32
Best Local Similarity: 21.88% Mismatches: 61
Query Match: 9.56% Indels: 58
DB: 3 Gaps: 5

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-487-596-7 (1-1828)
QY 24 LeuLeuLeuSerLeuThrValPheSerIleVal----- 34
Db 1016 GTACTTGTCTTCTTGAAGAGATATTTCTTCTGTTATTGAAGAGATCATCATCTTCA 1075
QY 35 -----SerValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSer 50
Db 1076 AAAGTCATACCTCTAATTCGAGAGATCTCTGGTATTACCATGATTTTGTGACACTGTCA 1135
QY 51 PheArgIleTyrlsGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1136 ATTATGTAACCGTCTTCGCTATCAACATTCATCATCTCTCTCCCAACATAATGCC 1195
QY 71 ArgAlaTyrlLeu----- 74
Db 1196 ATGGCGCCTTTGGTCCGCAAGATATTTCTTCACAGCTTCCCAAACTGTTTGCATGAGA 1255
QY 75 -----GluSerGlu-ValAlaIleSerGluGl 83
Db 1256 AGTCATGTAGACAGGTAATCTCACTCAGAAAGAGAACTGAGAGTGTGTGACCAAAA 1315
QY 83 uLeuValGlnLysTyrlSerAsnSerAlaLeuGlyHisValAsnCystrIleLysGluLe 103
Db 1316 TCTTCTAGAAACACATFG-GAAGTCGCTCAATCTTCTTCGCTACATTACAGACACAT 1374
QY 103 uArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe----- 118
Db 1375 CATGAAGAAATGATGTCGTCGAGGTGTGTAAGATTGGAATTCATGACCCAGGTCT 1434
QY 119 ----AlaValLeuMetTrpValPheThrTyrlValGlyAlaLeuPheAsnGlyLeuThrIe 137
Db 1435 TCATCGGATGTTTCTGTCGACTTTTCTTTCTGTTCA----- 1471
QY 137 uLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrlGluArgHisGlnAl 157
Db 1472 ----ATGTGTGATCTCTGGGCTTTT---GTTCCTGTATTATTATAATGGCAATAT 1524
QY 157 aGlnIleAspHisTyrlLeuGlyLeuAlaAsnLys 168
Db 1525 ATTAATACCAAGTTTCATATTGGAATGCAATAG 1558

RESULT 37
US-08-660-451A-7
; Sequence 7, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
```

Qy 83 uleuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLe 103  
Db 1316 TCCTCTAGAAACACATTG-GAAGCTGGCTCAATTCTATTGCTACATTACAGACACAT 1374  
Qy 103 uArgLeuPheLeuValAspLeuValAspSerLeuLysPhe----- 118  
Db 1375 CATGAAGAAATGATGTCGCGTGGAGTGTGTTGAAGATTGGAAATTCATAGCCAGGTTCT 1434  
Qy 119 ---AlaValLeuMetTrrPheThrTrrValGlyAlaLeuPheAsnGlyLeuThrLe 137  
Db 1435 TCATCGGAGTTTCTGTGACTTTCTTTTCGTTTCA----- 1471  
Qy 137 uleuIleLeuAlaLeuIleSerPheSerValProValIleTyrGluArgHisGlnAl 157  
Db 1472 ---ATTGTTGGATCTCTGGGCTTTT---GTTCTGTATTATTATAAATGGCAAAATAT 1524  
Qy 157 aGlnIleAspHisTyrLeuGlyLeuAlaAsnLys 168  
Db 1525 ATTAATACCAAGTTATATGGAAATGCAAAATAG 1558  
RESULT 38  
US-09-462-136-1  
; Sequence 1, Application US/09462136  
; Patent No. 6426198  
; GENERAL INFORMATION:  
; APPLICANT: Carstee, et al.  
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease  
; FILE REFERENCE: 4239-53894  
; CURRENT APPLICATION NUMBER: US/09/462,136  
; CURRENT FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: PCT/US98/13862  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/051,682  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4550  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3837)  
US-09-462-136-1  
Alignment Scores:  
Pred. No.: 0.32 Length: 4550  
Score: 88.50 Matches: 39  
Percent Similarity: 42.11% Conservative: 25  
Best Local Similarity: 25.66% Mismatches: 51  
Query Match: 9.51% Indels: 37  
DB: 3 Gaps: 7  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-462-136-1 (1-4550)  
Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 1792 AATCTGACCATTTCTTCTGCTGCTGAAGATATTGAAGATGAAGTAAATCGTGAAGT 1851  
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85  
Db 1852 GACAGTGTATGCTTC-----ACCGTTGTAATTAGCTATGCCATCATG 1893  
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArg 105  
Db 1894 TTCTATATATTTCTCCCTAGCCCTTGGGCAC-----ATCAAAAGCTGTGCAGG 1941  
Qy 106 LeuPheLeuValAspAsp-----LeuValAspSerLeu 116  
Db 1942 CTT-----CTGGTGGATTCGAAGTCTCCTAGGCATCGCGGGCATCTTGATCGTGTGAGC 1998  
Qy 117 LysPheAlaValLeuMetTrrPheThrTrrValGlyAlaLeuPheAsnGlyLeuThr 136

Db 1999 TCGGTGGCTTGCTCTCTGGGTGTCTTCTAGCTACATTGGGGTTG-----CCCTTGACC 2049  
Qy 137 LeuLeuIleLeuAlaLeuIle-----SerLeuPhe 146  
Db 2050 CTCATTGTGATTGAAGTCATCCCGTCTGCTGGTGTGGAGTGAGCAACATCTTC 2109  
Qy 147 SerValProValIleTyrGluArgHisGln-----AlaGlnIleAspHisTyr 162  
Db 2110 ATTCTGGTGGCAGGCTTACCAGAGATGAACGCTCTTCAAGGGGAACCTCGATCAGCAG 2169  
Qy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174  
Db 2170 CTGGCAGGCTCTAGGAGAAAGTGGCTCCCATGATG 2205  
RESULT 39  
US-09-949-016-4281  
; Sequence 4281, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4281  
; LENGTH: 4661  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-4281  
Alignment Scores:  
Pred. No.: 0.332 Length: 4661  
Score: 88.50 Matches: 39  
Percent Similarity: 42.11% Conservative: 25  
Best Local Similarity: 25.66% Mismatches: 51  
Query Match: 9.51% Indels: 37  
DB: 4 Gaps: 7  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-4281 (1-4661)  
Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 1913 AATCTGACCATTTCTTCTGCTGCTGAAGATATTGAAGATGAAGTAAATCGTGAAGT 1972  
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85  
Db 1973 GACAGTGTATGCTTC-----ACCGTTGTAATTAGCTATGCCATCATG 2014  
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArg 105  
Db 2015 TTCTATATATTTCTCCCTAGCCCTTGGGCAC-----ATCAAAAGCTGTGCAGG 2062  
Qy 106 LeuPheLeuValAspAsp-----LeuValAspSerLeu 116  
Db 2063 CTT-----CTGGTGGATTCGAAGTCTCCTAGGCATCGCGGGCATCTTGATCGTGTGAGC 2119  
Qy 117 LysPheAlaValLeuMetTrrPheThrTrrValGlyAlaLeuPheAsnGlyLeuThr 136  
Db 2120 TCGGTGGCTTGCTCTCTGGGTGTCTTCTAGCTACATTGGGGTTG-----CCCTTGACC 2170  
Qy 137 LeuLeuIleLeuAlaLeuIle-----SerLeuPhe 146  
Db 2171 CTCATTGTGATTGAAGTCATCCCGTCTCTGGTGTGGTGTGGAGTGGCAACATCTTC 2230

QY 147 SerValProValIleTyrGluArgHisGln-----AlaGlnIleAspHisTyr 162  
DQ 2231 ATTCTGGTGCAGCCCTACAGAGAGATGAACGCTTCAAGGGGAAACCCCTGGATCAGCAG 2290  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174  
DQ 2291 CTGGGAGGGTCTTAGGAGAGTGGCTCCAGTATG 2326

## RESULT 40

US-09-814-915A-100  
; Sequence 100, Application US/09814915A  
; Patent No. 6750015  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Kathryn  
; APPLICANT: Richer, Jennifer  
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Related  
; TITLE OF INVENTION: Thereto  
; FILE REFERENCE: 2848-39  
; CURRENT APPLICATION NUMBER: US/09/814,915A  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: 60/214,870  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 100  
; LENGTH: 4673  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-814-915A-100

Alignment Scores:  
Pred. No.: 0.334 Length: 4673  
Score: 88.50 Matches: 39  
Percent Similarity: 42.11% Conservative: 25  
Best Local Similarity: 25.66% Mismatches: 51  
Query Match: 9.51% Indels: 37  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-814-915A-100 (1-4673)

QY 46 SerValProValIleTyrGluArgHisGln-----AlaGlnIleAspHisTyr 162  
DQ 1915 AATCTGACCATTTCTCTCTGCTGAGAGAGTATTGAAGTGAACATAATCGTGAAGT 1974  
QY 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85  
DQ 1975 GACAGTGATGCTCTC-----ACCGTTGTAATTAGCTATGCAATCATG 2016  
QY 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105  
DQ 2017 TTCTATATATTTCCCTAGCCTTGGGGCAC-----ATCAAAAGCTGTCGAGG 2064  
QY 106 LeuPheLeuValAspAsp-----LeuValAspSerLeu 116  
DQ 2065 CTT---CTGGTGATTCGAGGTCTCATTAGGCATCGGGGCTCTTGATCGCTGAGC 2121  
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 136  
DQ 2122 TCGGTGGCTTGCCTTCTGGGTGCTTTCAGCTACATGGGTG-----CCCTTGACC 2172  
QY 137 LeuLeuIleLeuAlaLeuIle-----SerLeuPhe 146  
DQ 2173 CTATTGTGATGAAGTCAATCCCGTCTCGGTGCTGCTGCTGAGTGGAGAACATCTTC 2232  
QY 147 SerValProValIleTyrGluArgHisGln-----AlaGlnIleAspHisTyr 162  
DQ 2233 ATTCTGGTGCAGCCCTACAGAGAGATGAACGCTTCAAGGGGAAACCCCTGGATCAGCAG 2292  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174  
DQ 2293 CTGGGAGGGTCTTAGGAGAGTGGCTCCAGTATG 2328

## RESULT 41

US-09-949-016-5725  
; Sequence 5725, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 20712  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5725  
; LENGTH: 1273  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5725

Alignment Scores:  
Pred. No.: 0.0484 Length: 1273  
Score: 88.00 Matches: 42  
Percent Similarity: 38.54% Conservative: 32  
Best Local Similarity: 21.88% Mismatches: 61  
Query Match: 9.45% Indels: 58  
DB: 4 Gaps: 5

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-5725 (1-1273)

QY 24 LeuLeuLeuSerLeuThrValPheSerIleVal----- 34  
DQ 605 GTACTGTGCTCTTGTGACTGCTCTCTCTGCTGCTTATTGAAGAGATCATCATCTTCA 664  
QY 35 -----SerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50  
DQ 665 AAGATCATACCTTAATTGGAGAGATCTGTGATTATTACCATGATTTTGTGACACTGTCA 724  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
DQ 725 ATTATGGTAACCGTCTTCCTATCAACATTCATCATCGTCTCTCTCAACACATATGCC 784  
QY 71 ArgAlaTyrLeu----- 74  
DQ 785 ATGGCGCCTTGTGTCGCAAGATATTCTTTCACAGCTTCCCAAACTGCTTTGCATGAGA 844  
QY 75 -----GluSerGlu-ValAlaIleSerGlu 83  
DQ 845 AGTCATGTAGACAGGTACTTCTCAGAAAGAGAACTGAGAGTGTGTAGTGACCAAAA 904  
QY 83 uLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLe 103  
DQ 905 TCTTCTAGAAACACATG-GAGCTGCGCTCGATTCCTATTCCTACATTCACAGACAT 963  
QY 103 uArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe----- 118  
DQ 964 CATGAAGGAAATGATGTCGTCGAGTGTGTAAGATTGGAAATTCATGCCAGGTCT 1023  
QY 119 ---AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLe 137  
DQ 1024 TCATCGGATGTTTCTGTGGACTTTCTTTCTGCTTCA----- 1060  
QY 137 uLeuLeuLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAl 157  
DQ 1061 ----ATTGTTGATCTCTTGGGCTTTT---GTTCTGTTATTATAATGGCAATAT 1113  
QY 157 aGlnIleAspHisTyrLeuGlyLeuAlaLeuLys 168  
DQ 1114 ATTAATACCAGTTTCATATTGGAAATGCAAAATAG 1147

RESULT 42  
US-09-134-000C-2072  
; Sequence 2072, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2072  
; LENGTH: 1779  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-2072

Alignment Scores:  
Pred. No.: 0.0975 Length: 1779  
Score: 87.50 Matches: 48  
Percent Similarity: 38.53% Conservative: 41  
Best Local Similarity: 20.78% Mismatches: 65  
Query Match: 9.40% Indels: 77  
DB: 4 Gaps: 10

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-134-000C-2072 (1-1779)

Qy 7 TyrTrpArgAspIleLysValThrGlyValValPheGlyAlaSerLeuPheLeuLeu 26  
Db 133 TTCTGGAAACAGTGAACGT-----TTATTTCGATACATG 168

Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuLeuLeuSer 46  
Db 169 TCTAAACGAATGCTGCAATTATTGCTGTC-----TTAGTATTAGCAATTCGACCC 219

Qy 47 ValThrIleSerPheArg-----IleTyrLys 55  
Db 220 GTCTGTTTCCAAATTCAAACACCAAAAGTATTAGCACAGCGCAACCACTGAAATTTTAA 279

Qy 56 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla----- 72  
Db 280 GCGGTCATGAAGAGCGCTGCTGAATAGAAACAAAGCGCTTAAATAAACATCTTTTCCAAAT 339

Qy 73 -----TyrLeuGluSerGlu 77  
Db 340 GATTTTGACAAATTTGGTCAATTTTATTAATTTGTTATGTCATGCTATTCTGCT 399

Qy 78 Val-----Ala 79  
Db 400 GTCTTTAATTTCTTCAGCAAGTAAATTATGACACGTGTTTCACAGCAACAGTTTATGAA 459

Qy 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-----His 95  
Db 460 TTACGTCGAAGTATGAGACGCAAAATGAACAAAGTTCCCAATTTCTATTATGATATTCT 519

Qy 96 ValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuLeuSer 115  
Db 520 AGTAATGGGACATTATGTCACACGCAATTAACGACATGATTAATTTCCGAGTACT 576

Qy 116 LeuLys-----PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132  
Db 577 TTACAGCAAACTTAAACCAATTAATACCAGTATCGTGACATTTGTGGGTGACTTTGG 636

Qy 133 AsnGlyLeuThrLeu-----LeuIleLeuAlaIleSerLeuPheSerValproValle 151  
Db 637 ATGATGCTGACCATTAGCTGGCAGTTAACTAAATTTGCTTTAGCAACAGTCCCAATTAGT 696

Qy 152 Tyr-----GluArgHisGlnAlaGlnIleAspHis 161

Db 697 TTAATTGTTGTGATGGTTGTGGCGCTCGCTCGCAAAACATTTTGGCGCTCAACAAAA 756  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172  
Db 757 AGCTTAGGATTATTGAATAACCAAGTCGAAGAA 789

RESULT 43  
US-09-134-001C-2168  
; Sequence 2168, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 2168  
; LENGTH: 3156  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-2168

Alignment Scores:  
Pred. No.: 0.245 Length: 3156  
Score: 87.50 Matches: 44  
Percent Similarity: 41.15% Conservative: 35  
Best Local Similarity: 22.82% Mismatches: 68  
Query Match: 9.40% Indels: 45  
DB: 3 Gaps: 8

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-134-001C-2168 (1-3156)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 1138 ATCGTTATCTCTCTGTTTAAAGAAATATAAGAACTACAGCTATT----- 1182

Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal----- 36  
Db 1183 -----TCAATTGTATCTATACCAATGTCAATATTA 1212

Qy 37 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 56  
Db 1213 ATTGCGCTCATAGCATTAAATAATTAAAGCAACGTATCATTAATAATTCTTACTTTAGGTGCA 1272

Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
Db 1273 TTAACGGTTGCAATCGGCGCA-----GTTATAGATGAT 1305

Qy 77 GluValAlaIleSerGluLeuValGlnLysTyrSer-----AsnSerAlaLeuGly 94  
Db 1306 TCTATAGTTGCTGTTGAGATATATTATTAAGAGATTCTGATCCGAATGACAGCTCAAA 1365

Qy 95 HisValAsnCysThrIleLysGluLeuArgArgLeuPhe-----LeuValAspAsp 111  
Db 1366 GGTCAAAATTTAATTATAAGCGCTACTAGAGAAGTATTAAACCTATTATGTCTCGACC 1425

Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131  
Db 1426 CTTGTTACTAGTAGTGTGTTTACCACCTAGTGTGTCAGGTTCTAGTAGGTAATG 1485

Qy 132 PheAsn-----GlyLeuThrLeuLeuIleLeuAla-----LeuIleSerLeu 145  
Db 1486 TTTAGACCATTTGCGCTAGCCATTTAGTTTATAGTTTACTTCTACTTCTGTTTCTGAT 1545

Qy 146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165  
Db -----

```

Db      1546  ACCCTAGTGCCTCTCTTTAGGTGCAACATTTTTTAAAAAT-----GGCGTT 1590

Qy      166  AlaAsnLysAsnValLysAspAlaMetAlaLysIle 177
        |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      1591  AAAAATAGGGAACAAAAAAGAGGTCTAGGAACAGTT 1626

```

RESULT 44

```

US-09-313-294A-81
; Sequence 81, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCES: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 81
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inbyte ID No. 6476212 700548479H1
; NAME/KEY: unsure
; LOCATION: 109
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-81

```

Alignment Scores:		
Prod. No.:	0.00893	Length: 236
Score:	86.00	Matches: 26
Percent Similarity:	58.54%	Conservative: 22
Best Local Similarity:	31.71%	Mismatches: 26
Query Match:	9.24%	Indels: 9
DB:	4	Gaps: 3

US-09-830-972-29 COPY 990 1178 (1-189) X US-09-313-294A-81 (1-296)

Qy		114	AspSerLeuLysPheAlaValLeu-----MetTrpValPheThrTyrValGlyAla	130
Dd		48	GATCTAAAGAAATTCCTAATTGTATCGCAGGCTCTCTGGCTCCCTTCAGTTCTTTGGGAGC	107
Qy		131	LeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerValProVal	150
Dd		108	CNTGC-AACTTCTGNACACTGTTCTATATTGTCTTTTGGCACGTGTACACTATACTTGTT	166
Qy		151	IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaLeuLysAsnVal	170
Dd		167	CTGTATGAGAATAATGAGGACAAGGTTGATGCTTTTGGTGAGAAGGCTATGATCGCAACTG	226
Qy		171	LysAspAlaMetAla-----LysIleGlnAlaLysIlePro-----GlyLeuLys	185
Dd		227	AAGAAGTATTATGCCATCTTCATGAGAAGATGCCCTATCGAAGATTCCAAAGGGCCCTCAG	286
Qy		186	ArgLys	187
Dd		287	GATAAG	292

## RESULT 45

RES001 43  
US-08-956-171E-322  
; Sequence 322, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon

```

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
;
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 322:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1302 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 322:
;
US-08-956-171E-322

Alignment Scores:
Pred. No.: 0.132 Length: 1302
Score: 85.00 Matches: 42
Percent Similarity: 40.41% Conservative: 36
Best Local Similarity: 21.76% Mismatches: 756
Query Match: 9.13% Indels: 40
DR: 4 Gaps: 7

```

US-09-830-972-29 COPY 990 1178 (1-189) x US-08-956-171E-322 (1-1302)

Qy	2	VaIValAspLeuLeuTyTrpArgAspIleLysLysThrGlyVal---	ValPheGlyAla	20
		::::	::::	
Db	68	ATAGTATTTTTGCTGTTTTTAAGAACAATTCGTACGCGCAATTTC	TATTATATCATGCATT	127
		::::	::::	
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle	40	
		::::	::::	
Db	128	CGGTTATCATTCTTATGCGCTT-----ATT	154	
		::::	::::	
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyLyserGlyValIleGlnAla	60	
		::::	::::	
Db	155	GCTCTGAATTTGAGTGATGTTTTCATTGAATATATACTAACGGTAGGTGCATTAAACAGTAGCG	214	
		::::	::::	
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80	
		::::	::::	
Db	215	ATTGACGTF-----GTGATACAGATTGCTATTGTAGTT	247	
		::::	::::	
Qy	81	SerGluGluLeuValGlnLysTy-SerAsnSer-----AlaLeuGlyHisValAsnCys	98	
		::::	::::	
Db	248	CITTGAAATATTATTCGACCGCTTAACAGATTCAGAGAACAACACTAAAAGGTGAAATTTA	307	
		::::	::::	
Qy	99	ThrIleLysGluLeuArgLeuPhe-----LeuValAspLeuValAspSer	115	
		::::	::::	
Db	308	ATTATCAGTCCGACAACCTGAAGTATTTAAACCATAATGTCATCCGACATAGTTACTATT	357	
		::::	::::	



```

; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-149

Alignment Scores:
Pred. No.: 5,96 Length: 12566
Score: 84,50 Matches: 40
Percent Similarity: 46,39% Conservative: 37
Best Local Similarity: 24,10% Mismatches: 58
Query Match: 9,08% Indels: 31
DB: 3 Gaps: 8

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-961-527-149 (1-12566)
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 344 TCATAGTCTTACTATTGACGGCCACCTGATGCTGCTAGTCTAGTATTGCTTTTCG 403
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 404 ---CTGACCTTTATGAGTCTGACCTGATTTATCGGATC---AAATCCCTTCGTGAGCA 457
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 458 GGGATTCGGTTAATAGCTGGT-----GAGAGCTTGTTCGAGTT 496
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 497 GCT-----CTCAGACGACGGTTA 514
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 515 GAAGATGTGAGACAGCTT---ATCTGCTCAGTCTGCTGATCCAGTCTTTTGGGATTCGGG 571
QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 572 ATTCCTGG-----TATCAAGGTGCTGTTTATGGCAACGGTGCATCGTCATC 622
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 623 ATTGCTCTTCTACTTTATGATGATGACCTTGGCAGGATTTCTACCTTACTTAAGTGTGCTC 682
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 683 TATCTACTTGGTTTACAGAAATAGTCTGGTGGATCTA-----TTGAAAGGGAAA 733
QY 181 IleProGlyLeuLysArg 186
Db 734 CTCCT---CTCAACGT 748

RESULT 48
US-08-961-527-104
; Sequence 104, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6735 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-104

Alignment Scores:
Pred. No.: 2,57 Length: 6735
Score: 84,00 Matches: 54
Percent Similarity: 46,49% Conservative: 32
Best Local Similarity: 29,19% Mismatches: 66
Query Match: 9,02% Indels: 33
DB: 3 Gaps: 11

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-961-527-104 (1-6735)
QY 11 IleLysLysThrGlyValValPhe-----GlyAlaSerLeuPheLeuLeu 25
Db 2885 ATTCAATCTACAGGAGTACTTCCCTTCTTATCCAGGGTGGAAATAGTCTTCTAGTC 2944
QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu 45
Db 2945 TTATCAGTGGCAGTAGCTTCTCTTAAATATTGATGTCAGTGAACCAACGCTAAATTG 3004
QY 46 -----SerValThrIle-SerPheArgIleTyrIleGly 56
Db 3005 TACCAGAAATGGAAATCAACCAATGACCTTCTGTTGAAGT---AGGATAAGAAAGG 3061
QY 56 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSe 76
Db 3062 ATAGTTTATGTCCTCTCAAAAATTA---GAAATATTAGTATAAAGTGTGCAAGA 3118
QY 76 rGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVa 96
Db 3119 AGAAGTCTTGATTTCTAACAGAAATTACTGGAAGATATTACTAAAAATATGCTTGGCC 3178
QY 96 IAsnCys---ThrIleLysGluLeuArgArgLeuPheLeuValAspAsp----- 111
Db 3179 GACCTTTGAAAAAATAATACAGTTGAAAGAAATTATCAACGAGGAAGATTATCAAGGTC 3238
QY 112 -----LeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValG 129
Db 3239 AAACCGTCTAGTACTAGTCTTATCAATGATCAATGGTCTATATTTCACGCTAT----- 3293
QY 129 yAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuAlaLeuIleSerLeuPheSerValPr 149
Db 3294 -----TTCTCTATCTGCTCTTTTGATT-----AATAATTCA--GAGGATGTGA 3337
QY 149 oValIleTyrGlu---ArgHisGlnAlaGlnIleAspHis---TyrLeuGlyLeuAla 167
Db 3338 TTAGCTTATGAATCAATCATCAAAATAATTGATCAGGACTATTTAGTAAATATTC 3397
QY 167 nLysAsnValLys 171
Db 3398 TACAACGATTAA 3410

RESULT 49
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
```



```

GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
Alignment Scores:
Pred. No.: 2.12e+04 Length: 1830121
Score: 84.00 Matches: 62
Percent Similarity: 33.71% Conservative: 28
Best Local Similarity: 23.22% Mismatches: 80
Query Match: 9.02% Indels: 97
DB: 4 Gaps: 13
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-557-884-1 (1-1830121)
Qy 6 LeuTyrTrp-----ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe 23
Db 37676 CTTATTGGATTTTACAAACGCTAGCCATCCAGTCAGTCGCTTTAGTTTGGCATTTT 37735
Qy 24 LeuLeuSerLeuThr----- 29
Db 37736 CTTTGGTGGCTTTTACCAATGGGAAACAAATTTGGAGTTTGCAGCGGTATCTT 37795
Qy 30 -----ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
Db 37796 TCACCTAAAGTAGCATTAACCTATCTTATCTTCTGCTTATGTTGCAATGACATTA 37855
Qy 45 LeuSerValThrIleSerPhe-----ArgIleTyrLysGlyValIleGlnAlaIle 61
Db 37856 CTTAGCGTAGCATGAGCGCTTGTAAATTTCTGAGTGGTATAAAATATGTATACCTCATTTG 37915
Qy 62 GlnLysSerAspGluGlyHisProPhe----- 70
Db 37916 CAAGAAATTAATGAA---CATGTATTTTGGCAACAAATGGGCTTATCTGGTCAATGCCA 37972
Qy 71 -----ArgAlaTyrLeuGluSerGluValAlaIle--- 80
Db
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
Alignment Scores:
Pred. No.: 2.12e+04 Length: 1830121
Score: 84.00 Matches: 62
Percent Similarity: 33.71% Conservative: 28
Best Local Similarity: 23.22% Mismatches: 80
Query Match: 9.02% Indels: 97
DB: 4 Gaps: 13
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-557-884-1 (1-1830121)
Qy 6 LeuTyrTrp-----ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe 23
Db 37676 CTTATTGGATTTTACAAACGCTAGCCATCCAGTCAGTCGCTTTAGTTTGGCATTTT 37735
Qy 24 LeuLeuSerLeuThr----- 29
Db 37736 CTTTGGTGGCTTTTACCAATGGGAAACAAATTTGGAGTTTGCAGCGGTATCTT 37795
Qy 30 -----ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
Db 37796 TCACCTAAAGTAGCATTAACCTATCTTATCTTCTGCTTATGTTGCAATGACATTA 37855
Qy 45 LeuSerValThrIleSerPhe-----ArgIleTyrLysGlyValIleGlnAlaIle 61
Db 37856 CTTAGCGTAGCATGAGCGCTTGTAAATTTCTGAGTGGTATAAAATATGTATACCTCATTTG 37915
Qy 62 GlnLysSerAspGluGlyHisProPhe----- 70
Db 37916 CAAGAAATTAATGAA---CATGTATTTTGGCAACAAATGGGCTTATCTGGTCAATGCCA 37972
Qy 71 -----ArgAlaTyrLeuGluSerGluValAlaIle--- 80
Db
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
Db 37973 GCAAAGTTCTGTTTCAGCAGCATTAAGTATATTATTAGAACCAAGCTTCGTCAATCAAC 38032
Qy 81 -----SerGluGluLeuValGlnLys-----Tyr 88
Db 38033 TGGATTGAATGGCTTACGAGCAGCTTGTTAATAATGATGGCACATCGCGCTATTATAC 38092
Qy 89 SerAsnSerAlaLeuGlyHis-----Val 96
Db 38093 AAAACACAGTATTATCAGAAAAATCTTGATAACCCCGATCAACGATTATTCACAAGATGTG 38152
Qy 97 AsnCysThrIleLysGluLeuArgArgLeuPhe-----LeuValAspAspLeuValAsp 114
Db 38153 CAATCTTATGTAAACACACGCTTTCTTTAAGCACTGGCGTCATTGATGCGGTACACCTCG 38212
Qy 115 SerLeuLysPheAlaValLeuMetTrp----- 123
Db 38213 ATGATCTCTTACACGATTTTGTATGGGATTAGCCGGTCCAAATGATAGTCTTGGTGTGA 38272
Qy 124 -----ValPheThrTyrValGlyAlaLeuPheAsnGly 134
Db 38273 GAAATTCGCATATGATGGTATTTTGTATGTTTGGTTATGTC-----ATTTTCAACACC 38326
Qy 135 LeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArg 154
Db 38327 CTCATCGCATTTCTGGCTCGGTGCG---CCATTAATCTCAATTTTATTATTAATGAACGC 38383
Qy 155 HisGlnAlaGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysAsnValLysAspAlaMe 174
Db 38384 CTAACGCCAACTAT---CGTTATCTTTAATTCGCATTAAGAATATGCTGAAGACATT 38440
Qy 174 tAlaLysIleGlnAlaLys 180
Db 38441 GCTTTTATGAGCGGAGAA 38459
RESULT 50
US-09-643-990A-1
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
```

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1

## Alignment Scores:

Pred. No.: 2,12e-04 Length: 1830121  
Score: 84.00 Matches: 62  
Percent Similarity: 33.71% Conservative: 28  
Best Local Similarity: 23.22% Mismatches: 80  
Query Match: 9.02% Indels: 97  
DB: 4 Gaps: 13

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-643-990A-1 (1-1830121)

QY 6 LeuTyrTrp-----ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe 23  
DB 37676 CTTATTGGATTGTTAAAGCGTAGCCATCACCTCAGTCGTCTTAGTTTGGCAATTTT 37735  
QY 24 LeuLeuSerLeuThr----- 29  
DB 37736 CTTTGGTGGTGTATACCAATGCGGAAACAATTTTGGATGTTTGCAGCGGTTATCTT 37795  
QY 30 -----ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44  
DB 37796 TCACCTAAACGTAGCAATTAACCTATCTTATCTTCTGCTTATTGTTGCAATGACATTA 37855  
QY 45 LeuSerValThrIleSerPhe-----ArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 37856 CTTAGCGTAGTACGCTTGTAAATCTGAGTGTATATAAATATGATATACCTCATGTG 37915  
QY 62 GlnLysSerAspGluGlyHisProPhe----- 70  
DB 37916 CAAGAAATTTAAAGAA---CATGTATTTTGGCAAAATGGGCTTATCTCGTCATCGCA 37972  
QY 71 -----ArgAlaTyrLeuGluSerGluValAlaIle----- 80  
DB 37973 GCAAGTTCTGTTTTCAGCAGCATTTAGTAAGCTATTTATAGAGCAACGTTTTCGTCAACA 38032  
QY 81 -----SerGluGluLeuValGlnLys-----Tyr 88  
DB 38033 TGGATTGAATGGCTTAACGAGCAGCTTGTATATAATGATGGCAGCATCGCGCTATTAC 38092  
QY 89 SerAsnSerAlaLeuGlyHis-----Val 96  
DB 38093 AAAACACAGATTTTATCAGAAATCTTGATAACCCGATCAAGTATTCAACAAGATGTG 38152  
QY 97 AsnCysThrIleLysGluLeuArgLeuPhe-----LeuValAspAspLeuValAsp 114  
DB 38153 CAATCTTATGTAACCAACCGCTTCTTTAAGCACTGGCGCTCATGTCGGTCACTCG 38212  
QY 115 SerLeuLysPheAlaValLeuMetTrp----- 123  
DB 38213 ATGATCTCTACAGATTGTTGATGGGATAGCCGCTCCCAATGATGATGTTGGTGTGTA 38272  
QY 124 -----ValPheThrTyrValGlyAlaLeuPheAsnGly 134  
DB 38273 GAAATTCGCATATGATGTTATTTTAGTTGTTGTTATGTC-----ATTTCACAACC 38326  
QY 135 LeuThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIleTyrGluArg 154  
DB 38327 CTCATCGCAATCTCGGTCGGTCGC-----CCATTAACTCTCAATTAATTAATGAACGC 38383  
QY 155 HisGlnAlaGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysAsnValLysAspAlaMe 174  
DB 38384 CTAAACGCAAACTAT---CGTTATTTTAAATTCGCAATTAAGAATATGCTGAACGATT 38440

QY 174 tAlaLysIleGlnAlaLys 180  
DB 38441 GCTTTTATGAGCGGCAAA 38459

## RESULT 51

US-09-543-681A-2003  
Sequence 2003, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 2003  
LENGTH: 843  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-543-681A-2003

## Alignment Scores:

Pred. No.: 0.107 Length: 843  
Score: 83.50 Matches: 38  
Percent Similarity: 38.71% Conservative: 34  
Best Local Similarity: 20.43% Mismatches: 68  
Query Match: 8.97% Indels: 46  
DB: 4 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-543-681A-2003 (1-843)

QY 2 ValValAspLeuLeuTyr---TrpArgAspIleLysLysThr----- 14  
DB 58 GTGGTAGGATCATTTTATGATGG-----ATPAAACGCTCTCTACCCCTAAACAGT 111  
QY 15 -----GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeu 28  
DB 112 ATGAAATATCTCTGGGAGGAGTAAATAGTAGGAATACTACTCTCTATTCTTTAGTCTTT 171  
QY 29 ThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThr 48  
DB 172 AGCAATTTATGGGTATTTAGCTCCTTAGAAGATATCTGGCAATCTCTGTTTATGGTTATG 231  
QY 49 IleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln---LysSerAspGluGly 67  
DB 232 ATGGAATCATTCCTGCTGCTTAAATTTTCAGATGGTCTATTGGATGAACAACAGT 291  
QY 68 HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLys 87  
DB 292 AATCACTAAAGCAATATCGAAAC-----GAATTGACACAAAA 333  
QY 88 TyrSerAsnSerAlaLeu----- 93  
DB 334 ACGCAACACAAAGTCTCTGGGGGATTTTACTGATCATCGCCATTGCCATTCCGAGAGAA 393  
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 104  
DB 394 GGCAGGAAGTGGTGGTTTTCCTATCAAGCCATATTATGGTCTCACAGCACAAACCGCG 453  
QY 105 ArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
DB 454 TTGCTCTTCTGATTGAAGTATTCCTGGCCCTATTGATAGCGGACTAATCTATGGTTA 513  
QY 125 PheThrTyrValGlyAlaLeu-PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIle 144  
DB 514 TTTTGTCTAACATCAAAATGATTTCTGGCGGTAAATTTCTTTGTTATTATCCGGAATTTTA 573  
QY 144 rLeuPheSerValPro 149  
DB 144 rLeuPheSerValPro 149





FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 11397  
LENGTH: 1665  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-11397

Alignment Scores:  
Pred. No.: 0.44 Length: 1665  
Score: 82.50 Matches: 39  
Percent Similarity: 42.58% Conservative: 27  
Best Local Similarity: 25.16% Mismatches: 56  
Query Match: 8.86% Indels: 33  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-252-991A-11397 (1-1665)

Qy	15	GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleVal	34
Db	478	GGCGCGGTGTTCGGCAAG-----CTGATCGAGCTGGCGCGCTTCTCCCGCTCC	525
Qy	35	SerValThrAlaTyrlleAlaLeu-----AlaLeuLeuSerValThrIle	49
Db	526	ATCGTCGGCGCGCGATCCGCTGCTCGGCACCGCGCGATGCTGGCGATCGTACTG	585
Qy	50	-----SerPheArgIleTyrlsGly-----ValIleGlnAlaIleGln	62
Db	586	GTCTGGCGCGCTGTCACTACGCGCGCGCTCGCTCTTCTGCTGTGTGTTCGGGTC	642
Qy	63	LysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSerGlu	82
Db	643	-----TACCGGTTCGGCGCGGAGATGTTCCGCGAGAGCGACATCCCAAG	687
Qy	83	GluLeuValGlnLysTyrlSerAsnSerAlaLeuGlyHisValAsnCystrIleLeuGlu	102
Db	688	CGATTGATTCCG-----CGGACCATCGCCCTCGCGCGCTTTCTTTCACCATGGACGG	741
Qy	103	LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLeuPheAlaValLeuMet	122
Db	742	CTGCCCGGACCCCGCAGATCCAGAACATCATCCCTCGACCTTCTTCGGCACCACGCC	801
Qy	123	TrpValPheThrTyrlValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu	142
Db	802	TGGCGCGCGCCCTGGCTCGGACC-----CTCGCGCGCG	834
Qy	143	IleSerLeuPheSerValProValIleTyrlGluArgHisGlnAla	157
Db	835	CTGTTCGTCTTCGCGTGGCGCTGCTACTACCTGCGACGCCAGCGC	879

RESULT 58  
US-08-853-659A-28  
Sequence 26, Application US/08853659A  
Patent No. 5925522  
GENERAL INFORMATION:  
APPLICANT: Wong, K.K.; Saffer, J.D.  
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection  
TITLE OF INVENTION: Of A  
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Paul W. Zimmerman  
ADDRESSEE: Intellectual Property Services  
ADDRESSEE: Battelle Memorial Institute  
ADDRESSEE: PNNL P.O. Box 999  
STREET: Washington Way  
CITY: Richland

Alignment Scores:  
Pred. No.: 0.372 Length: 350  
Score: 82.50 Matches: 39  
Percent Similarity: 42.58% Conservative: 27  
Best Local Similarity: 25.16% Mismatches: 56  
Query Match: 8.86% Indels: 33  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-252-991A-11439 (1-1500)

QY	15	GlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleVal	34
DB	1200	GGCGCGGTGTGGCAAG-----CTGATCGAGCTGCGCGGCTTCTCCGCTCC	1153
QY	35	SerValThrAlaTyrlleAlaLeu-----AlaLeuLeuSerThrIle	49
DB	1152	ATGTCGCGCGGGGATCCGCTGCTCGGCACCGCAGCGATGCTGGCGATCGTACTG	1093
QY	50	-----SerPheArgIleTyrlsGly-----ValIleGlnAlaIleGln	62
DB	1092	GTCGCGCGGTCTCACCTACGCGCGGCTCTCGCTGTTCTGCTGTGTGTTCGCGGTC	1036
QY	63	LysSerAspGluGlyHisProPheArgAlaTyrlsLeuSerGluValAlaIleSerGlu	82
DB	1035	-----TACCCGTTTCGCGCGGAGATGTTCCGCCAGAGCGACATCCCAAG	991
QY	83	GluLeuValGlnIysTyrlsSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu	102
DB	990	CGATTGATTCG-----GGCAGCATCGCCTCGCGCGGTTTTTCCTTCACCATGGACGG	937
QY	103	LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet	122
DB	936	CTCGCGGCGACCCCGCAGATCCAGAACATCATCCCTCGACCTTCCTGGCACCCACGCC	877
QY	123	TripValPheThrTyrlsValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu	142
DB	876	TGGGCGCGCGCTGGCTCGGACC-----CTCGCGCGG	844
QY	143	IleSerLeuPheSerValProValIleTyrlsGluArgHisGlnAla	157
DB	843	CTGTGCTGCTTCGCGGTGGCGCTGCTACTCTCGGACGCCAGCGG	799

RESULT 57  
US-09-252-991A-11397  
; Sequence 11397, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```

; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1797 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: the coding nucleotides of SEQ ID
; OTHER INFORMATION: NO:28 correspond to nucleotides 22630 through
; OTHER INFORMATION: 24426 of SEQ ID NO:2
;
US-08-853-659A-28

Alignment Scores:
Pred. No.: 0.688 Length: 1797
Score: 81.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-28 (1-1797)

QY 8 TTPARGASPIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
DB 487 TGGAAATGAGTTTCAGAAAAATTAACCCCGTTTATTAAACTCGATCTTCAACGTATAGCC 546
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
DB 547 GATATTCGAATATTATTATATTTCTCATTTGTTATATATGTAATTTAGTCTGGTTGTT 606
QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
DB 607 ATTGTACCTATTACCATGTTTATCGTCTCTATTATTATTTCTCCTCGTTAACCCATTAT 666
QY 57 ValIleGlnAlaIleGlnLysSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 76
DB 667 ACTAATGAGTTTAAATGAACAAACAAAGAGGACAGACAGAGGAGGAGGAGGAGGAGGAGGAG 726
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
DB 727 GAAGTTTCTTATCTATTAATAAGATCCATACCTTAATAATTAACAGTTTACTTTTGAT 786
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105
DB 787 TGGGTTAATACATCAATGAACAGTCGTATCTTAACCTGAAGATAAGGAATAATTAATCTT 846
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
DB 847 ATCTCAATCTATATTTGGGAGTATGTCATCTATTACCCTAACTAATCTATTATGTAATA 906
QY 124 ValPheThrTyrVal-----GlyValAlaLeuPheAsnGlyLeuThr 136
DB 907 GCCTTTTATGTTATCAAGGATGATGTTACTACTGGCGCAATGTTTCATCTGTCATT 966
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerValProValIle 151
DB 967 GTCTCTGGCGGATTTCCGGGATCATTTCCGAATTTTCTTCTACATTAATC 1017

RESULT 59
US-08-853-659A-6
; Sequence 6, Application US/08853659A
; Patent No. 592522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:6 corresponds to
; OTHER INFORMATION: nucleotides 15735 through 24701 of SEQ ID NO:2
;
US-08-853-659A-6

Alignment Scores:
Pred. No.: 9.13 Length: 8967
Score: 81.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-6 (1-8967)

QY 8 TTPARGASPIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
DB 7382 TGGAAATGAGTTTCAGAAAAATTAACCCCGTTTATTAAACTCGATCTTCAACGTATAGCC 7441
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
DB 7442 GATATTCGAATATTATTATATTTCTCATTTGTTATATATGTAATTTAGTCTGGTTGTT 7501
QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
DB 7502 ATTGTACCTATTACCATGTTTATCGTCTCTATTATTATTTCTCCTCGTTAACCCATTAT 7561
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSer 76
DB 7562 ACTAATGAGTTTAAATGAACAAACAAAGAGGACAGACAGACAGACAGACAGACAGACAGAC 7621
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
DB 7622 GAAGTTTCTTATCTTATTAAATGATCCATACCTTAATAATGATCCATACCTTAATAATGAT 7681
```



```
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-64 (1-8967)

Qy      8 TTPARGAsPtleIysLysThrGlyValvalPhelgYAlaserLeuPhe----LeuLeuLeu 26
|||    :~::~:|||||          |||:::|||
Db     7382 UGGAAGUGAGUUUCAGAAAUAUAAACCGGUUUUUAUAAACUCGUAUCUUCUUAACCAUGAUAGCC 7441
|||    :~::~:|||||          |||:::|||
Qy     27 SerLeuThrValPheSerileValSerValThralatYrilelaleuAlaleu----- 44
|||    :~::~:|||||          |||:::|||
Db     7442 GAUAUCCAUAUUUAUUAUUAUUCUCAUGUUAUAUAUGUAAAAUUUAGCUGGUGUUU 7501
|||    :~::~:|||||          |||:::|||
Qy     45 -----LeuSerValThrIleSerPheArgIleTyrlLySgly 56
|||    :~::~:|||||          |||:::|||
Db     7502 AUUGUAACCUUAUUAACAUGUUUAUUGGCUCUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7561
|||    :~::~:|||||          |||:::|||
Qy     57 ValIleGlNalalieGlnLySserASpGLuglyHisProPheArgAlATyrLeuGIuSer 76
|||    :~::~:|||||          |||:::|||
Db     7562 ACUAUGAGUUUAUGAACCAAACAAAAGAAGAGGACAGAGAACAGAGAAUAUUUUUAUCUCA 7621
|||    :~::~:|||||          |||:::|||
Qy     77 GluValAlalateSerGIuGIuLeuValGlnLyTyrSerAenSerAlaleu----- 93
|||    :~::~:|||||          |||:::|||
Db     7622 GAAGUUUUUUAUCUAUUAUAAUUAUGCAUACCUAAAUAAUUAUUAUUAUUAUUAUUAUUAUUAU 7681
|||    :~::~:|||||          |||:::|||
Qy     94 -----GlyHieValasnCystrIleIlysGluLeua-GArG 105
|||    :~::~:|||||          |||:::|||
Db     7682 UGGGUUAUAUAUCAUAAUUAUGAAGACGUCGUUAUCUUAUACCUGAAGAAUAAAGGAAUUAUUAUUAU 7741
|||    :~::~:|||||          |||:::|||
Qy     106 LeuPhe-----LeuValaspLeuValaspSerLeuLysPheAlaValLeuMetTrp 123
|||    :~::~:|||||          |||:::|||
Db     7742 AUCUAUCAAUCUAUUAUUGGGAGUUAUGCUAUUAUACCCCAAUAUAUUAUGGUUAUA 7801
|||    :~::~:|||||          |||:::|||
Qy     124 ValPheThrTyrVal-----GlyAlalaLeuPheAenGlyLeuThr 136
|||    :~::~:|||||          |||:::|||
Db     7802 GCCUUUUUUUAUGGUUAUAAUAAAGGGUGUUAUACUGCGCGCAUAUUGUUUAUCUGUGUAU 7861
|||    :~::~:|||||          |||:::|||
Qy     137 Leu-----LeuIleLeuAlaIleuleSerLeuPheSerValProvallie 151
|||    :~::~:|||||          |||:::|||
Db     7862 GUCUCUGGCCGUAUUUCCGGGAUCAUUUCCGAUUUUUUUUUUAUUAUUAUUAUUAUUAUUAUUAU 7912
|||    :~::~:|||||          |||:::|||

RESULT 62
US-08-853-659A-67/c
; Sequence 67, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
```

; FILING DATE: N/A  
 ; INFORMATION FOR SEQ ID NO: 67:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8967 bases  
 ; TYPE: nucleotide  
 ; STRANDEDNESS: single stranded  
 ; TOPOLOGY: linear  
 ;  
 US-08-853-659A-67

Alignment Scores:  
 Pred. No.: 9.13 Length: 8967  
 Score: 81.50 Matches: 36  
 Percent Similarity: 41.24% Conservative: 37  
 Best Local Similarity: 20.34% Mismatches: 71  
 Query Match: 8.75% Indels: 33  
 DB: 2 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-853-659A-67 (1-8967)  
 Qy 8 TTPArgAspIleLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26  
 Db 1586 TGAATGAGTTTCGAAATAATTAACCGGTTTATTAACTCGATCTTTACAGTATAGCC 1527  
 Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44  
 Db 1526 GATATTCCAATAATTATTATATTCTCTGTTTATATATGTAATTTAGGCTCGGTGTT 1467  
 Qy 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56  
 Db 1466 ATTGTACCTATTACCAGTTTATCGTCTCTATTATTATTTCCTCGTTAACCACTTAT 1407  
 Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
 Db 1406 ACTAATGAGTTAATGAACAAACAAAGGAGACAGAAACAGGAATATTTTATCTCA 1347  
 Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93  
 Db 1346 GAAGTTTCTCTATTCTATAATGATCCATACCTTAAATAATCAAGGTTTACTTTTGAT 1287  
 Qy 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105  
 Db 1286 TGGTTAATACATCAATGACAGTCTGATCTTAACTGAAGNATAGGAATTAATCTT 1227  
 Qy 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTyr 123  
 Db 1226 ATCTATCAATCTATATTGGGGAGTATGTCATCTATTACCACAAATAACTATTATGGTAATA 1167  
 Qy 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136  
 Db 1166 GCCTTTTATGTTAATCAAGGTGATGTGTACTACGCGCAATGTTTCATCTGTCATT 1107  
 Qy 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerValProValIle 151  
 Db 1106 GTCTCTGGCGGTATTTCCGGGATCAATTCGAATTTTCTTCTACATAATC 1056

RESULT 63  
 US-08-853-659A-2  
 ; Sequence 2, Application US/08853659A  
 ; Patent No. 5925522  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wong, K.K.; Saffer, J.D.  
 ; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection  
 ; TITLE OF INVENTION: Of A  
 ; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella  
 ; NUMBER OF SEQUENCES: 67  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Paul W. Zimmerman  
 ; ADDRESSEE: Intellectual Property Services  
 ; ADDRESSEE: Battelle Memorial Institute  
 ; ADDRESSEE: FNNL P.O. Box 999  
 ; STREET: Washington Way  
 ; CITY: Richland  
 ; STATE: Washington



COUNTRY: U.S.A.  
ZIP: 99352  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (WordPerfect 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/853,659A  
FILING DATE: Unknown  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: none  
FILING DATE: n/a  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24701 bases  
TYPE: nucleotide  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-853-659A-2

Alignment Scores:  
Pred. No.: 46.6 Length: 24701  
Score: 81.50 Matches: 36  
Percent Similarity: 41.24% Conservative: 37  
Best Local Similarity: 20.34% Mismatches: 71  
Query Match: 8.75% Indels: 33  
DB: 2 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-853-659A-2 (1-24701)

QY 8 TrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26  
DB 23116 TGGATGAGTTTCAGAAATTAACCCGTTTATTAACTCGATCTTTCAACGTATAGCC 23175  
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyIleAlaLeuAlaLeu----- 44  
DB 23176 GATATTCGAATTTATTATATTTCTCATTTGTTATATATGTAATTTAGGTCGTGTT 23235  
QY 45 -----LeuSerValThrIleSerPheArgIleTyIysGly 56  
DB 23236 ATTGACCTATTACCAGTGTTCCTCTCTCTATTATTATTTTCCCTCGTTAAACCCATTAT 23295  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyIleuGluSer 76  
DB 23296 ACTAATGAGTTTATGAACAAACAAAGAGGACAGAGACAGAGATATTTTATCTCA 23355  
QY 77 GluValAlaIleSerGluLeuValGlnLysTyIerSerAsnSerAlaLeu----- 93  
DB 23356 GAAGTTTCTTATCTATTAAATGATCCATACCTTAATATCAAGTTTACTTTTTCAT 23415  
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105  
DB 23416 TGGGTTAATACATCAATGAACAGTCGTATCTTAACCTGAAGATAAGGAATTAATCTT 23475  
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123  
DB 23476 ATCTATCAATCTATATGGGAGTATGTCATCTATTACCAATTAATATTATGGTAATA 23535  
QY 124 ValPheThrTyIerVal-----GlyAlaLeuPheAsnGlyLeuThr 136  
DB 23536 GCCTTTATGTTAATCAAGGTCATGTTACTACTGGCGCAATGTTTCTCATCTGTCATT 23595  
QY 137 Leu-----LeuIleAlaLeuIleSerLeuPheSerValProValIle 151  
DB 23596 GTCCTGCGCGTATTTCCGGGATCATCTTCGAATTTTCTTACATTAATC 23646

## RESULT 64

US-08-853-659A-3/c  
Sequence 3, Application US/08853659A  
Patent No. 5925522  
GENERAL INFORMATION:

APPLICANT: Wong, K.K.; Saffer, J.D.  
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection  
TITLE OF INVENTION: Of A  
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Paul W. Zimmerman  
ADDRESSEE: Intellectual Property Services  
ADDRESSEE: Battelle Memorial Institute  
ADDRESSEE: PNNL P.O. Box 999  
STREET: Washington Way  
CITY: Richland  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 99152

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (WordPerfect 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/853,659A  
FILING DATE: Unknown  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: none  
FILING DATE: n/a  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24701 bases  
TYPE: nucleotide  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-853-659A-3

## Alignment Scores:

Pred. No.: 46.6 Length: 24701  
Score: 81.50 Matches: 36  
Percent Similarity: 41.24% Conservative: 37  
Best Local Similarity: 20.34% Mismatches: 71  
Query Match: 8.75% Indels: 33  
DB: 2 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-853-659A-3 (1-24701)

QY 8 TrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26  
DB 1586 TGGATGAGTTTCAGAAATTAACCCGTTTATTAACTCGATCTTTCAACGTATAGCC 1527  
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyIleAlaLeuAlaLeu----- 44  
DB 1526 GATATTCGAATTTATTATATTTCTCATTTGTTATATGTAATTTAGGTCGTGTTGTT 1467  
QY 45 -----LeuSerValThrIleSerPheArgIleTyIysGly 56  
DB 1466 ATTGACCTATTACCAGTGTTCCTCTCTCTATTATTATTTCCCTCGTTAAACCCATTAT 1407  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyIleuGluSer 76  
DB 1406 ACTAATGAGTTTATGAACAAACAAAGAGGACAGAGACAGAGATATTTTATCTCA 1347  
QY 77 GluValAlaIleSerGluLeuValGlnLysTyIerSerAsnSerAlaLeu----- 93  
DB 1346 GAAGTTTCTTATCTATTAAATGATCCATACCTTAATATCAAGTTTACTTTTTCAT 1287  
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105  
DB 1286 TGGGTTAATACATCAATGAACAGTCGTATCTTAACCTGAAGATAAGGAATTAATCTT 1227  
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123  
DB 1226 ATCTATCAATCTATATGGGAGTATGTCATCTATTACCAATTAATATTATGGTAATA 1167



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Db 1586 TGAATAGCTTTTCAGAAAATAAACCCTTTTATTAACTCGATCTTTCAACGTATAGCC 1527
Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 1526 GATATTCATATTTATTATATTTCTCATGTGTATATATGTAATTTAGTCTGGTGTGTT 1467
Qy 45 -----LeuSerValThrIleSerPheArgIleTyrIleGly 56
Db 1466 ATTGTACCTATTACCATGTTTATCGTCTCTATTATTATTTCCCTCGTTAAACCATTTAT 1407
Qy 57 ValIleGlnAlaIleGlnIleSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 1406 ACTAATAGCTTAAATCAACAAACAAAGAGGACAGACAGGAATATTTTATCTCA 1347
Qy 77 GluValAlaIleSerGluLeuValGlnIleTyrSerAsnSerAlaLeu----- 93
Db 1346 GAAGTTTTCTTATCTATTAAATGATCCATACCTTAATAATATCAAGGTTTACTTTTGTAT 1287
Qy 94 -----GlyHisValAsnCysThrIleIleGluLeuArg 105
Db 1286 TGGGTTAATACATCAATGAACAGTCGTATCTTAACCTGAAGATAAGGAATTAATCTT 1227
Qy 106 LeuPhe-----LeuValAspLeuValAspSerLeuIlePheAlaValLeuMetTrp 123
Db 1226 ATCTATCAATCTATATTGGGGAGTATGTCATCTATTACCAAATAACTATTATGTAATA 1167
Qy 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 1166 GCCTTTTATGTAATCAAGGGTGATGTTACTACTGGCGCAATGTTTCATCTGTCAAT 1107
Qy 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerValProValIle 151
Db 1106 GTCTCTGGCGGATTTCCGGGATCATTTTCAATTTTCTTACATTAATC 1056

RESULT 67
US-09-795-927-6
; Sequence 6, Application US/09795927
; Patent No. 6531309
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James A.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Revelli, Jean-Pierre
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6531309el Human Transporter Proteins and Polynucleotides Encod
; FILE REFERENCE: LEX-0141-USA
; CURRENT APPLICATION NUMBER: US/09/795,927
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,956
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2913
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-795-927-6

Alignment Scores:
Pred. No.: 1.76 Length: 2913
Score: 81.00 Matches: 48
Percent Similarity: 42.93% Conservative: 37
Best Local Similarity: 24.24% Mismatches: 69
Query Match: 8.70% Indels: 44
DB: Gaps: 10

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-795-927-6 (1-2913)
Qy 21 SerLeuPheLeuLeu-----SerLeuThrValPheSerIle 33
||||| ||||||| |||||
```

```
Db 1102 AGCTCTTTCTGCTCATATTTCTGGCAAGAAGATTGCCAGTCTTTCACAATTTACAGTGTG 1161
Qy 34 ValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPhe----- 51
Db 1162 AATTCCAACAGGATTTAATAGCCATCGCCTTTTGCATGTGCTGAGTTCATTTTTCAGA 1221
Qy 52 -----ArgIleTyrIleGlyValIleGlnAlaIleGlnIleSerAsp 65
Db 1222 TCTTGTGTGTTTACTGGTGTCTATTCTAGGACTATTATCCAG-----GATAAATCTGA 1275
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Db 1276 GGAAGACAAACAGTTTGCATCTCTGTAGGCGAGGTGTGATGCTGCTC-----CTGATG 1329
Qy 86 GlnIleTyrSer-----AsnSerAlaLeuGlyHisValAsnCys 98
Db 1330 GTGAAGATGGGACACTTTTCTACACACTGCCAATGCTGTGCTGGCTGATTTATTCTG 1389
Qy 99 -----ThrIleIleGluLeuArgLeuPheLeuValAsp 110
Db 1390 AGCAACGTCATTCCTTACCTTGAACCATTTTAACTACCAGCTGTGGAGGCGAGAC 1449
Qy 111 AspLeuValAspSerLeuIlePheAlaValLeuMetTrpValPheThrTyrValGlyAla 130
Db 1450 -----CAATATGACTGTGCTCTTTGGATGATGACATTTCTCATCTTCA 1491
Qy 131 LeuPheAsnGlyLeuThrLeu-----LeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
Db 1492 ATTTTCTGGGACTGGACATTTGGACTAATTTATCTCAGTAGTTCCTTCTTCTATCAC 1551
Qy 150 ValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnIleAsn 169
Db 1552 ACTGTT---CGTTCACACAGAGACTAAGATTCTTCTCTGGGTCAATCCCTAACACCAAC 1608
Qy 170 ValIleAspAlaMetAlaIleGln-----AlaIleProGlyLeuIle 185
Db 1609 ATTTATAGAGCATCAATGATTATCGGAGATCATCACCATTCTCTGGGTGAAA 1662

RESULT 68
US-09-762-724-1/c
; Sequence 1, Application US/09762724
; Patent No. 6664053
; GENERAL INFORMATION:
; APPLICANT: Kovacs, et al.
; TITLE OF INVENTION: Identification of a region of the major surface
; FILE REFERENCE: 4239-58054
; CURRENT APPLICATION NUMBER: US/09/762,724
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US99/18750
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,805
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3042
; TYPE: DNA
; ORGANISM: Pneumocystis carinii sp. f. hominis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3042)
US-09-762-724-1

Alignment Scores:
Pred. No.: 1.89 Length: 3042
Score: 81.00 Matches: 26
Percent Similarity: 54.41% Conservative: 11
Best Local Similarity: 38.24% Mismatches: 14
Query Match: 8.70% Indels: 17
DB: Gaps: 2

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-762-724-1 (1-3042)
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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal-----16
Db 2864 GTCGTGGAGGTGCTGTATGGTGTGACGCTTTGTGACCCACGCTGCTGTGTGCTGAGA 2805
QY 17 -----ValPheGlyAlaSerLeuPheLeuLeuSer 27
Db 2804 GATTGTCATTCTCTCCGCTCTCTACTGTTTCTCTGCTCTCT-----TTGACTGTTTCT 2751
QY 28 LeuThrValPheSerIleValSerValThrAlaTyrIleAla-LeuAlaLeuLeuSerVa 47
Db 2750 GTGACTGTTGTTATGTTGGTTCCTGCTACTGTTTATTTATTCATGGCTTTACTTTCAGT 2691
QY 47 lThrIleSerPheArgIleTyr 54
Db 2690 GGTTCCTATTATTTAAACATATTT 2669
RESULT 69
US-09-795-927-8
; Sequence 8, Application US/09795927
; Patent No. 6531309
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James A.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Revelli, Jean-Pierre
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6531309el Human Transporter Proteins and Polynucleotides Enc
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0141-USA
; CURRENT APPLICATION NUMBER: US/09/795,927
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,956
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3749
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-795-927-8
Alignment Scores:
Pred. No.: 2.64 Length: 3749
Score: 81.00 Matches: 48
Percent Similarity: 42.93% Conservative: 37
Best Local Similarity: 24.24% Mismatches: 69
Query Match: 8.70% Indels: 44
DB: 4 Gaps: 10
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-795-927-8 (1-3749)
QY 21 SerLeuPheLeuLeuLeu-----SerLeuThrValPheSerIle 33
Db 1577 AGCTCTCTTTCTGTCATATTTCTGGCAAGAGATTGCCAGTCTTCACAAATTACAGTGTC 1636
QY 34 ValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSerPhe-----51
Db 1637 AATTCCACAGGATTATAGCCATCGGCTTGCATGTCAGTTCATTTTCAGA 1696
QY 52 -----ArgIleTyrIleGlyValIleGlnAlaIleGlnIleSerAsp 65
Db 1697 TCTTGTGTTTACTGCTGCTATTGTAGACTATTATCCAG-----GATAAATCTGGA 1750
QY 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 1751 GGAAGACAAACAGTTTCATCTCTGTTAGGCGCAGGTGTGTGCTGCTC-----CTGATG 1804
QY 86 GlnLysTyr-Ser-----AsnSerAlaLeuGlyHisValAsnCys 98
Db 1805 GTGAGATGGGACACTTTTCTACACACTGCCAAATGCTGCTGCTGGTATTATTTCTG 1864
```

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QY 99 -----ThrIleLysGluLeuLeuArgLeuPheLeuValAsp 110
Db 1865 AGCAACGTCATTCCCTACCTTGAACACCATTTCTAACCTACCAGCCTGTGGAGGAGGAC 1924
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAla 130
Db 1925 -----CAATATGACTGTGCTCTTTGGATGATGACATTTCTCATCTTCA 1966
QY 131 LeuPheAsnGlyLeuThrLeu-----LeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
Db 1967 ATTTTCTGGAGCTGACATTTGGACTAATATCTCAGTAGTTTCTTCTTCTCATCACC 2026
QY 150 ValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn 169
Db 2027 ACTGTT--CGTTACACAGAGCTAAGATTCTTCTCTGGGTCAAAATCCCTAACCAAC 2083
QY 170 ValLysAspAlaMetAlaLysIleGln-----AlaLysIleProGlyLeuLys 185
Db 2084 ATTTATAGAGCATCAATGATTATCGGAGATCATCACATTTCTGGGGTGAA 2137
RESULT 70
US-09-328-352-740
; Sequence 740, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 740
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-740
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Score: 80.50 Matches: 35
Percent Similarity: 43.84% Conservative: 29
Best Local Similarity: 23.97% Mismatches: 44
Query Match: 8.65% Indels: 39
DB: 4 Gaps: 7
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QY 26 LeuSerLeuThrValPheSerIleVal-----SerValThrAlaTyrIle 40
Db 832 GCCCAGTATCTCACTTCTAATTTATGGCCCTGAGTTACCACATATACCCAGCAAT 891
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QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 934 -----CCTGAAACATATTTTCCGTTTGAACCTGAAACGCGGTGAGACTTTG 978
QY 81 SerGluGlu-----LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn--- 97
Db 979 GCTCAGCAACCTACACAGTTTCAAGTTATAGC-----ATTGGGAAATTCGAAG 1029
QY 98 -----CysThrIleLysGluLeu 103
Db 1030 GCATGCTCTCCATTTGCTATTATTTAAACGGTAATGGTCACGATTTGGAGCGCTTAAGCAATTT 1089
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QY 124 ValPheThrTyrValGly 129
Db 1149 GTATTACACAAATTTGGT 1166

RESULT 71
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; FILE REFERENCE: jannaschii
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
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APPLICATION NUMBER: 333,155  
FILING DATE: 04-APR-1989  
SEQ ID NO: 5  
LENGTH: 1990  
5518916-5

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Percent Similarity:	37.89%	Conservative:	36
Best Local Similarity:	22.03%	Mismatches:	64
Query Match:	8.59%	Indels:	77
DB:	6	Gaps:	11

US-09-830-972-29\_COPY\_990\_1178 (1-189) x 5518916-5 (1-1990)

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Db 718 CATGGT-----AGCCATATAGATACCTGTTGTGACAGATATTCAACATCGGTAGTTCC 665  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp----- 65  
Db 664 TTCCTCGTCGACAACTTGTGTTCAA-----CAGACCAGTGACAGAGTAGTGGTAATC 611  
QY 66 -----GluGlyHisProPheArgAlaTyrLeuGluSerGluVal 78  
Db 610 ACCATGGTTCGTCCTTCTTGAACGCAACCTTCGCGTTTAC----- 566  
QY 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCys 98  
Db 565 -----GCTGTTCTTGCAGGGTTCGATGC 542  
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Db 541 ACTCTCTTTGAACAATCTGAACGACGATCCAACTGGTAAGGTTTGGAGAGATAGAGG 482  
QY 103 -----LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe 118  
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QY 184 -LeuLysArgLysAlaGlu 189  
Db 196 ATTGTGGCGAAAGCAGAC 178

## RESULT 77

US-08-916-421B-1/c  
Sequence 1, Application US/08916421B  
Patent No. 6503729  
GENERAL INFORMATION:  
APPLICANT: Bult et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii  
Patent No. 6503729  
TITLE OF INVENTION: jannaschii

FILE REFERENCE: PB275  
CURRENT APPLICATION NUMBER: US/08/916,421B  
CURRENT FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: US 60/024,428  
PRIOR FILING DATE: 1996-08-22  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
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FEATURE:	
NAME/KEY: misc feature	
LOCATION: (713652) .. (713652)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (741684) .. (741684)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (779455) .. (779455)	OTHER INFORMATION: n equals a, t, c, or g





Alignment Scores:		
Pred. No.:	0.981	Length: 1500
Score:	79.50	Matches: 41
Percent Similarity:	40.38%	Conservative: 22
Best Local Similarity:	26.28%	Mismatches: 50
Query Match:	8.54%	Indels: 43

RESULT 82

Alignment Scores:

US-09-830-972-29 COPY 990 1178 (1-189) x US-09-949-016-15236 (1-147840)

Qy 18 PheGlyAlaSerLeuPheLeuLeuLeuSerLeu-----Thr 29





```
Db 476 AGACACTTATCAAAATGTTT- - - - - GAATCATGTTT 444
Qy 87 LysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeu 106
Db 443 AAATACAGTAATTTATCATTAATGAATTAAGTTTACAAATAAAGTAAGTATCCAGTAC 384
Qy 107 PheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThr 126
Db 383 TTGTGATA- - - - - ATTAATATCATAAAGTTTATCAATCTTTTAATAGCACTTACA 333

RESULT 85
US-09-949-016-3567
; Sequence 3567, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3567
; LENGTH: 3811
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3567

Alignment Scores:
Pred. No.: 5,17 Length: 3811
Score: 79.00 Matches: 44
Percent Similarity: 41.32% Conservative: 25
Best Local Similarity: 26.35% Mismatches: 52
Query Match: 8.49% Indels: 46
DB: 4 Gaps: 8

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-3567 (1-3811)
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerIleu 22
Db 723 ATTCAAGTAATTTATTGACAGACTTGGGGTCTTACATCAAAATGCCCTACTCAATCTC 782
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 783 TCTTTAGACCTGTCCCTGAACCTATGAACCTTTATCCCAACGAGTGCAATTTAAAGAAAT 842
Qy 43 AlaLeuLeuSerValThrIle- - - - - SerPheArgIleTyrLysGlyVal 57
Db 843 AGGCTTCATAGCTGACCTTTAAGAAATAATTTGTAGTATTTAATGTAATGAAGAACTGT 902
Qy 58 IleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGlu 77
Db 903 ATTCAAGGCTGTG- - - - - GCTGGTTTAGAAGTCCAT 932
Qy 78 ValAlaIle- - - - - SerGluGluLeuValGlnLysTyrSerAsnSerAla 92
Db 933 CGTTTGGTTCTGGGAGAAATTTAGAAATGAAGGAAACTTGGAAAGATTTGACAAATCTGCT 992
Qy 93 Leu- - - GlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeu- - - - - 108
Db 993 CTAGAGGCCCTGTGCAATTTGACCAATTTGAAGATTTCCGATTTAGCATCTTAGACTACTAC 1052
Qy 109 ValAspLeuValAspSerLeuLysPheAlaValLeuMetTyrPheThrTyrVal 128
Db 1053 CTCGATGATATTAATTGAC- - - - - 1070
```

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Qy 129 GlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSer- - - 147
Db 1071 - - - - - TATTTAATGTTTGACA- - - - - AATGTTTCTTCATTTCCCTG 1109
Qy 148 ValProValIleTyrGluArg 154
Db 1110 GTGAGTGTGACTATTGAAAGG 1130

RESULT 86
US-08-836-687B-29
; Sequence 29, Application US/08836687B
; Patent No. 6448034
; GENERAL INFORMATION:
; APPLICANT: Gasson, Michael John
; APPLICANT: Dodd, Helen Mair
; TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
; FILE REFERENCE: 20747/70
; CURRENT APPLICATION NUMBER: US/08/836,687B
; CURRENT FILING DATE: 1995-11-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 7454
; TYPE: DNA
; ORGANISM: Lactococcus sp.
US-08-836-687B-29

Alignment Scores:
Pred. No.: 15,2 Length: 7454
Score: 79.00 Matches: 35
Percent Similarity: 39.44% Conservative: 36
Best Local Similarity: 19.44% Mismatches: 77
Query Match: 8.49% Indels: 32
DB: 3 Gaps: 5

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-836-687B-29 (1-7454)
Qy 5 LeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPheLeu 24
Db 2746 CTGTCGTATCTTCAGATATTCAGAAATAGTACAAACCTGGGTGGAAATCTATCTTC 2805
Qy 25 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
Db 2806 CTA- - - - - AGATATACTGATCCTAAACCATATTAGATTGGGTATA 2847
Qy 45 LeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSer 64
Db 2848 AAATGTTTCAGATTTA- - - - - TTTTAGCTTACGGATCTATCTTGAATCTTAAAGAGT 2904
Qy 65 AspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeu 84
Db 2905 CGGAAAAATAGTAATAATGTCAACTTTT- - - - - GATATTTCTATTATGATCAAGAA 2955
Qy 85 ValGlnLysTyr- - - - - Ser 89
Db 2956 GTAGAAAGATATGTTGGATTGATCTTTAGAGTTATCCGAAGCAATATTTTGTGCCGAT 3015
Qy 90 AsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuVal 109
Db 3016 TCTAAATATTATCCAAATTTGCTTACATTGATAAAGATACTAATAATGATTGGAAGTC 3075
Qy 110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTyrPheThrTyrValGly 129
Db 3076 GATGATGTA- - - - - TCAATCTTGGTGAATTAATTTATCTGAAA 3114
Qy 130 AlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
Db 3115 TGCTTCTTCAGATGATGATACAAAAGATCTTAATTTTGAATTTAGTTAGTCTCTAAA 3174
Qy 150 ValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn 169
Db 3175 AAGGTTAAAGAAATGTCAATGAAAGATTGAACATTATCTTAAAGCTTCTGAAAGTTAAT 3234
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RESULT 87
US-09-949-016-15309
; Sequence 15309, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15309
; LENGTH: 15346
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15309

Alignment Scores:
Pred. No.: 48.6 Length: 15346
Score: 79.00 Matches: 44
Percent Similarity: 41.32% Conservative: 25
Best Local Similarity: 26.35% Mismatches: 52
Query Match: 4.49% Indels: 46
DB: 8 Gaps: 8

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-15309 (1-15346)
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 10258 ATTCAAAGTATTATTATTCACAGACTTGGCGGTTCTACATCAAAATGCCCTACTCATCTC 10317
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 10318 TCTTTAGACTGTCCCTGAACCTATGAACCTTATCCACAGGTCGATTAAGAAAT 10377
QY 43 AlaLeuLeuSerValThrIle-----SerPheArgIleTyrLysGlyVal 57
Db 10378 AGCGTTCAATAGCTGACTTTAAGAAATAATTTTGATAGTTAAATGTAATGAATACTGT 10437
QY 58 IleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGlu 77
Db 10438 ATTCAGAGGTCGT-----GCTCGTTTAGAAGTCCAT 10467
QY 78 ValAlaIle-----SerGluGluLeuValGlnLysTyrSerAsnSerAla 92
Db 10468 CGTTTCGTTCTGGAGAAATTAGAAATGAGGAACTTGGAAAGTTTGACAAATCTGCT 10527
QY 93 Leu---GlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeu-----108
Db 10528 CTAGAGGCGCTGTGCAATTGACCAATTGAAGAAATTCGATAGCACTTAGACTACTAC 10587
QY 109 ValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrVal 128
Db 10588 CTCGATGATATTATTGAC-----10605
QY 129 GlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSer---147
Db 10606 -----TTATTAAATTGTTGACA-----AATGTTCTTCAITTTCCCTG 10644
QY 148 ValProValIleTyrGluArg 154
Db 10645 GTGAGTGTGACTATTGAAAGG 10665

RESULT 88
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```
US-09-949-016-13877
; Sequence 13877, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13877
; LENGTH: 20211
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc.feature
; LOCATION: (1).....(20211)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877

Alignment Scores:
Pred. No.: 3.07e+03 Length: 20211
Score: 79.00 Matches: 35
Percent Similarity: 42.64% Conservative: 20
Best Local Similarity: 27.13% Mismatches: 32
Query Match: 8.49% Indels: 42
DB: 4 Gaps: 9

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-13877 (1-20211)
QY 68 HisProPheArg---AlaTyrLeuGlu-----SerGluValAlaIleSer--- 81
Db 169976 TATCCTTTTAGATAATCTTATCTGGAACATGTTTAAATTTCTAGTGTGTTCTTTT 170035
QY 82 -----GluGluLeuValGlnLysTyr-----SerAsnSerAlaLeuGlyHis 95
Db 170036 TAAAGTGACACTTCAAGATAACTCAAAAGCCATTTGAATGAGGAATCCTTCTGACAT 170095
QY 96 ValAsnCysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSer 115
Db 170096 TTACAATGCTTCCCGACACTTTGACAAAATTTGATTTTATGATAGTGTGTTTCATTC 170155
QY 116 LeuLysPheAlaValLeuMetTrpValPhe-----ThrTyrValGly 129
Db 170156 ---AGATTGCGCTATCTC---TCGTTTTTCCAACTAAATTCAACTTAGTGTATTATAGGA 170209
QY 130 AlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerVal--- 148
Db 170210 GCCAAATTT-----GTTTATATTTTGCCTTTTATGTAACATTTATTTAAGTTGA 170257
QY 149 -----ProValIle 151
Db 170258 TGAATTTAAACATTTTAAAGCAAGTCAGTGGAATAAATAAGTTTAAACAAAGTGATT 170317
QY 152 TyrGluArgHisGlnAlaGlnIleAsp 160
Db 170318 TTTGATAACCATATAATTCACAACAGAT 170344

RESULT 89
US-09-949-016-14543/C
; Sequence 14543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14543  
; LENGTH: 387902  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(387902)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14543

Alignment Scores:  
Pred. No.: 8.78e+03 Length: 387902  
Score: 79.00 Matches: 43  
Percent Similarity: 38.46% Conservative: 22  
Best Local Similarity: 25.44% Mismatches: 57  
Query Match: 8.49% Indels: 47  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-14543 (1-387902)

Qy 8 TrpArgAspIle-----LysLysThrGlyValValPhe-----Gly 19  
Db 105633 TGGCATGAATTTTAAATTTGAAATTTGCGATGGAATGCTACATTCACCATGTAATGGG 105574  
Qy 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
Db 105573 GAGGCTTTAAATTTGCTATTTAGATAATATTTTGTAGAGGTAGGGTGTGTCATAT 105514  
Qy 40 IleAlaLeu---AlaLeuLeuSerValThrIleSerPhe----- 51  
Db 105513 GTGTGTATATATACATGTATGCTTCCACAGATACAGCTGACCATTCAAAAGAAATAAG 105454  
Qy 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63  
Db 105453 AAGGATTTCTGGAGCTCACGGGAGAAATAAGCGTGGGTAGACTCTTCCATAGAATCC 105394  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyrLeuGluSerGluVal 78  
Db 105393 AGTCTGAAGGCCATCTTGCTGAAATAATCCTGTGCAGAGCC----- 105352  
Qy 79 AlaIleSerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHis----- 95  
Db 105351 -----TCCTACTCTAACTTAGATTTTGCAGAAAAGACTGGA 105316  
Qy 96 ValAenCys-ThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSe 115  
Db 105315 CAGAGTTGTGGTGGTTTGGGAGCTAGAAAGACGGTCTCTTGTATCATAGTGGTTTC 105256  
Qy 115 rLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLe 135  
Db 105255 CTGCAAGGTAGGTGTAAAGTTTGCACATCAGAAACAGATGAAGAGTACTAGCAGGAGC 105196  
Qy 135 uThrLeuLeuLeuAlaLeuLeu 143  
Db 105195 TACCTTGCTCTCTTAGCTCTTTGTG 105171

RESULT 90

US-09-949-016-12557/c  
; Sequence 12557, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12557  
; LENGTH: 421883  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(421883)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12557

Alignment Scores:  
Pred. No.: 1e+04 Length: 421883  
Score: 79.00 Matches: 43  
Percent Similarity: 38.46% Conservative: 22  
Best Local Similarity: 25.44% Mismatches: 57  
Query Match: 8.49% Indels: 47  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-12557 (1-421883)

Qy 8 TrpArgAspIle-----LysLysThrGlyValValPhe-----Gly 19  
Db 105633 TGGCATGAATTTTAAATTTGAAATTTGCGATGGAATGCTACATTCACCATGTAATGGG 105574  
Qy 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
Db 105573 GAGGCTTTAAATTTGCTATTTAGATAATATTTTGTAGAGGTAGGGTGTGTCATAT 105514  
Qy 40 IleAlaLeu---AlaLeuLeuSerValThrIleSerPhe----- 51  
Db 105513 GTGTGTATATATACATGTATGCTTCCACAGATACAGCTGACCATTCAAAAGAAATAAG 105454  
Qy 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63  
Db 105453 AAGGATTTCTGGAGCTCACGGGAGAAATAAGCGTGGGTAGACTCTTCCATAGAATCC 105394  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyrLeuGluSerGluVal 78  
Db 105393 AGTCTGAAGGCCATCTTGCTGAAATAATCCTGTGCAGAGCC----- 105352  
Qy 79 AlaIleSerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHis----- 95  
Db 105351 -----TCCTACTCTAACTTAGATTTTGCAGAAAAGACTGGA 105316  
Qy 96 ValAenCys-ThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSe 115  
Db 105315 CAGAGTTGTGGTGGTTTGGGAGCTAGAAAGACGGTCTCTTGTATCATAGTGGTTTC 105256  
Qy 115 rLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLe 135  
Db 105255 CTGCAAGGTAGGTGTAAAGTTTGCACATCAGAAACAGATGAAGAGTACTAGCAGGAGC 105196  
Qy 135 uThrLeuLeuLeuAlaLeuLeu 143  
Db 105195 TACCTTGCTCTCTTAGCTCTTTGTG 105171

RESULT 91

US-09-543-681A-2407  
; Sequence 2407, Application US/09543681A

```
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2407
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Proteus mirabilis
; US-09-543-681A-2407

Alignment Scores:
Pred. No.: 1.13 Length: 1341
Score: 78.50 Matches: 34
Percent Similarity: 37.00% Conservative: 40
Best Local Similarity: 17.00% Mismatches: 55
Query Match: 8.43% Indels: 71
DB: 4 Gaps: 8

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-543-681A-2407 (1-1341)

QY 15 GlyValValPheGlyAlaSerLeuPhe----- 23
Db 199 GGGCTTTTATTGGTACCTCAGCTTTTGGCTATATTGGACAAAGTAGGCGCCGTAAA 258
QY 24 ---LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 259 ATGTCCTCGTTCATATTGGCTATTGGCTATTGGCTGATTCT-----ATTGGCACC 306
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 307 ATGTTTGTTCACACCAATAGGTTGTAGTATCGCTTCCTTATTGGGATTGTG--- 363
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 364 -----ATTGGCGCTGACTATCCTATTGCAACT 390
QY 83 GluLeuValGlnLysTyrSerAsn-----Ser 91
Db 391 TCGATGATCACCAGAAATTTCCAAATAAAAGCAACGTCCTTTGCGGTGGATTATTGCT 450
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgAlaGluPheLeuValAspAsp 111
Db 451 GCTATGGTATATCGGTGGACATGTGCCAATTTAGTGGT---TATCTTTTATATGAT 507
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
Db 508 GTTCAAGATGGCTGGCGT-----TGGATG-----TTAGCAGTGTCT 543
QY 132 PheAsnGlyLeuThrLeuLeuLeuAla----- 141
Db 544 TTATTCTTGGCTTATTATTCTAATTGGTTCGCTTTGATCTCCCTGAATCAGCGCTTTGG 603
QY 142 -----LeuIleSerLeuPheSerVal 148
Db 604 TTAATACCGCAAGGACGTATTAAAGAGTGTAAATAATGATGATCAACTCTTTGCGGAG 663
QY 149 ProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLys 168
Db 664 CCTGTGCTTTTGAAGCAGAAGATGCTAAACACGCCGTTTATCGAATTATTATAATAA 723

RESULT 92
US-09-489-039A-5041
; Sequence 5041, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
```

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5041
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-5041

Alignment Scores:
Pred. No.: 0.674 Length: 879
Score: 78.00 Matches: 38
Percent Similarity: 39.87% Conservative: 25
Best Local Similarity: 24.05% Mismatches: 65
Query Match: 8.38% Indels: 30
DB: 4 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-489-039A-5041 (1-879)

QY 6 LeuTyrTrpArgAspIleLysLys-----ThrGlyValValPheGly 19
Db 82 CTGCTGTGGCGCGCATTTGATGAAGACCATATGACACCTCGCGGGAACTTCGCTAT 141
QY 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39
Db 142 GGTCTATTACTCTCTGCTGGTGGCTGATTGCGGTGCTGCTGCTGCTGCTGCTGCTT 201
QY 40 IleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 59
Db 202 CCTATGTTCTCCGAAGTCAGCGTCAGATCCGCTCATTTTATCTGCCAATTTATTCCG 261
QY 60 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79
Db 262 GCG-----ACCGGGATGTAATCCAGGGATATATCAGCAGATTTCGTGGCC 306
QY 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr 99
Db 307 AACTCCAGCGCATG-----ACCGGTAGGCGCTTTGCGCTGATC 348
QY 100 IleLysGluLeuArgAlaGluPheLeuValAspAspLeuValAspSerLeu----- 116
Db 349 GTCACTCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 408
QY 117 -----LysPheAlaValLeuMetTrpValPheThrTyrVal 128
Db 409 ACGCGCAGCGCGCCCAAGTTTATCTTTGCGGT-----TACTGGATGATCTCGACCCCTC 465
QY 129 GlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla---LeuIleSerLeu 145
Db 466 GGCCCGCTGCTGGCGGGCGCCAGCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 519

RESULT 93
US-09-949-016-12900
; Sequence 12900, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
```

; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12900  
; LENGTH: 462589  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12900

Alignment Scores:  
Pred. No.: 1.61e+04 Length: 462589  
Score: 78.00 Matches: 45  
Percent Similarity: 38.17% Conservative: 26  
Best Local Similarity: 24.19% Mismatches: 49  
Query Match: 8.38% Indels: 66  
DB: 4 Gaps: 8

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-12900 (1-462589)

Qy 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyriLeAlaLeuAla 43  
Db 110616 CTACTTTGTCTAGTATCTAC-----ATTACACCGATTAACTTAATCAGT 110663  
Qy 44 LeuLeu-----SerValThrIleSerPheArgIleTyriLysGly 56  
Db 110664 GTCATGTGCTCTGCTAACTGCAATTAATTTGTCTGTATTTTCATTCGGCATCTCAAAAATG 110723  
Qy 57 VallileGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyriLeuGluSer 76  
Db 110724 GTAATAAACATA-----GGACATATTTTATAGGGCTATATATTGAAT 110765  
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyriSerAsnSerAlaLeuGlyHisVal 96  
Db 110766 -----GTATTAAATGAGAAATCCTTCAGTATTCCTTAGCACTGTGCTAGAACATGAA 110819  
Qy 97 Asn-----CysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 110820 AACTCTTAATAAGCTTGGCTATTAGTCTGTGTAACCGTAAGACTGTTCTGCTTAT 110879  
Qy 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrp-----123  
Db 110880 CCCTTGTTATCCCACTTCTTTCACAGAACCTTGTGGCAGCAGATTAATCATAGAAA 110939  
Qy 124 -----ValPheThr-----126  
Db 110940 TTATTGAATAAATTAATGGTCCCATTTTTCCTAGTCCACTGTGGTGAAGTCTCAGAT 110999  
Qy 127 -----TyrValGlyAlaLeuPheAsnGlyLeu-----135  
Db 111000 TCCCAAGGATGTGGTGTGTGCAGATAGTTCCATGTGCCAGGGCTCTTGTTCAGTTTA 111059  
Qy 136 -----ThrLeuLeuLeuAlaLeuLeuSerLeuPheSerValPro 149  
Db 111060 GTGATTATTCTGCCACACTTGTCTTAATCCAGATTGATTGCTTTTATATGAAGATA 111119  
Qy 150 VallileTyriGluArgHis 155  
Db 111120 GTAATATATGGAGGCAT 111137

## RESULT 94

US-09-949-016-12412  
; Sequence 12412, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12412  
; LENGTH: 476044  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12412

Alignment Scores:  
Pred. No.: 1.68e+04 Length: 476044  
Score: 78.00 Matches: 45  
Percent Similarity: 38.17% Conservative: 26  
Best Local Similarity: 24.19% Mismatches: 49  
Query Match: 8.38% Indels: 66  
DB: 4 Gaps: 8

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-12412 (1-476044)

Qy 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyriLeAlaLeuAla 43  
Db 124072 CTACTTTGTCTAGTATCTAC-----ATTACACCGATTAACTTAATCAGT 124119  
Qy 44 LeuLeu-----SerValThrIleSerPheArgIleTyriLysGly 56  
Db 124120 GTCATGTGCTCTGCTAACTGCAATTAATTTGTCTGTATTTTCATTCGGCATCTCAAAAATG 124179  
Qy 57 VallileGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyriLeuGluSer 76  
Db 124180 GTAATAAACATA-----GGACATATTTTATAGGGCTATATATTGAAT 124221  
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyriSerAsnSerAlaLeuGlyHisVal 96  
Db 124222 -----GTATTAAATGAGAAATCCTTCAGTATTCCTTAGCACTGTGCTAGAACATGAA 124275  
Qy 97 Asn-----CysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 124276 AACTCTTAATAAGCTTGGCTATTAGTCTGTGTAACCGTAAGACTGTTCTGCTTAT 124335  
Qy 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrp-----123  
Db 124336 CCCTTGTTATCCCACTTCTTTCACAGAACCTTGTGGCAGCAGATTAATCATAGAAA 124395  
Qy 124 -----ValPheThr-----126  
Db 124396 TTATTGAATAAATTAATGGTCCCATTTTTCCTAGTCCACTGTGGTGAAGTCTCAGAT 124455  
Qy 127 -----TyrValGlyAlaLeuPheAsnGlyLeu-----135  
Db 124456 TCCCAAGGATGTGGTGTGTGCAGATAGTTCCATGTGCCAGGGCTCTTGTTCAGTTTA 124515  
Qy 136 -----ThrLeuLeuLeuAlaLeuLeuSerLeuPheSerValPro 149  
Db 124516 GTGATTATTCTGCCACACTTGTCTTAATCCAGATTGATTGCTTTTATATGAAGATA 124575  
Qy 150 VallileTyriGluArgHis 155  
Db 124576 GTAATATATGGAGGCAT 124593

## RESULT 95

US-09-198-452A-1

; Sequence 1, Application US/09198452A  
; Patent No. 655294

## GENERAL INFORMATION:

; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849

[illegible]

NAME/KEY: misc feature  
LOCATION: (705001)..(720000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (720001)..(735000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (735001)..(750000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (750001)..(765000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (765001)..(780000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (780001)..(795000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (795001)..(810000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (810001)..(825000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (825001)..(840000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (840001)..(855000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (855001)..(870000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (870001)..(885000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (885001)..(900000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (900001)..(915000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature

Alignment Scores:  
Pred. No.: 7.64e+04 Length: 1230025  
Score: 78.00 Matches: 34  
Percent Similarity: 40.41% Conservative: 25  
Best Local Similarity: 23.29% Mismatches: 65  
Query Match: 8.38% Indels: 23  
DB: 4 Gaps: 5

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-198-452A-1 (1-1230025)

Qy 6 LeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu 25  
Db 1042940 ATGTTTGGATGGACTTCTGCAGGAACC-ATGTCCTTGTGCTCTGGGCTTTATTTTC 1042998  
Qy 26 LeuSerLeu-----ThrValPheSerIleValSerValThrAlaTyRileAlaLeuAla 43  
Db 1042999 GTAGCTCTAAGAAGTCTTACAATTCCTATAGCTCAAGATGTGGCTTATGTTTATAGCTGCT 1043058  
Qy 44 LeuLeuSerValThrIleSerPheArgIleTyRlyGlyValIleGlnAlaIleGlnLys 63  
Db 1043059 CTGTAGGGGCTTGTATCGGATCTTATGGTATAATGTTTCCCGGCCACGCTCTTCATG 1043118  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyRileuGlu 75  
Db 1043119 GGAGATACCGGGTCACTACTTCTAGGGGCTGCTAGGAGCTCGCTGTTATGCTGGC 1043178  
Qy 76 SerGlu-----ValAlaIleSerGluGluLeuValGlnLysTyRAsnSerAla 92  
Db 1043179 GCAGATGCATCCTAGTCTGATCGGAGGAGTTTTTGTGTGAAGCGGGATCTGTCAATT 1043238

Qy 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 1043239 CTACAGTACTAGTTGTAGATTAAAGGAAA---AAACGCCCTTTCTTATGCTCTCCATTG 1043295  
Qy 113 -----ValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
Db 1043296 CATCACCATTATGAATATCAGGGCTCCAGAGACTAAATATCGTCATCGCTTTTGGATC 1043355  
Qy 125 PheThrTyRValGlyAla 130  
Db 1043356 TTTAGTTTGTATGCGCA 1043373  
RESULT 96  
US-09-438-185A-1  
; Sequence 1, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438.185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1230230  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-438-185A-1

Alignment Scores:  
Pred. No.: 7.64e+04 Length: 1230230  
Score: 78.00 Matches: 34  
Percent Similarity: 40.41% Conservative: 25  
Best Local Similarity: 23.29% Mismatches: 65  
Query Match: 8.38% Indels: 23  
DB: 4 Gaps: 5

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-438-185A-1 (1-1230230)

Qy 6 LeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu 25  
Db 1032818 ATGTTTGGATGGACTTCTGCAGGAACC-ATGTCCTTGTGCTCTGGGCTTTATTTTC 1032876  
Qy 26 LeuSerLeu-----ThrValPheSerIleValSerValThrAlaTyRileAlaLeuAla 43  
Db 1032877 GTAGCTCTAAGAAGTCTTACAATTCCTATAGCTCAAGATGTGGCTTATGTTTATAGCTGCT 1032936  
Qy 44 LeuLeuSerValThrIleSerPheArgIleTyRlyGlyValIleGlnAlaIleGlnLys 63  
Db 1032937 CTGTAGGGGCTTGTATCGGATCTTATGGTATAATGTTTCCCGGCCACGCTCTTCATG 1032996  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyRileuGlu 75  
Db 1032997 GGAGATACCGGGTCACTACTTCTAGGGGCTGCTAGGAGCTCGCTGTTATGCTGGC 1033056  
Qy 76 SerGlu-----ValAlaIleSerGluGluLeuValGlnLysTyRAsnSerAla 92  
Db 1033057 GCAGATGCATCCTAGTCTGATCGGAGGAGTTTTTGTGTGAAGCGGGATCTGTCAATT 1033116  
Qy 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 1033117 CTACAGTACTAGTTGTAGATTAAAGGAAA---AAACGCCCTTTCTTATGCTCTCCATTG 1033173

```
QY 113 -----ValAspSerLeuLysPheAlaValLeuMetTrpVal 124
Db 1033174 CATCACCATTATGAATATCAGGCGCTCCAGAGACTAAATCGTCATGCGCTTTTGGATC 1033233
QY 125 PheThrTyrValGlyAla 130
Db 1033234 TTAGTTTGTATGCGCA 1033251

RESULT 97
US-09-248-796A-730
; Sequence 730, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 730
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-730

Alignment Scores:
Pred. No.: 1,22 Length: 1152
Score: 77.50 Matches: 35
Percent Similarity: 34.72% Conservative: 15
Best Local Similarity: 24.31% Mismatches: 27
Query Match: 67 Indels: 67
DB: 5 Gaps: 5

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-248-796A-730 (1-1152)
QY 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSer 32
Db 91 AAAACTTCATTAATGAAATCATCAAAACACTC-----CTGACACTATTATT 135
QY 33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArg 52
Db 136 ATGATTTCCTTAAGGCGCAGTAATCGCACTTATCTTTTACCACCTTAATTTATTATTGTT 195
QY 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAla 72
Db 196 TTAATCAAA-----TATCCATTT----- 213
QY 73 TyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAla 92
Db 213 ----- 213
QY 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAspLeu 112
Db 214 TTCGGGGGTAAACCTTATATCAAG-----AATGATTG 249
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyr----- 127
Db 250 GTCAATTCTTGAATTAACCGTTTATCAAGCATTAACTCAATTTCCCACTTGATGATGTT 309
QY 128 -----ValGlyAlaLeuPhe 132
Db 310 CATATTTTTCATAATTTCTGCTGAATTTGTTATCAATAAAGCTGTTGGTAAATTATAT 369
QY 133 AsnGlyLeuThr 136
Db 370 CCTGGTTTAAACA 381

RESULT 98
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```
US-09-543-681A-215/c
; Sequence 215, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 215
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-215

Alignment Scores:
Pred. No.: 1,25 Length: 1167
Score: 77.50 Matches: 30
Percent Similarity: 43.85% Conservative: 27
Best Local Similarity: 23.08% Mismatches: 42
Query Match: 8.32% Indels: 31
DB: 4 Gaps: 5

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-543-681A-215 (1-1167)
QY 30 ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIle 49
Db 395 GTTTTCTCGTAATCGCGCTTCAATTTTGTTCATCAAGTTTATG-----GTA 345
QY 50 SerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro 69
Db 344 TCTGGACGAATATCGACAACAACAATAGTCGCACCACGTAACA----- 300
QY 70 PheArgAlaTyr-----LeuGluSerGluVal----- 78
Db 299 ---AAGCGGTTCCGAATCGAAATCGAAACAAAGTGAACCTCGGCATATCATCTTCATCGCGGGT 243
QY 79 -----AlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91
Db 242 TTGATATTCAGAGATAGCCGCCATTTCTTAACGATGCTGTACAGAAGGTGTTAACAGC 183
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
Db 182 GTCATTATGACAATGAATTTGTTCTTCTTAACCACTTTTTCACATTTTTCGTGAAGTTGCCA 123
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr-----Tyr 127
Db 122 TCACCACAGAGCTTGCACACTTTCCATCGCTGTTTCATATATACTACTTAATTTCTGTGCCAACA 63
QY 128 ValGlyAlaLeuPheAsnGlyLeuThrLeu 137
Db 62 ACGGGTGGTTTATTAAACGAATCATATTA 33

RESULT 99
US-09-620-312D-751
; Sequence 751, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
```



APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yuning  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pt\_FL\_genes Version 1.0  
SEQ ID NO 751  
LENGTH: 2020  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (222)..(1196)  
US-09-620-312D-751

Alignment Scores:  
Pred. No.: Length: 2020  
Score: 3.02  
Percent Similarity: 77.50  
Best Local Similarity: 42.98%  
Query Match: 28.10%  
Indels: 44  
Gaps: 25  
DB: 4

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-620-312D-751 (1-2020)

Qy 75 GluSerGluValAlaIleSer-----GluGluLeuValGlnLysTySerAsnSerAla 92  
Db 189 GAACTGAATTGTCTATTTCACCTGAAGAAAATGATAGACAAAATCAAACTGTGTT 248  
Qy 93 LeuGly-----HisValAsnCysThrIleLysGluLeuArgLeuPhe 107  
Db 249 GTAGCAGAGGATTCGTGCCCTATATGATTCTCTGATTTCATCTCGAAGAAATGGTTT 308  
Qy 108 LeuValAspAspLeuValAspSerLeuLysPheAla-----ValLeuMetTrpValPheThr 126  
Db 309 GGTGGGAGCAGTTCGAGGACTATTGTGAATTTGCAAACTATCTCTGTGGGTTTTTACA 368  
Qy 127 TyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPhe 146  
Db 369 -----CCACTAATCTTTTAATCTTCTTACTTCTTACTTACTTCTTT 407  
Qy 147 SerValProval-----IleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 408 CTCTCTACCTTACTTATTATTTCCTACACTTTATTAAGAGAAAGATGTTTGAAGAA 467  
Qy 161 HistyrLeuGlyLeuAlaAsnLysAspValLysAspAlaMetAlaLeuIleGlnAlaLys 180  
Db 468 GCCTAC-----TCTCATAAATTTATGGGATGTCGAAGGAAACACAGTGGCAACT 515  
Qy 181 Ile 181  
Db 516 CTG 518

RESULT 100

US-09-949-016-12735  
Sequence 12735, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12735  
LENGTH: 80355  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12735  
Alignment Scores:  
Pred. No.: Length: 80355  
Score: 1.13e+03  
Percent Similarity: 77.50  
Best Local Similarity: 57.14%  
Query Match: 42.86%  
Indels: 20  
Gaps: 1  
DB: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-12735 (1-80355)  
Qy 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProphearg 71  
Db 42680 AGAGTAGGGTCTGGGATGATACAGCTCTTCTCAG---GACTCTGGGAACCCCTTTAAGG 42736  
Qy 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTySerAsnSer 91  
Db 42737 GCCTGCTTGAACCTCAGAGTGGTGGCTCAGCCAGCAGCTCTCTGTCCTATTTCTGTGTC 42796  
Qy 92 AlaLeuGlyHisValAsnCysThrIle 100  
Db 42797 GCGTTGATATCACACACTTGTGATGTG 42823  
Search completed: June 19, 2005, 05:38:14  
Job time : 2629.5 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 03:56:06 ; Search time 445.5 Seconds  
(without alignments)  
2633.504 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SVDDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

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Xgapop 10.0 , Xgapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_0/US09830972/runat\_16062005\_153944\_18950/app\_query.fasta\_1.654  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500  
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-NO MMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSPELLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
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6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
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9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
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15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	931	100.0	600	21	US-10-956-157-9764	Sequence 9764, Ap
2	931	100.0	1400	21	US-10-956-157-9763	Sequence 9763, Ap
3	931	100.0	2883	21	US-10-956-157-4529	Sequence 4529, Ap
4	931	100.0	3478	21	US-10-956-157-4528	Sequence 4528, Ap
5	931	100.0	3579	9	US-09-789-386-1	Sequence 1, Appli
6	931	100.0	3579	9	US-09-789-386-22	Sequence 22, Appl
7	931	100.0	3579	18	US-10-327-502-212	Sequence 212, App
8	931	100.0	3579	19	US-10-327-213-8	Sequence 8, Appli
9	931	100.0	3579	19	US-10-466-258-8	Sequence 8, Appli
10	931	100.0	3579	20	US-10-810-653-22	Sequence 22, Appl
11	931	100.0	4053	9	US-09-758-140-5	Sequence 5, Appli
12	931	100.0	4053	9	US-09-758-140-5	Sequence 5, Appli
13	931	100.0	4053	19	US-10-717-597-310	Sequence 310, App
14	931	100.0	4623	21	US-10-956-157-4532	Sequence 4532, Ap
15	931	100.0	4632	14	US-10-060-036-53	Sequence 53, Appl
16	927	99.6	799	18	US-10-660-946-2	Sequence 2, Appli
17	927	99.6	1122	9	US-09-789-386-5	Sequence 5, Appli
18	927	99.6	1160	14	US-10-175-523-156	Sequence 156, App
19	927	99.6	1609	21	US-10-956-157-4527	Sequence 4527, Ap
20	927	99.6	1610	9	US-09-765-205-5	Sequence 5, Appli
21	927	99.6	1610	21	US-10-347-669-5	Sequence 5, Appli
22	927	99.6	1785	17	US-10-439-388-62	Sequence 62, Appl
23	927	99.6	1785	21	US-10-956-157-1705	Sequence 1705, Ap
24	927	99.6	2050	21	US-10-956-157-4530	Sequence 4530, Ap
25	927	99.6	2052	19	US-10-466-258-3	Sequence 3, Appli
26	927	99.6	2226	21	US-10-956-157-4531	Sequence 4531, Ap
27	927	99.6	2235	14	US-10-060-036-54	Sequence 54, Appl
28	921	98.9	1980	17	US-10-220-891-22	Sequence 22, Appl
29	918	98.6	994	11	US-09-978-360A-110	Sequence 110, App
30	914	98.2	2610	18	US-10-641-643-382	Sequence 382, App
31	908	97.5	4684	9	US-09-893-348-17	Sequence 17, Appl
32	908	97.5	4684	20	US-10-810-653-17	Sequence 17, Appl
33	905	97.2	2782	15	US-10-205-194-165	Sequence 165, App
34	904.5	97.2	3492	18	US-10-267-502-214	Sequence 214, App
35	886	95.2	1798	19	US-10-466-258-10	Sequence 10, Appl
36	872	93.7	1400	21	US-10-956-157-9765	Sequence 9765, Ap
37	867	93.1	1514	9	US-09-823-245A-349	Sequence 349, App
38	805	86.5	1400	21	US-10-956-157-9762	Sequence 9762, Ap
39	805	86.5	1400	21	US-10-956-157-9767	Sequence 9767, Ap
40	718	77.1	1400	21	US-10-956-157-9766	Sequence 9766, Ap
41	695	74.7	422	9	US-09-960-352-8477	Sequence 8477, Ap
42	682	73.3	1520	15	US-10-084-817-333	Sequence 333, App
43	682	73.3	2331	18	US-10-267-502-213	Sequence 213, App
44	682	73.3	3202	9	US-09-954-456-210	Sequence 210, App
45	682	73.3	3202	17	US-10-172-118-386	Sequence 386, App

# ALIGNMENTS

## RESULT 1

US-10-956-157-9764  
; Sequence 9764, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956.157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9764

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; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9764

Alignment Scores:
Pred. No.: 2,566-107 Length: 600
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-9764 (1-600)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 31 TCAGTTGTTGACCTCTCTGCTACTGGAGAGACATTAAAGACACTGGAGTGGTGTGGTGC 90
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 91 AGCCTATTCTCTGCTTTTCATTGACAGTATTACAGCAATTTGAGCGTAAACAGCTACATT 150
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 151 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 210
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 211 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAACTTGTCTATA 270
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 271 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTTGGTCAATGTAAGTGCACGATA 330
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 331 AAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 390
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 391 TTGATGTGGTATTTACCTATGTTGGTGCCTTGTATTAATGGTCTGCACACTACTGATTTTG 450
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 451 GCTCTCAATTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 510
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 511 CATTTATCTAGGACTTGCAAAATGAAGATGTTAAGATGCTATGGCTTAAATCCAGCAAAA 570
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 571 ATCCCTGGATTGAAGCGCAAGCTGAA 597

RESULT 2
US-10-956-157-9763
; Sequence 9763, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9763
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-956-157-9763

Alignment Scores:
Pred. No.: 9,8e-107 Length: 1400
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-9763 (1-1400)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 488 TCAGTTGTTGACCTCTCTGCTACTGGAGAGACATTAAAGACACTGGAGTGGTGTGGTGC 547
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 548 AGCCTATTCTCTGCTTTTCATTGACAGTATTACAGCAATTTGAGCGTAAACAGCTACATT 607
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 608 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 667
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 668 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAACTTGTCTATA 727
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 728 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTTGGTCAATGTAAGTGCACGATA 787
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 788 AAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 847
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 848 TTGATGTGGTATTTACCTATGTTGGTGCCTTGTATTAATGGTCTGCACACTACTGATTTTG 907
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 908 GCTCTCAATTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 967
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 968 CATTTATCTAGGACTTGCAAAATGAAGATGTTAAGATGCTATGGCTTAAATCCAGCAAAA 1027
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 1028 ATCCCTGGATTGAAGCGCAAGCTGAA 1054

RESULT 3
US-10-956-157-4529
; Sequence 4529, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4529
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4529

Alignment Scores:
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Pred. No.: 3.08e-106 Length: 2883
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-4529 (1-2883)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 2314 TCAGTTGTGACCTCTGCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTCC 2373
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 2374 AGCCTATTCTGCTCTTCATTGACAGTATTGACATTTGAGCGTAAACGCTACATT 2433
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 2434 GCCTTGGCCCTGCTCTGTCGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 2493
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 2494 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCGCATATCTGGAATCTGAAAGTTGCTATA 2553
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 2554 TCTGAGGAGTGGTTCAGAGTACAGTAATTTCTGCTTGTGTCATGTGACGACGATA 2613
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 2614 AAGCAACTCAGCGCGCTCTCTTAGTTGATTTAGTTAGTTCTCTGAAAGTTGACGTG 2673
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 2674 TTGATGTGGGTATTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTTG 2733
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 2734 GCTCTCATTTACCTTCAGTGTTCCTGTTATTATGAACGCGCATCAGGACAGATAGAT 2793
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 2794 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 2853
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 2854 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2880

RESULT 4
; Sequence 4528, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4528
; LENGTH: 3478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4528

Alignment Scores:
Pred. No.: 4.14e-106 Length: 3478
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-4528 (1-3478)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 2566 TCAGTTGTGACCTCTGCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTCC 2625
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 2626 AGCCTATTCTGCTCTTCATTGACAGTATTGACATTTGAGCGTAAACGCTACATT 2685
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 2686 GCCTTGGCCCTGCTCTGTCGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 2745
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 2746 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCGCATATCTGGAATCTGAAAGTTGCTATA 2805
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 2806 TCTGAGGAGTGGTTCAGAGTACAGTAATTTCTGCTTGTGTCATGTGAACTGACGATA 2865
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 2866 AAGCAACTCAGCGCGCTCTCTTAGTTGATTTAGTTAGTTCTCTGAAAGTTGACGTG 2925
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 2926 TTGATGTGGGTATTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTTG 2985
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 2986 GCTCTCATTTACCTCTTCAGTGTTCCTGTTATTATGAACGCGCATCAGGACAGATAGAT 3045
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3046 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 3105
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 3106 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3132

RESULT 5
US-09-789-386-1
; Sequence 1, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789.386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1

Alignment Scores:
Pred. No.: 4.33e-106 Length: 3579

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Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-789-386-1 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTTGACCTCTCTGCTGACCATTAAGAGACTGGAGTGGTGTGGTGC 3069
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTrile 40
Db 3070 AGCTATTCTCTGCTCTTTCATTGACGATTTACGAGTGTGAGCGTAACAGCCTACATT 3129
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGACCATCAGTTTAGATATACAAGGTTGTATCCAGCT 3189
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLile 80
Db 3190 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTCAGAAAGTACAGTAATTCCTGCTTGTGTCATGTGAACGCACGATA 3309
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGGCGCTCTCTTCTAGTATGATTTAGTTAGTTCTCTGAACTTTCAGTGT 3369
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGCTGACACTACTGATTTTG 3429
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCATTTTCACTCTTCTAGTGTCTGTTTATTAAGACGCATCAGCGCGAGATAGAT 3489
QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCAGGACTTGCATAAATAAGAAATCTTAAAGATGCTATGGCTTAAATCCACGAAAA 3549
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 6
US-09-893-348-22
; Sequence 22, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22

; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22

Alignment Scores:
Pred. No.: 4,33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-893-348-22 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTTGACCTCTCTGCTGACCATTAAGAGACTGGAGTGGTGTGGTGC 3069
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTrile 40
Db 3070 AGCTATTCTCTGCTCTTTCATTGACGATTTACGAGTGTGAGCGTAACAGCCTACATT 3129
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGACCATCAGTTTAGATATACAAGGTTGTATCCAGCT 3189
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLile 80
Db 3190 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTCAGAAAGTACAGTAATTCCTGCTTGTGTCATGTGAACGCACGATA 3309
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGGCGCTCTCTTCTAGTATGATTTAGTTAGTTCTCTGAACTTTCAGTGT 3369
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGCTGACACTACTGATTTTG 3429
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCATTTTCACTCTTCTAGTGTCTGTTTATTAAGACGCATCAGCGCGAGATAGAT 3489
QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCAGGACTTGCATAAATAAGAAATCTTAAAGATGCTATGGCTTAAATCCACGAAAA 3549
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 7
US-10-267-502-212
; Sequence 212, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212
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; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-327-213-8

Alignment Scores:
Pred. No.: 4.33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-327-213-8 (1-3579)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTGACCTCCCTGCTACTCGAGAGACATTAAGAAGACTGGAGTGGTGGTGC 3069
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCCTGCTGCTTTCATTCAGCAGTATTCAGCATTTGAGCGTAACAGCCTACATT 3129
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 3189
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAAATCTGAAGTTGCTATA 3249
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTGTCATGTGAACTGCACGATA 3309
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCAGTG 3369
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3370 TTGATGTGGTATTTACTATGTTGGTGGCTTGTGTTAATGGTCTGACACTACTGATTTTG 3429
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCATTTCCATCTTCAGTTCCTGTTTATTTATGAACGGCATCAGGCGCAGATAGAT 3489
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 9
US-10-466-258-8
; Sequence 8, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3579)
US-10-466-258-8
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; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-267-502-212

Alignment Scores:
Pred. No.: 4.33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-267-502-212 (1-3579)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTGACCTCCCTGCTACTCGAGAGACATTAAGAAGACTGGAGTGGTGGTGC 3069
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCCTGCTGCTTTCATTCAGCAGTATTCAGCATTTGAGCGTAACAGCCTACATT 3129
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 3189
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAAATCTGAAGTTGCTATA 3249
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTGTCATGTGAACTGCACGATA 3309
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCAGTG 3369
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3370 TTGATGTGGTATTTACTATGTTGGTGGCTTGTGTTAATGGTCTGACACTACTGATTTTG 3429
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCATTTCCATCTTCAGTTCCTGTTTATTTATGAACGGCATCAGGCGCAGATAGAT 3489
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 8
US-10-327-213-8
; Sequence 8, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 8
; LENGTH: 3579
; TYPE: DNA
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Alignment Scores:
Pred. No.: 4,33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-466-258-8 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 3010 TCAGTTGTGTACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC 3069

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3070 AGCCTATTCTCTGCTCTTCATTCAGAGTATTCAGCATTTGAGGTTAACAGCCTACATT 3129

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3189

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249

QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100
DB 3250 TCTGAGGAGTTGGTTCAGAGTACAGTAATCTCTGTCTTGGTCATGTGACGAGATA 3309

QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3310 AAGGAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTG 3369

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140
DB 3370 TTGATGGGTATTTACCTATCTTGGTCCCTTGTATTGATGCTGACACTACTGATTTTG 3429

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 3430 GCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTATGAAGCGCATCAGCGGAGATAGAT 3489

QY 161 HistyrLeuGlyLeuAlaAsnLysAenValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3490 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAA 3549

QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 10
US-10-810-653-22
; Sequence 22, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-10-810-653-22

Alignment Scores:
Pred. No.: 4,33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-810-653-22 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 3010 TCAGTTGTGTACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC 3069

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3070 AGCCTATTCTCTGCTCTTCATTCAGAGTATTCAGCATTTGAGGTTAACAGCCTACATT 3129

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3189

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249

QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100
DB 3250 TCTGAGGAGTTGGTTCAGAGTACAGTAATCTCTGTCTTGGTCATGTGACGAGATA 3309

QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3310 AAGGAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTG 3369

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140
DB 3370 TTGATGGGTATTTACCTATCTTGGTCCCTTGTATTGATGCTGACACTACTGATTTTG 3429

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 3430 GCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTATGAAGCGCATCAGCGGAGATAGAT 3489

QY 161 HistyrLeuGlyLeuAlaAsnLysAenValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3490 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAA 3549

QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 11
US-09-758-140-5
; Sequence 5, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
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; CURRENT FILING DATE: 2001-01-12  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(3710)  
; OTHER INFORMATION: Human mRNA for No. US2002001295A1 protein (KIAA0886, GenBank  
; OTHER INFORMATION: Accession No. US2002001295A1 AB020693)  
US-09-758-140-5

Alignment Scores:  
Pred. No.: 5,28e-106 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-758-140-5 (1-4053)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	3144	TCAGTTGTTGACCTCTCTGACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCC	3203
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	3204	AGCCTATTCTCTGCTCTTCAATTCACAGATATTCAGCATTTGTGACGTAACAGCCTACATT	3263
Qy	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	3264	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT	3323
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	3324	ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATCTCGAATCTGAAGTTGCTATA	3383
Qy	81	SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	3384	TCTGAGGAGTTGGTTTCAGAAATCAGTAATCTCTCTTGTCTATGTGAATCTGAAAGTTGCAAGT	3443
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	3444	AAGGAATCTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTG	3503
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	3504	TTGATGTGGGTATTACCTATGTTGGTCCCTTGTGTTAATGCTGACACTACTGATTTTG	3563
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	3564	GCTCTCATTTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGAT	3623
Qy	161	HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	3624	CATTATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAA	3683
Qy	181	IleProGlyLeuLysArgLysAlaGlu	189
Db	3684	ATCCCTGGATTGAAGCGCAAGACTGAA	3710

RESULT 12

US-09-972-599A-5

; Sequence 5, Application US/09972599A

; Patent No. US20020077295A1  
; GENERAL INFORMATION:  
; APPLICANT: STRITTMATTER, STEPHEN M.  
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
; FILE REFERENCE: C077 CIP US  
; CURRENT APPLICATION NUMBER: US/09/972,599A  
; CURRENT FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: PCT/US01/01041  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(3710)  
; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1 protein (KIAA0886, Ge  
; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)  
US-09-972-599A-5

Alignment Scores:  
Pred. No.: 5,28e-106 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-972-599A-5 (1-4053)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	3144	TCAGTTGTTGACCTCTCTGACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCC	3203
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	3204	AGCCTATTCTCTGCTCTTCAATTCACAGATATTCAGCATTTGTGACGTAACAGCCTACATT	3263
Qy	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	3264	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT	3323
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	3324	ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATCTCGAATCTGAAGTTGCTATA	3383
Qy	81	SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	3384	TCTGAGGAGTTGGTTTCAGAAATCAGTAATCTCTCTTGTCTATGTGAATCTGAAAGTTGCAAGT	3443
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	3444	AAGGAATCTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTG	3503
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	3504	TTGATGTGGGTATTACCTATGTTGGTCCCTTGTGTTAATGCTGACACTACTGATTTTG	3563
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	3564	GCTCTCATTTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGAT	3623
Qy	161	HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180

Db 3624 CATTATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3683  
QY 181 ileProGlyLeuLysArgLysAlaGlu 189  
Db 3684 ATCCCTGGATTGCAAGCGCAAAAGCTGAA 3710  
RESULT 13  
US-10-717-597-310  
; Sequence 310, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dornier, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; PRIORITY FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 310  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-310

Alignment Scores:  
Pred. No.: 5,286-106 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-717-597-310 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3144 TCAGTTGTTGACCTCTCTGACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGCC 3203  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3204 AGCCTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACAGCCTACATT 3263  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3264 GCCTTGGCCCTGCTCTCTGTGACCAATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCT 3323  
QY 61 ileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3383  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3384 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAAATCTCTGCTTTGGTCAATGTAAGTGCACGATA 3443  
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTGG 3503  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3504 TTGATGTGGGTTATTTACCTATGTTGGTGCTTGTGTTTAAATGCTGTGACACTACTGATTTTG 3563

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3564 GCTCTCATTTTCACTCTTCACTGTTTATTTATGAACCGCATCAGGCACAGATAGAT 3623  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3624 CATTATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3683  
QY 181 ileProGlyLeuLysArgLysAlaGlu 189  
Db 3684 ATCCCTGGATTGCAAGCGCAAAAGCTGAA 3710

## RESULT 14

US-10-956-157-4532  
; Sequence 4532, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4532  
; LENGTH: 4623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4532

## Alignment Scores:

Pred. No.: 6,5e-106 Length: 4623  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-4532 (1-4623)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3151 TCAGTTGTTGACCTCTCTGACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGCC 3210  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACAGCCTACATT 3270  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCT 3330  
QY 61 ileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3390  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3391 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAAATCTCTGCTTTGGTCAATGTAAGTGCACGATA 3450  
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTGG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3511 TTGATGTGGGTTATTTACCTATGTTGGTGCTTGTGTTTAAATGCTGTGACACTACTGATTTTG 3570  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3571 GCTCTCATTTTCACTCTTCACTGTTTCTGTTTATTTATGAACCGCATCAGGCACAGATAGAT 3630



Db 108 GTTGTTCACCTCTCTGTACTGGAGACATTAAGAACCTGGAGTGTGTTTGGTGCCAGC 167  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
Db 168 CTATTCTCTGCTCTCTCAATGACAGTATTACAGCATTTGAGCGTAACAGCCTACATTTGCC 227  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
Db 228 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 288 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGCTATATCT 347  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101  
Db 348 GAGGAGTTGGTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGCTGAAGTGCAGATAAG 407  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 408 GAACTCAGCGGCTCTCTTAGTTAGTGAATTTAGTTGATTTCTCTGAAGTTTGCAGTTTG 467  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 468 ATGTGGGTATTTACCTATGTTGGTGTCTGTTGTTTAAATGGTCTGACACTACTGATTTGGCT 527  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 528 CTCATTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587  
QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 588 TATCTAGGACTTGCATAAATGAAGTGTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 647  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 648 CTGGATTGAAGCGCAAAAGCTGAA 671

## RESULT 17

US-09-789-386-5  
; Sequence 5, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; TITLE OF INVENTION: PRINJHA, RABINDER KUMAR  
; FILE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1122  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-5

Alignment Scores:  
Pred. No.: 2,21e-106 Length: 1122  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-789-386-5 (1-1122)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 556 GTTGTTCACCTCTCTGTACTGGAGACATTAAGAACCTGGAGTGTGTTTGGTGCCAGC 615  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
Db 616 CTATTCTCTGCTCTCTCAATGACAGTATTACAGCATTTGAGCGTAACAGCCTACATTTGCC 675  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 676 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 736 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGCTATATCT 795  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101  
Db 796 GAGGAGTTGGTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGCTGACACTAGATAGAT 855  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 856 GAACTCAGCGGCTCTCTTAGTTAGTGAATTTAGTTGATTTCTCTGAAGTTTGCAGTTTG 915  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 916 ATGTGGGTATTTACCTATGTTGGTGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 975  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 976 CTCATTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035  
QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1036 TATCTAGGACTTGCATAAATGAAGTGTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 1095  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1096 CTGGATTGAAGCGCAAAAGCTGAA 1119

RESULT 18  
US-10-175-523-156  
; Sequence 156, Application US/10175523  
; Publication No. US20030096264A1  
; GENERAL INFORMATION:  
; APPLICANT: Brockman, Jeffrey  
; APPLICANT: Evans, David  
; APPLICANT: Hook, Derek  
; APPLICANT: Klimczak, Leszek  
; APPLICANT: Laeng, Pascal  
; APPLICANT: Palfreyman, Michael  
; APPLICANT: Rajan, Prithi  
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)  
; FILE REFERENCE: 3235/IJ795-US3  
; CURRENT APPLICATION NUMBER: US/10/175,523  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/299,151  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/317,828  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/325,150  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/333,047  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 60/349,936  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/361,834  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 156  
; LENGTH: 1160  
; TYPE: DNA

ORGANISM: Homo sapiens  
US-10-175-523-156

Alignment Scores:  
Pred. No.: 2,338-106 Length: 1160  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 14 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-175-523-156 (1-1160)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB GTTGTGACCTCCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 287  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB CTATTCTCTGCTGCTTTCATTGACAGTATTGACAGTATTGAGCGTAAACAGCCTACATTGCC 347  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 407  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 467  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB GAGGAGTTGGTTTCAGAACTACAGTAATCTGCTCTGTGTCATGTAAGCTGACGATAAAG 527  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121  
DB GAACCTACGCGCCTCTCTTGTAGTATGATTTAGTTGATCTCTGAACTTTGCAAGTGTG 587  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGTTCTGACACTACTGATTTGGCT 647  
QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB CTCATTTTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 707  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB TATCTAGGACTTGCATAATGAAGTGTAAAGATGCTATGGCTAAATAATCCAAGCAAAATC 767  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 768 CTGATTTGAAGCGCAAGCTGAA 791

## RESULT 19

US-10-956-157-4527  
; Sequence 4527, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4527  
; LENGTH: 1609  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4527

## Alignment Scores:

Pred. No.: 3,91e-106 Length: 1609  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-4527 (1-1609)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB GTTGTGACCTCCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 199  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB CTATTCTCTGCTGCTTTCATTGACAGTATTGACAGTATTGAGCGTAAACAGCCTACATTGCC 259  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 319  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 379  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB GAGGAGTTGGTTTCAGAACTACAGTAATCTGCTCTGTGTCATGTAAGCTGACGATAAAG 439  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121  
DB GAACCTACGCGCCTCTCTTGTAGTATGATTTAGTTGATCTCTGAACTTTGCAAGTGTG 499  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGTTCTGACACTACTGATTTGGCT 559  
QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB CTCATTTTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 619  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB TATCTAGGACTTGCATAATGAAGTGTAAAGATGCTATGGCTAAATAATCCAAGCAAAATC 679  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 680 CCTGGATTGAAGCGCAAGCTGAA 703

## RESULT 20

US-09-765-205-5  
; Sequence 5, Application US/09765205  
; Patent No. US20020034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1610  
; TYPE: DNA  
; ORGANISM: human  
US-09-765-205-5

## Alignment Scores:

Pred. No.: 3,91e-106 Length: 1610  
Score: 927.00 Matches: 188

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.57%	Indels:	0
DB:	9	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-765-205-5 (1-1610)

Qy	2	ValValAspLeuLeuTyrTrpAraGspIlleLysLysThrGlyValValPheGlyAlaSer	21
Db	687	GTWTTTGACCTCCTGTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCCAGC	746
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	747	CTATTCCTGCTGCTTCATTCAGACGTATTCAGCATTCGTGCGGTAAACAGCCTACATTGCC	806
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	807	TTGGCCCTGCTCTCTGTGACATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC	866
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	867	CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	926
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	927	GAGGAGTTGGTTTCAGAAAGTACAGTAAATTCCTCTGCTCATGTGTCACATCCAGATAAAG	986
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	987	GAACCTCAGGGCCCTCTCTTTAGTTGATGATTTAGTTGATTCCTCTGAAGTTTGCAGTGTTG	1046
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	1047	ATGTGGGTATTTACCTATGTTGGTGCCTCTGTTAAATGTCCTGACACACTGATTTTGGCT	1106
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	1107	CTCATTTTCACTCTTCAGTGTTCCTGTTATTATTTATGAACGGCATCAGGCACAGATAGATCAT	1166
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	1167	TATCTAGGACTTGCATAATAGATGTTTAAAGATGCTATGGCTAAATATCCAGGCANAAATC	1226
Qy	182	ProGlyLeuLysArgLysAlaGlu	189
Db	1227	CCTGGATTGAAGCGCAAGCTGAA	1250

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RESULT 21
US-10-347-669-5
; Sequence 5, Application US/10347669
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-10-347-669-5

Alignment Scores:
Pred. No.: 3,91e-106
Score: 927.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 99.57%
Matches: 188
Conservative: 0
Mismatches: 0
Indels: 0
Length: 1610

```

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-439-388-62 (1-1785)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 247 GTTGTGACCTCTGCTGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 306  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLysIleAla 41  
Db 307 CTATTCTCTGCTCTTTCATTGACAGTATTCAGCAATGTGAGCGTAAACAGCTTACATTGCC 366  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGCTATC 426  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 427 CAGAAATCAGATGAAGCCACCATTACGGGCATATCTGGAATCTGAAGTTGCTATATCT 486  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 487 GAGGAGTTGGTTTCAGAAGTACAGTAATCTCTGCTCTTGGTCATGTGAACCTGCACGATAAG 546  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 547 GAACCTCAGCGCCCTCTCTTCTAGTGTGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 606  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 607 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAATGGTCTGACACTACTGATTTGGCT 666  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 667 CTCATTTCACTCTTCAGTGTCTCTGTTTATGAACGGCATCAGGCACAGATAGATCAT 726  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 727 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAATC 786  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 787 CTGGATTGAAGCGCAAAAGCTGAA 810

## RESULT 23

US-10-956-157-1705  
; Sequence 1705, Application US/10956157  
; Publication No. US20050118625A1

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1705  
; LENGTH: 1785  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-1705

Alignment Scores:  
Pred. No.: 4.61e-106 Length: 1785  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-1705 (1-1785)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

Db 247 GTTGTGACCTCTCTGCTGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 306  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLysIleAla 41  
Db 307 CTATTCTCTGCTCTTTCATTGACAGTATTCAGCAATGTGAGCGTAAACAGCTTACATTGCC 366  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGCTATC 426  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 427 CAGAAATCAGATGAAGCCACCATTACGGGCATATCTGGAATCTGAAGTTGCTATATCT 486  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 487 GAGGAGTTGGTTTCAGAAGTACAGTAATCTCTGCTCTTGGTCATGTGAACCTGCACGATAAG 546  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 547 GAACCTCAGCGCCCTCTCTTCTAGTGTGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 606  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 607 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAATGGTCTGACACTACTGATTTGGCT 666  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 667 CTCATTTCACTCTTCAGTGTCTCTGTTTATGAACGGCATCAGGCACAGATAGATCAT 726  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 727 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAATC 786  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 787 CTGGATTGAAGCGCAAAAGCTGAA 810

## RESULT 24

US-10-956-157-4530  
; Sequence 4530, Application US/10956157  
; Publication No. US20050118625A1

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4530  
; LENGTH: 2050  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4530

Alignment Scores:  
Pred. No.: 5.74e-106 Length: 2050  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-4530 (1-2050)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

Db 622 GTTGTGACCTCTCTGCTGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 681







Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTATAGGATATACAAGGGTGTGATCCAAAGCTATC 876  
Qy 62 GlnlySerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 877 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGGAATCTGATATATCT 936  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 937 GAGGAGTTGGTTCAGAGGTACAGTAATCTCTGCTCTTGTGTCATGTGACCTGACAGATAAG 996  
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 997 GAACTCAGCGGCTCTCTCTAGTATGATTTAGTTAGTTCTCTGAAGTTGTCAGTGTG 1056  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 1057 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTGGCT 1116  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1117 CTCATTTTACCTTCAGTTCCTGTTTATATGAAACGGCATCAGGCACAGATAGATCAT 1176  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1177 TATCTAGGACTTGCATAAAGAACTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATC 1236  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1237 CCTGGATTGAAGCGCAAGCTGAA 1260

## RESULT 27

US-10-060-036-54

; Sequence 34, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yugu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; PRIOR FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 54

; LENGTH: 2235

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-060-036-54

Alignment Scores:  
Pred. No.: 6,588-106 Length: 2235  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 14 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-060-036-54 (1-2235)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 697 GTTGTGACCTCTGCTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 756  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThralaTyrIleAla 41  
Db 757 CTATTCTCTGCTCTTCTATTCAGAGTATTCAGCATTTGAGCGCTAACAGCCTACATTCGCC 816

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTATAGGATATACAAGGGTGTGATCCAAAGCTATC 876  
Qy 62 GlnlySerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 877 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGGAATCTGATATATCT 936  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 937 GAGGAGTTGGTTCAGAGGTACAGTAATCTCTGCTCTTGTGTCATGTGACCTGACAGATAAG 996  
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 997 GAACTCAGCGGCTCTCTCTAGTATGATTTAGTTAGTTCTCTGAAGTTGTCAGTGTG 1056  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 1057 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTGGCT 1116  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1117 CTCATTTTACCTTCAGTTCCTGTTTATATGAAACGGCATCAGGCACAGATAGATCAT 1176  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1177 TATCTAGGACTTGCATAAAGAACTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATC 1236  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1237 CCTGGATTGAAGCGCAAGCTGAA 1260

## RESULT 28

US-10-220-891-22

; Sequence 22, Application US/10220891

; Publication No. US20030207286A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWARA, AKIRA

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED

; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS

; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE

; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS

; FILE REFERENCE: 73888-73435

; CURRENT APPLICATION NUMBER: US/10/220,891

; CURRENT FILING DATE: 2003-03-07

; PRIOR APPLICATION NUMBER: JP 2000/140387

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: JP 2000/159195

; PRIOR FILING DATE: 2000-03-07

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 22

; LENGTH: 1980

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-220-891-22

Alignment Scores:  
Pred. No.: 3,181-105 Length: 1980  
Score: 921.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.93% Indels: 0  
DB: 17 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-220-891-22 (1-1980)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 1006 TCAGTGTGTGACCTCTGCTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCC 1065  
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThralaTyrIle 40

Db 1066 AGCTATTCCAGCTGCTTTCATTGACAGATTTTCAGCATTTGTCAGCGTAACAGCCTACATT 1125  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAGCT 1185  
QY 61 IleGlnLysSerAspGluCluYHisProPheArgAlaTyrIleGluSerGluValAlaIle 80  
Db 1186 ATCCAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 1245  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 1246 TCTGAGAGTGTGTTTCCAGAGTACAGTAATTCCTCTCTTGGTCATGTGAACTGCAGATA 1305  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 1306 AAGGAACCTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGGAGTTGTCAGTG 1365  
QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 1366 TTGATCTGGGTATTTACCTATGTTGTCGCTTGTGTTAAATGGTCTGCACACTACTGATTTTG 1425  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 1426 GCTCTCATTTCACTTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 1485  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1486 CATTATCTAGGACTTCGAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAACAAA 1545  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 1546 ATCCCTGGATTGAAGCGCAAAGCTGAA 1572

RESULT 29

US-09-978-360A-110  
; Sequence 110, Application US/09978360A  
; Publication No. US20040110939A1  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine  
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
; FILE REFERENCE: 56.US4.CIP  
; CURRENT APPLICATION NUMBER: US/09/978,360A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: US 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: US 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: US 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: US 60/099,273  
; PRIOR FILING DATE: -09-04  
; PRIOR APPLICATION NUMBER: US 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 09/215,435  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: PCT/IB98/02122  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: US 09/247,155  
; PRIOR FILING DATE: 1999-02-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 810  
; SOFTWARE: Patent.pm  
; SEQ ID NO 110  
; LENGTH: 994

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 35..631  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 35..160  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 8.6  
; OTHER INFORMATION: seq ASLFLLLSLTVFS/IV  
; FEATURE:  
; NAME/KEY: polyA\_signal  
; LOCATION: 901..906  
; FEATURE:  
; NAME/KEY: polyA\_site  
; LOCATION: 979..994  
US-09-978-360A-110  
Alignment Scores:  
Pred. No.: 2,49e-105 Length: 994  
Score: 918.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 98.60% Indels: 0  
DB: 11 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-978-360A-110 (1-994)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 68 GTTGTGACCTCTCTGTACTGGAGAGACATTAGAGACTGGAGTGGTGTGGTGGCAGC 127  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 128 CTATTCTCTGCTCTTCATTGACAGTATTTCAGCATTTGTCAGCGTAACAGCCTACATTGC 187  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
Db 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 247  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 248 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 307  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 308 GAGGAGTTGGTTTCCAGAAATACAGTAATTCCTCTCTTGGTCAATGTAACGATGCAAGTAAAG 367  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 368 GAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGAGTGTG 427  
QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 428 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTAAATGGTCTGCACACTACTGATTTGGCT 487  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 488 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 547  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 548 TATCTAGTACTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAACAAAATC 607  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 608 CTTGGATTGAGCGCAAAGCTGAA 631

RESULT 30

US-10-641-643-382  
; Sequence 382, Application US/10641643  
; Publication No. US20040077003A1

GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
Susan G. Stuart  
Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
GENE EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
FILING DATE: 14-Aug-2003  
APPLICATION NUMBER: US/10/641,643  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 382:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2610 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT14  
CLONE: 1508778  
SEQUENCE DESCRIPTION: SEQ ID NO: 382 :  
US-10-641-643-382  
Alignment Scores:  
Pred. No.: 3,688-104 Length: 2610  
Score: 914.00 Matches: 188  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 0  
Query Match: 98.17% Indels: 1  
DB: 18 Gaps: 0  
US-09-830-972-29\_copy\_990\_1178 (1-189) x US-10-641-643-382 (1-2610)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 1311 GTTGTGACCTCTCTGTTGAGGACATTAAGAGACTGGAGTGTGTGGTCCAGC 1370  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41  
Db 1371 CTATTCTCTGCTTTCATTGACATTTACGATTTGAGCGGTAAACAGCCTACAATTGC 1430  
Qy 41 aleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaI 61  
Db 1431 CTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTAT 1490  
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 1491 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATCTCGGAATCTGAAGTTGCTATATC 1550  
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIlely 101

Db 1551 TCAGGAGTTGGTTCAGAAAGTACAGTAATTCGTCTCTTGGTCAATGTGAACGACGATAA 1610  
Qy 101 sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValle 121  
Db 1611 GGAACCTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 1670  
Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl 141  
Db 1671 GATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGGTCTGCACACTACTGATTTGGC 1730  
Qy 141 aleuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
Db 1731 TCTCATTTCACTCTCTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1790  
Qy 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIl 181  
Db 1791 TTAICTAGGACTTGCATAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAT 1850  
Qy 181 eProGlyLeuLysArgLysAlaGlu 189  
Db 1851 CCCTGGGTGAAGCGCAAGCTGAA 1875  
RESULT 31  
US-09-893-348-17  
; Sequence 17, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US-  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 4684  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (253)..(3744)  
; OTHER INFORMATION:  
US-09-893-348-17  
Alignment Scores:  
Pred. No.: 5,318-103 Length: 4684  
Score: 508.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 97.53% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-29\_copy\_990\_1178 (1-189) x US-09-893-348-17 (1-4684)  
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 3175 TCAGTTGTGACCTCTCTGAGAGACATTAAGAGACTGGAGTGTGTGGTCC 3234  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3235 AGCTATTCTCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAACGGCCTACATT 3294

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGCT 3354  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3355 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGAAATCTCAAGTTGCTATA 3414  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 3415 TCAGAGGAATTTGGTTCAGAAATACAGTAATTTCTGCTCTTGGTCATGTGACACCAATA 3474  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3475 AAGAAGACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGTG 3534  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140  
DB 3535 TTGATGTGGGTGTTTACTTATGTGTGGTCTTGTTCATAGTGGTCTGACACTACTGATTTTA 3594  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 3595 GCTCTGATCTCACTCTCTCAGTATCTCTGTTATTTATGACGGCATCAGGTGCAGATAGT 3654  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3655 CATTATCTAGGACTTCGAAACAAGAGTGTAAAGGATGCCATGGCCAAAATCCAAGCAAAA 3714  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
DB 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741  
RESULT 32  
US-10-810-653-17  
; Sequence 17, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michel  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 4684  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (253)..(3744)  
; OTHER INFORMATION:  
US-10-810-653-17  
Alignment Scores:  
Pred. No.: 5,31e-103 Length: 4684  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 97.53% Indels: 0  
DB: 20 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-810-653-17 (1-4684)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3175 TCAGTTGTTGACCTCTCTACTTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC 3234  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3235 ACCTTATTCTCTGCTGCTCTCTGACAGTTCAGCATTTGTCAGTGTAAAGCGCCTACATT 3294  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGCT 3354  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3355 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGAAATCTCAAGTTGCTATA 3414  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 3415 TCAGAGGAATTTGGTTCAGAAATACAGTAATTTCTGCTCTTGGTCATGTGACACCAATA 3474  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3475 AAGAAGACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGTG 3534  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140  
DB 3535 TTGATGTGGGTGTTTACTTATGTGTGGTCTTGTTCATAGTGGTCTGACACTACTGATTTTA 3594  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 3595 GCTCTGATCTCACTCTCTCAGTATCTCTGTTATTTATGACGGCATCAGGTGCAGATAGT 3654  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3655 CATTATCTAGGACTTCGAAACAAGAGTGTAAAGGATGCCATGGCCAAAATCCAAGCAAAA 3714  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
DB 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741  
RESULT 33  
US-10-205-194-165  
; Sequence 165, Application US/10205194  
; Publication No. US20030134301A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Finnock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018201  
; CURRENT APPLICATION NUMBER: US/10/205,194  
; CURRENT FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 165  
; LENGTH: 2782  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Foccen-m2 reticulon  
US-10-205-194-165  
Alignment Scores:  
Pred. No.: 5,31e-103 Length: 4684  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3

Pred. No.: 5,57e-103 Length: 2782  
Score: 905.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 4  
Best Local Similarity: 96.83% Mismatches: 2  
Query Match: 97.21% Indels: 0  
DB: 15 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-205-194-165 (1-2782)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValValPheGlyAla 20  
Db 1271 GCAGTGTGTGACCTCTCTACTGGAGACATTAAGAAGACTGGAGTGTGTTGGTGCC 1330

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 1331 AGCTTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCCCTACATT 1390

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleYsThrGlyValIleGlnAla 60  
Db 1391 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGCATCCAGGCT 1450

Qy 61 IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 1451 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCCATATTTAGAAATCTGAAAGTTGCTATA 1510

Qy 81 SerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnCyseThrIle 100  
Db 1511 TCAGAGGAATTTGGTTTCAGAAATACAGTAATTTCTGCTTGTGTCATGTGAACAGCACATA 1570

Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuIysPheAlaVal 120  
Db 1571 AAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTTCCCTGAAGTTTGCAGTG 1630

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140  
Db 1631 TTGATGTGGTGTGTTACTTATGTGTTGTCCTTTGTTCAATGCTCTGACACTACTGATTTTA 1690

Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 1691 GCTCTGATCTCCTCTTCAGTATCTCTGTTATTTATGAAAGCCATCAGTGCAGATAGAT 1750

Qy 161 HistYrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1751 CATTTATCTAGACTTGCACAAACAGAGCTGTAAAGATGCGCATGCGCAAAATCCAAAGCAAA 1810

Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 1811 ATCCCTGGATTGAAGCGCAAGCAGAT 1837

RESULT 34  
US-10-267-502-214  
; Sequence 214, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 214  
; LENGTH: 3492  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-267-502-214

Alignment Scores:  
Pred. No.: 9,22e-103 Length: 3492  
Score: 904.50 Matches: 186  
Percent Similarity: 98.95% Conservatives: 2  
Best Local Similarity: 97.89% Mismatches: 1

Query Match: 97.15% Indels: 1  
DB: 18 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-267-502-214 (1-3492)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValVal---PheGly 19  
Db 2920 TCAGTTGTGACCTCTCTGCTACTGGAGACATTAAGAAGACTGGAGTGTGTTTGGT 2979

Qy 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
Db 2980 GCCAGCTTATTTCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCCCTAC 3039

Qy 40 IleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleYsThrGlyValIleGln 59  
Db 3040 ATTGCTTGGCCCTGCTCTCTGTCAGTATCAGCTTTAGGATATATAAGGTGTGATCCAA 3099

Qy 60 AlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79  
Db 3100 GCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCCATATTTGGAATCTGAAAGTTGCC 3159

Qy 80 IleSerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnCyseThr 99  
Db 3160 ATATCAGAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTTGTGTCATGTGAACAGCACA 3219

Qy 100 IleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAla 119  
Db 3220 ATAAAGAAATTTGAGCGCTCTCTCTTAGTTGATGATTTAGTTGATTTCCCTGAAGTTTGA 3279

Qy 120 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 139  
Db 3280 GTGTTGATGTGGTGTGTTTACTTACGTTGTCCTTGTTCATGTTGTTGACACTACTGATT 3339

Qy 140 LeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle 159  
Db 3340 TTACTCTGATCTCCTCTTCAGTATTTCTGTTATATATGAACGGCATCAGGCGCAGATA 3399

Qy 160 AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla 179  
Db 3400 GATCATTTATCTAGACTTGCACAAACAGAGCGTTAAGGATGCGTCCAAATCCAAAGCA 3459

Qy 180 LysIleProGlyLeuLysArgLysAlaGlu 189  
Db 3460 AAAATCCCTGGATTGAAGCGCAAGCAGAA 3489

RESULT 35  
US-10-466-258-10  
; Sequence 10, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 1798  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (215)..(814)  
US-10-466-258-10

Alignment Scores:  
Pred. No.: 6,98e-101 Length: 1798  
Score: 886.00 Matches: 187  
Percent Similarity: 98.94% Conservatives: 0  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 95.17% Indels: 2  
DB: 19 Gaps: 0

```
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-466-258-10 (1-1798)
QY 2 ValValAspLeuLeuThrTrpArgAspLeuLeuThrGlyValValPheGlyAlaSer 21
Db 248 GTTGTGACCTCTCTGTTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCAGC 307
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 308 CTAATCTGCTGCTCTCTCATTCAGAGTATTTCAGCAATGTGAGCGTAACAGCCTACATTGCC 367
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61
Db 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCAAGCTATC 427
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 428 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGGAATCTGCTATATCT 487
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 488 GAGGAGTGTGGTTTCAGAAATGACAGTAAATCTGCTCTTGGTTCATGTGAACCTGCACGATAAAG 547
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuPheAlaValLeu 121
Db 548 GAACCTCAGCGCGCTCTCTTAGTGTGATGATTTAGTGTGATTTCTGAAAGTTTCAGTGTG 607
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 608 ATGTGGGTATTACCTATGTTGGTGGCTGTTGTTTAAATGGTCTGACACTACTGATTTGGCT 667
QY 142 LeuIleSerLeu-PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161
Db 668 CTCAATTCACCTCTTCAGTGTTCCTGTTATTTA-GAAACGGCATCAGGCACAGATAGATCA 726
QY 161 sTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 727 TTATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAGCAAAAT 786
QY 181 eProGlyLeuLysArgLysAlaGlu 189
Db 787 CCTGTGATTGAAGCGCAAAAGCTGAA 811
RESULT 36
US-10-956-157-9765
; Sequence 9765, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9765
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9765
Alignment Scores:
Pred. No.: 2,75e-99 Length: 1400
Score: 872.00 Matches: 178
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.66% Indels: 0
DB: 21 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-9765 (1-1400)

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-823-245A-349 (1-1514)
QY 12 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 31
Db 2 AAGAAGACTGGAGTGGTGTGGTGCCAGCCTATTCTGCTGCTTTCATTGACAGATTTC 61
QY 32 SerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPhe 51
Db 62 AGCATTTGAGCGGTAAACAGCCTACATTGCTTGGCCCTGCTCTCTGTGACCATCAGCTTT 121
QY 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71
Db 122 AGGATATACAAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCCAG 181
QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91
Db 182 GCATATCTGGAATCTGAAAGTTGCTATATCTGAGGAGTGGTTTCAGAAATGACAGTAAATCT 241
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGlnLeuArgArgLeuPheLeuValAspAsp 111
Db 242 GCTCTTGGTTCATGTGAACCTGCACGATAAAGAACTCAGCGGCTCTCTTAGTGTGATGAT 301
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
Db 302 TTAGTGTGATTTCTCTGAAGTTTGCAGTGTGATGTGGTATTACCTATGTTGGTGGCTTG 361
QY 132 PheAsnGlyLeuThrLeuLeuIleLeuAlaIleSerLeuPheSerValProValIle 151
Db 362 TTATATGCTGTGACACTACTGATTTGGTCTCTCACTTCACTTCTCAGTGTTCCTGTATT 421
QY 152 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLys 171
Db 422 TATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATAAATAAGAAATGTTAAA 481
QY 172 AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189
Db 482 GATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAAAGCTGAA 535
RESULT 37
US-09-823-245A-349
; Sequence 349, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 349
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-349
Alignment Scores:
Pred. No.: 1.33e-98 Length: 1514
Score: 867.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.13% Indels: 0
DB: 9 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-823-245A-349 (1-1514)
```

QY 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSer 32  
DB 3 AAGACTGGAGTGGTGGTGGCCAGCCTATTCCTGCTGCTTCATTGACAGTATTCAGC 62  
QY 33 IleValSerValThrAlaTyrlleAlaLeuLeuLeuSerValThrIleSerPheArg 52  
DB 63 ATGTGTGAGCGTAACAGCCTACATTCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 122  
QY 53 IleTyrlsGlyValIleGlnAlaIleGlnIlySerAspGluGlyHisProPheArgAla 72  
DB 123 ATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCATTCAGGGCA 182  
QY 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnIlyTyrlsSerAsnSerAla 92  
DB 183 TATCTCGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAGTACAGTAATTCCTGT 242  
QY 93 LeuGlyHisValAsnCysThrIleGlySerGluLeuArgLeuPheLeuValAspLeu 112  
DB 243 CTGTGCTCATGTGAACGACGATAAAGAACTCAGCGCCTCTCTTAGTTGATGATTTA 302  
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132  
DB 303 GTTGATCTCTGAAGTTGACAGTGTGATGGGTATTTACCTATGTTGGTCCCTGTGTTT 362  
QY 133 AsnGlyLeuThrLeuLeuAlaLeuIleSerLeuPheSerValProValIleTyr 152  
DB 363 AATGCTCTGACACTACTGATTTGGCTCTCATTTCACTTCAGTGTTCCTGTTATTTAT 422  
QY 153 GluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172  
DB 423 GAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAATAAGAAATGTTAAAGAT 482  
QY 173 AlaMetAlaIleGlnAlaIlySerProGlyLeuLysArgLysAlaGlu 189  
DB 483 GCTATGGCTAAATCAAGCAAAAAATCCCTGGATTGAAGCGCAAGCTGAA 533

RESULT 38  
US-10-956-157-9762  
; Sequence 9762, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9762  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9762

Alignment Scores:  
Pred. No.: 7,88e-91 Length: 1400  
Score: 805.00 Matches: 164  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.47% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-9762 (1-1400)

QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeuAlaLeuLeu 45  
DB 3 CTTTCATTGACAGTATTCAGCATTTGAGCGTAAACAGGCTACATTCCTTGGCCCTGCTC 62  
QY 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65

DB 63 TCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122  
QY 66 GluGlyHisProPheArgAlaTyrlleuGluSerGluValAlaIleSerGluLeuVal 85  
DB 123 GAAGCCACCATTCAGGGCATATCTGGAATCTGAAGTGTCTATATCTGAGGAGTTGGTT 182  
QY 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105  
DB 183 CAGAAGTACAGTAATTCCTGCTTCTGTCATGTGAACTGCACGATAAAGAACTCAGGCGC 242  
QY 106 LeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
DB 243 CTCCTTAGTTCATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTGTGATGGGTATTT 302  
QY 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeu 145  
DB 303 ACCTATGTTGGTCCCTGTTTAACTGCTGACACTACTGATTTGGCTCTCATTTCACTC 362  
QY 146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165  
DB 363 TTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCATTTCTAGGACTT 422  
QY 166 AlaLeuLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
DB 423 GCAATAAGAATGTTAAAGATGCTATGGCTAAATCCAAGCAAAAAATCCCTGGATTGAAG 482  
QY 186 ArgLysAlaGlu 189  
DB 483 CGCAAGCTGAA 494

RESULT 39  
US-10-956-157-9767  
; Sequence 9767, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9767  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9767

Alignment Scores:  
Pred. No.: 7,88e-91 Length: 1400  
Score: 805.00 Matches: 164  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.47% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-9767 (1-1400)

QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeuAlaLeuLeu 45  
DB 3 CTTTCATTGACAGTATTCAGCATTTGAGCGTAAACAGGCTACATTCCTTGGCCCTGCTC 62  
QY 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
DB 63 TCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122  
QY 66 GluGlyHisProPheArgAlaTyrlleuGluSerGluValAlaIleSerGluLeuVal 85  
DB 123 GAAGCCACCATTCAGGGCATATCTGGAATCTGAAGTGTCTATATCTGAGGAGTTGGTT 182  
QY 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105



Db 183 CAGAAATACAGTAATTCCTCTTGGTCATGTGAACCTGCACGATATAAGAACTCAGGCCG 242  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 243 CTCCTCTTAGTTCAGATTTAGTTAGTCTCTGAAAGTTTGCAGTTTGCAGTTTGGGTATTT 302  
Qy 126 ThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuLeuLeuSerLeu 145  
Db 303 ACCTATGTTGGTGCCTTGTATTAATGCTCTGACACTACTGATTTGGCTCTCATTTCACTC 362  
Qy 146 PheSerValProValIleTyrgluArgHisGlnAlaGlnIleAspHisTyrluGlyLeu 165  
Db 363 TTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTT 422  
Qy 166 AlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 423 GCATAATAGAGTGTAAAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAG 482  
Qy 186 ArgLysAlaGlu 189  
Db 483 CGCAAGCTGAA 494

## RESULT 40

US-10-956-157-9766  
; Sequence 9766, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9766  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9766

Alignment Scores:  
Pred. No.: 7,56e-80 Length: 1400  
Score: 718.00 Matches: 144  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 77.12% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-9766 (1-1400)

Qy 46 SerValThrIleSerPheArgIleTyrlsGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 3 TCTGTGACCATCAGCTTTTAGGATATACAAAGGGTGTGATCCAGCTATCCAGAAATCAGAT 62  
Qy 66 GluGlyHisProPheArgAlaTyrlsGluSerGluValAlaIleSerGluGluLeuVal 85  
Db 63 GAAGGCCACCCATTCAGGCGCATCTCGAATCTCGAAGTTGCTATATCTCAGGAGTTGGTT 122  
Qy 86 GlnLysTyrsSerAsnSerAlaLeuGlyHisValAsnGlyThrIleLysGluLeuArgArg 105  
Db 123 CAGAAATACAGTAATTCCTCTTGGTCATGTGTAACCTGCACGATAAAGAACTCAGGCCG 182  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 183 CTCCTCTTAGTTCAGATTTAGTTAGTCTCTGAAAGTTTGCAGTTTGGGTATTT 242  
Qy 126 ThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuLeuLeuSerLeu 145  
Db 243 ACCTATGTTGGTGCCTTGTATTAATGCTCTGACACTACTGATTTGGCTCTCATTTCACTC 302

Qy 146 PheSerValProValIleTyrgluArgHisGlnAlaGlnIleAspHisTyrluGlyLeu 165  
Db 303 TTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTT 362  
Qy 166 AlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 363 GCATAATAGAGTGTAAAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAG 422  
Qy 186 ArgLysAlaGlu 189  
Db 423 CGCAAGCTGAA 434

## RESULT 41

US-09-960-352-8477  
; Sequence 8477, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 8477  
; LENGTH: 422  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 36-LIB34-048-Q1-E1-A8  
US-09-960-352-8477

Alignment Scores:  
Pred. No.: 9,06e-78 Length: 422  
Score: 695.00 Matches: 140  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 74.65% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-960-352-8477 (1-422)

Qy 37 ThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrlsGly 56  
Db 2 ACGGCTACATTCGCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGCT 61  
Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrluGluSer 76  
Db 62 GTGATCCAGGCTATCCAGAAATCTCATGAAGGCCACCCATTCAGGCGCATTTTGGAACT 121  
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyrsSerAsnSerAlaLeuGlyHisVal 96  
Db 122 GAAGTTGCTATATCTCAGGAGTTGCTTCAAGACTACAGCAATCTGCTCTTGGTCATGT 181  
Qy 97 AsnGlyThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeu 116  
Db 182 AACTGCACAATAAAGAACTCAGACGCTCTCTTGTAGTTGATGATTTAGTTGATTTCTG 241  
Qy 117 LysPheAlaValLeuMetTrpValPheThrTyrlsGlyValGlyAlaLeuPheAsnGlyLeuThr 136  
Db 242 AAGTTGTCAGTGTGATGTTGGGTATTTACCTATGTTGGTGCCTTGTTCATGCTCGACA 301  
Qy 137 LeuLeuLeuLeuLeuLeuLeuSerLeuPheSerValProValIleTyrgluArgHisGln 156  
Db 302 CTACTAATTTGGCTCTGATTTCACTTTCAGTGTTCCTGTTATTTATCAACGCGCATCAG 361  
Qy 157 AlaGlnIleAspHisTyrluGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 176  
Db 362 GCGCAATAGATCATTTCTGGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCTAAA 421

## RESULT 42



US-10-084-817-333  
; Sequence 333, Application US/10084817  
; Publication No. US20030119009A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan Stuart  
; APPLICANT: Jed G. Nuchtern  
; APPLICANT: Sharon E. Plon  
; APPLICANT: Jason M. Shohet  
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
; FILE REFERENCE: PA-0046 US  
; CURRENT APPLICATION NUMBER: US/10/084,817  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/270,784  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 365  
; SOFTWARE: PERL Program  
; SEQ ID NO 333  
; LENGTH: 1520  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030119009A1 092267CBI  
US-10-084-817-333

Alignment Scores:  
Pred. No.: 3,01e-75 Length: 1520  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 15 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-084-817-333 (1-1520)

QY	3	ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu	22
DB	176	ATTGACCTCTGTATTGGCGGACATCAAGCAGACGGGCATCGTGTGGAGTTTCCTG	235
QY	23	PheLeuLeuLeuSerLeuThrValPheSerIleValSerLeuThrAlaTyrIleAlaLeu	42
DB	236	CTGCTGCTCTTCCTCCGTACCCAGTTCCAGCGTGGAGCGTCTACCTGGCCCTG	295
QY	43	AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln	62
DB	296	GCAGCACTTCAGCCACCATCAGTTTCGGCATCTACAGTCTGTTTACAGCAGTGCAG	355
QY	63	LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu	82
DB	356	AAACCGAGCAAGGCCACCCTTTCAAGCCCTACTTTGGAGCTTGAGATCACCTTTCTCAG	415
QY	83	GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu	102
DB	416	GAGCAGATTCAAGATACAGGACCTGCCTGCAGCTTCTACGTGAACACACACTTAAGGAA	475
QY	103	LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet	122
DB	476	CTGAGAGGCTCTTCTTGTTCAGACCTGGTGGATCTCTTAAATTTGAGTCTCTGATG	535
QY	123	TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu	142
DB	536	TGCTCTCCACCTACGTTGGCGCTCTCTTCAATGSCCTGACCCCTGCTCATGGCTGTG	595
QY	143	IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr	162
DB	596	GTTTCAATGTTTACTCTACTCTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT	655
QY	163	LeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIlePro	182
DB	656	CTGGAGCTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA	715
QY	183	GlyLeuLysArgLysAlaGlu	189

US-09-954-456-210

RESULT 44  
US-09-954-456-210

```
; Sequence 210, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-954-456-210

Alignment Scores:
Pred. No.:          9.8e-75          Length:          3202
Score:             682.00          Matches:         128
Percent Similarity: 85.03%          Conservative:    31
Best Local Similarity: 68.45%          Mismatches:     28
Query Match:       73.25%          Indels:         0
DB:                9              Gaps:            0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-954-456-210 (1-3202)
QY      3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db      1890 ATTGACCTGTTGATTGGCGGACATCAAGCAGCGGCGATCGTGTGGAGTTTCCTG 1949
QY      23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db      1950 CTGCTGCTCTTCTCCCTGACCCAGTTACCGTGTGAGCGTCTGCTGCGCTACCTGGCCCTG 2009
QY      43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
Db      2010 GCCGCACTCTCAGCCACCACATCAGTTTCCGCATCTACAAGTCTGTTTACAAGCAGTGCAG 2069
QY      63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db      2070 AAAACCGAGAGGCGCCCTTTCAAGGCTACTTGGAGCTTGAAGATCAACCTTTCTCAG 2129
QY      83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
Db      2130 GAGCAGATTCAAGATACAGGACTCCCTGCGAGTCTAGTCTGACAGACACTTAAGGAA 2189
QY      103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db      2190 CTGAGGAGGCTCTTCTTCTTCAGGACCTGTGGTTCCTTAAATTTTCAAGTCTCTGAG 2249
QY      123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAlaLeu 142
Db      1230 GAGCAGATTCAAGATACAGGACTCCCTGCGAGTCTAGTCTGACAGACACTTAAGGAA 2189

; Sequence 210, Application US/10172118
; Patent No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 386
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L10333
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-386

Alignment Scores:
Pred. No.:          9.8e-75          Length:          3202
Score:             682.00          Matches:         128
Percent Similarity: 85.03%          Conservative:    31
Best Local Similarity: 68.45%          Mismatches:     28
Query Match:       73.25%          Indels:         0
DB:                17              Gaps:            0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-172-118-386 (1-3202)
QY      3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db      1890 ATTGACCTGTTGATTGGCGGACATCAAGCAGCGGCGATCGTGTGGAGTTTCCTG 1949
QY      23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db      1950 CTGCTGCTCTTCTCCCTGACCCAGTTACCGTGTGAGCGTCTGCTGCGCTACCTGGCCCTG 2009
QY      43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
Db      2010 GCCGCACTCTCAGCCACCACATCAGTTTCCGCATCTACAAGTCTGTTTACAAGCAGTGCAG 2069
QY      63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db      2070 AAAACCGAGAGGCGCCCTTTCAAGGCTACTTGGAGCTTGAAGATCAACCTTTCTCAG 2129
QY      83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
Db      2130 GAGCAGATTCAAGATACAGGACTCCCTGCGAGTCTAGTCTGACAGACACTTAAGGAA 2189
QY      103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db      2190 CTGAGGAGGCTCTTCTTCTTCAGGACCTGTGGTTCCTTAAATTTTCAAGTCTCTGAG 2249
QY      123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAlaLeu 142
Db      1230 GAGCAGATTCAAGATACAGGACTCCCTGCGAGTCTAGTCTGACAGACACTTAAGGAA 2189
```

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuValPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGCTGGATTCCTTAAATTTGACGCTCTGATG 2249  
QY 123 TrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
Db 2250 TGGCTCTGACCTAGCTGGGCGCTCTCTCAATGGCCTGACCTCTGCTGCTGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHisTyrr 162  
Db 2310 GTTTCATGTTTACTCTACCTAGTGTATGTTAGCAGCCAGGACACAGTTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGCTAAGAGGACGCTGAG 2450

## RESULT 46

US-10-342-887-386  
; Sequence 386, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 60/380,710  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 386  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-386

Alignment Scores:  
Pred. No.: 9.8e-75 Length: 3202  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 0 Indels: 0  
Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-342-887-386 (1-3202)

QY 3 ValAspLeuLeuTyrrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCGTGTGTTGGAGTTCTCTG 1949  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAlaLeu 42  
Db 1950 CTGCTGCTCTCTCTCCCTGACCCAGTTTCAGCGGTGGAGCGTCTGCTGCTGCTGCTG 2009  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCCGCACTCTCAGCCACCATCATGTTTCGCGCATCTACAAGTCTGTGTTTACAAGCAGTGCG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSerGlu 82

Db 2070 AAAACCCGACGAAGGCCACCCTTTCAAGGCCTACTTTGGAGCTTGAGATCACCCCTTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnCythrIleLysGlu 102  
Db 2130 GAGCAGATTCTCAGAGTACACGAGCTGCTGAGTTCTACGTTGACGTAACAGACACTTAAGGAA 2189  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGCTGGATTCCTTAAATTTGACGCTCTGATG 2249  
QY 123 TrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
Db 2250 TGGCTCTGACCTAGCTGGGCGCTCTCTCAATGGCCTGACCTCTGCTGCTGCTGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHisTyrr 162  
Db 2310 GTTTCATGTTTACTCTACCTAGTGTATGTTAGCAGCCAGGACACAGTTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGCTAAGAGGACGCTGAG 2450

## RESULT 47

US-10-723-860-1480  
; Sequence 1480, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Nataasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1480  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-1480

Alignment Scores:  
Pred. No.: 9.8e-75 Length: 3202  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 0 Indels: 0  
Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-723-860-1480 (1-3202)

QY 3 ValAspLeuLeuTyrrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCGTGTGTTGGAGTTCTCTG 1949  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAlaLeu 42  
Db 1950 CTGCTGCTCTCTCTCCCTGACCCAGTTTCAGCGGTGGAGCGTCTGCTGCTGCTGCTG 2009  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCCGCACTCTCAGCCACCATCATGTTTCGCGCATCTACAAGTCTGTGTTTACAAGCAGTGCG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSerGlu 82

Db 2070 AAAACCGAGAGGCGACCCCTTTCAGGCTTACTTGAGCTTGAGATCAACCTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GAGCAGATTGAGAGTACAGGACTCCCTGCAGTTCTACGTGAAACAGCACACTTAAGGAA 2189  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTTCCTGTCAGGACCTGGTGGATTCCTTAAATTTTCAGTCCCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLysAlaLeu 142  
Db 2250 TGCTCCTGACCTACCTGCTGCTCTTCAATAGGCTGACCTGCTGCTCAGGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
Db 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGCACAGATTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGCTAAGAGGACGCTGAG 2450

## RESULT 48

US-10-843-641A-3237  
; Sequence 3237, Application US/10843641A  
; Publication No. US20050064454A1  
; GENERAL INFORMATION:  
; APPLICANT: Avalon Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
; TITLE OF INVENTION: Signature Gene Sets  
; FILE REFERENCE: 689290-189  
; CURRENT APPLICATION NUMBER: US/10/843,641A  
; CURRENT FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: US/09/873,367  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US/09/954,531  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/09/954,456  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,436  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,832  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/964,824  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/09/967,768  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US/09/968,007  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,347  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,708  
; PRIOR FILING DATE: 2001-10-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 8447  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3237  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-843-641A-3237

Alignment Scores:  
Pred. No.: 9.8e-75 Length: 3202  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0

DB: 21 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-843-641A-3237 (1-3202)  
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTTGATTGGCGGACATCAAGCAGACGGGCATCGTGTGTTGGAGATTTCCTG 1949  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 1950 CTGCTGCTCTTCTCCCTGACCTACCCAGTTACGCTGGTGGAGCGTCTGCTGCTGCTGCTG 2009  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCGGCACCTCTCAGCCACCATCATGTTCCGATCTCAAGTCTGTTTACAGCAGTGGCAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGAGAGGCGACCCCTTTCAGGCTTACTTGGAGCTTGAGATCACCCCTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GAGCAGATTGAGAGTACAGGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2189  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTTCCTGTCAGGACCTGGTGGATTCCTTAAATTTTCAGTCCCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLysAlaLeu 142  
Db 2250 TGCTCCTGACCTACCTGCTGCTGCTCTTCAATAGGCTGACCTGCTGCTGCTGCTGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
Db 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGCACAGATTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGCTAAGAGGACGCTGAG 2450  
RESULT 49  
US-10-723-860-5926  
; Sequence 5926, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5926  
; LENGTH: 3305  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-5926  
Alignment Scores:  
Pred. No.: 1.03e-74 Length: 3305  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0

```

DB:                20                Gaps:                0
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-723-860-5926 (1-3305)
QY      3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
DB      1890 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGACGGGATGCTGTTGGAGATTCTCTG 1949
QY      23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB      1950 CTGCTGCTCTCTCTCCCTGACCCAGTTACGCTGGGAGGCTGCTGGCCCTTACCTGGCCCTG 2009
QY      43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
DB      2010 GCGGACCTCTCAGCCACCATCAGTTTCCGCATCTACAGTCTGTTTACAGCAGTGCAG 2069
QY      63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
DB      2070 AAACCCGAGGAGGACCCCTTTCAAGGCTTACTTTGGAGCTTGAGATCACCCCTTTCTCAG 2129
QY      83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
DB      2130 GAGCAGATTCAGAGTACAGGACTGCTGCTGAGTCTACGTGAACAGCACACTTAAAGAA 2189
QY      103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
DB      2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGCTGGTGGATTCCTTAAATTTGCAGTCTGATG 2249
QY      123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
DB      2250 TGGCTCCTCAGCTAGCTGTTGGGCTCTCTTCAATGGCTGACCTGCTGCTGCTGCTGCTG 2309
QY      143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
DB      2310 GTTTCATGTTTACTCTACCTGATGTATGTAAGCACCAGCAGCAGATTCACCAATAT 2369
QY      163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
DB      2370 CTGGGACTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTCAGGCTAAATCCCA 2429
QY      183 GlyLeuLysArgLysAlaGlu 189
DB      2430 GCGCGTAAGAGGACCGCTGAG 2450

RESULT 50
US-10-205-219-94
; Sequence 94, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Allstair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: rS-Rex-s
US-10-205-219-94
Alignment Scores:
Pred. No.:          3,968-75          Length:          1502
Score:              681.00          Matches:          127

```

```

Percent Similarity: 85.03%      Conservative: 32
Best Local Similarity: 73.91%    Mismatches: 28
Query Match: 73.15%             Indels: 0
DB: 15                           Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-205-219-94 (1-1502)
QY      3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
DB      179 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGACGGGATGCTGTTGGAGATTCTCTG 238
QY      23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB      239 CTGCTGCTCTCTCTCCCTGACCCAGTTACGCTGGGAGGCTGCTGGCCCTTACCTGGCCCTG 298
QY      43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
DB      299 GCTGCCCTCTCTGCCACCATCAGCTTCCGCATCTACAAGTCCGTTCTACAAGCTGTGCAG 358
QY      63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
DB      359 AAACAGATGAGGTCACCCCTTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTCCCGAG 418
QY      83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
DB      419 GAGCAGATTCAGAGTACAGGACTGCTGCTGAGCTATACGTGAACAGCACACTTGAAGGAG 478
QY      103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
DB      479 CTAGGAGGCTCTCTCTGTCAGGACCTGGTGGATTCCTTAAATTTGCAGTCTCTCATG 538
QY      123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
DB      539 TGGCTCCTGACTAGTGGGCGCACTCTCAATGGCCTGACCTGCTGCTTATGCTGTG 598
QY      143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
DB      599 GTTTCGATGTTTACTCTACCTGCTGATATGTTAAGCACCAGGACACAGTTGACCAATAT 658
QY      163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
DB      659 CTGGGACTGTGAGGACTCACATAAACACCCGTTGTGGCAAGATTCAGGCTAAATCCCC 718
QY      183 GlyLeuLysArgLysAlaGlu 189
DB      719 GCGCGTAAGAGGACCGCTGAG 739

RESULT 51
US-10-267-502-215
; Sequence 215, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Galant, Ron
; APPLICANT: Kim, Jaeseob
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-267-502-215
Alignment Scores:
Pred. No.:          8e-75          Length:          2343
Score:              681.00          Matches:          127
Percent Similarity: 85.03%      Conservative: 32
Best Local Similarity: 73.91%    Mismatches: 28
Query Match: 73.15%             Indels: 0
DB: 18                           Gaps: 0

```

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US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-11567 (1-422)

Qy    21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40
Db    4 AACTTGTTCCTGCTCTCGCTGCAGAGTATTGACCAATTTGGAGCTGTAAACGCCCTACATT 63
Qy    41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAla 60
Db    64 GCCTTGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGGTGTGATCCAGGCT 123
Qy    61 IleGlnIysSerAspGluGlyHisProPheArgAlaTyrlleuGluSerGluValAlaIle 80
Db    124 ATCCAGAAATCTCATGAAGCCACCCTATTGAGGCATATTTGGAAATCTGAAGTTGCTATA 183
Qy    81 SerGluGluLeuValGlnLysTyrlsSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db    184 TCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCCTGCTCTTGGTCATGTTAAGTTCGACAATA 243
Qy    101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValaspSerLeuLysPheAlaVal 120
Db    244 AAAGAACCTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 303
Qy    121 LeuMetTrpValPheThrTyrlsValGlyValAlaIleuPheAsnGlyLeuThrLeuLeuLeu 140
Db    304 TTGATGTGGGTATTTTACCTATGTGTGGTGCCTTGTTCATGGTCTGACACACTACTAATTTTG 363
Qy    141 AlaLeuIleSerLeuPheSerValProValIleTyrlsGluArgHisGlnAlaGlnIle 159
Db    364 GCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGNACGGCATCAGCGCAAATA 420

RESULT 53
US-10-205-194-128
; Sequence 128, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brokebank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: C1-13 protein
US-10-205-194-128

Alignment Scores:
Pred. No.:      4,01e-73      Length:      1473
Score:          665.00       Matches:     127
Percent Similarity: 85.03%   Conservative: 32
Best Local Similarity: 67.91% Mismatches:     28
Query Match:     71.43%     Indels:       1
DB:              15         Gaps:        0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-205-194-128 (1-1473)

Qy    3 ValAspLeuLeuTyrlsArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db    146 ATTGACCTTCTGTACTGGCGGACATCAAGCAGACGGGATTTGTTTCGGGAGCTTCCTG 205
Qy    23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeu 42
Db    206 CTGCTGCTCTTCTCCCTGACCAGTTGACGCTTGTGACGCTGCTGCTACCTGCGCCCTG 265

```

Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
|||  
Db 266 GCTGCCCTCTCGCCACCATCAGCTTCGCATCTACAGTCGTTCTACAGCTGGCAG 325  
|||  
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
|||  
Db 326 AAAACAGATGAGGGTCACCTTTTCAAGGCTACCTGGAGCTGAGATCACCTGTCCCG 385  
|||  
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
|||  
Db 386 GAGCAGATCCAGAGTACAGACTGCTGCAGCTATAGTGAACAGACACTCTGAGGAG 445  
|||  
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
|||  
Db 446 CTACGAGGCTCTCTCTGTCACAGACCTAGTGGATTCCTAAATTTGACGTCCTCATG 505  
|||  
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
|||  
Db 506 TGGCTCTGACCTAGCTGTTGGCGCACTCTTCAATGGCTGACCTGCTGCTATGGCTGTG 565  
|||  
Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
|||  
Db 566 GTTTCGATGTTTACTCTCTGTTGATATGTTAAGCACCAGGACAGGTTGACCAATAT 625  
|||  
Qy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
|||  
Db 626 CTGGGACTTGTGAGGACTCACATAACACCGTTGTGGCAGATCCAGGCTAANAATCCCC 685  
|||  
Qy 183 GlyLeuLysArgLysAlaGlu 189  
|||  
Db 686 GCGCG-AAGAGGCGATGCTGAG 705  
|||

## RESULT 54

US-10-408-967-1  
; Sequence 1, Application US/10408967  
; Publication No. US20040063161A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia & Upjohn Company  
; APPLICANT: Yan, Riqiang  
; APPLICANT: Lu, Yifeng  
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease  
; FILE REFERENCE: 00925  
; CURRENT APPLICATION NUMBER: US/10/408,967  
; CURRENT FILING DATE: 2003-04-08  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-408-967-1

## Alignment Scores:

Pred. No.:	1,646-68	Length:	711
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	18	Gaps:	1

US-09-830-972-29\_copy\_990\_1178 (1-189) x US-10-408-967-1 (1-711)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
|||  
Db 139 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 198  
|||  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
|||  
Db 199 ACGTGTATCATCTGCTTCCCTGGCAGCTTTCAGTGTGATCAGTGTGTTCTTACCTC 258  
|||  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
|||

Db 259 ATCTGGCTCTTCTCTGTCCACCATCAGCTTCCAGGATCTACAGTCCGTCATCCAAAGCT 318  
|||  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
|||  
Db 319 GTACAGAAGTCAAGAAGAGGCCATCCATTCAAAGCTACCTGGAGCTAGACATTACTCTG 378  
|||  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
|||  
Db 379 TCCTCAGAAGCTTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTG 438  
|||  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
|||  
Db 439 AAACATCATTTATTCGCTCTTTCTGTGTAAGAAGATCTGTTGACTCTCCTTGAAGCTGGCTGC 498  
|||  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
|||  
Db 499 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTTTAACGGAAATCACCTTCTTAATCTT 558  
|||  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
|||  
Db 559 GCTGAACCTGCTCATTTTCAGTGTCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 618  
|||  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
|||  
Db 619 CACTATGTTGGCATGCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAAGCAAAA 678  
|||  
Qy 181 IleProGlyLeu--LysArgLysAlaGlu 189  
|||  
Db 679 CTCCTCGAATGCTGCCAAAAAAGGCAGAA 708  
|||

## RESULT 55

US-10-106-698-1945  
; Sequence 1945, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 1945  
; LENGTH: 1330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-106-698-1945

## Alignment Scores:

Pred. No.:	4,426-68	Length:	1330
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	15	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-106-698-1945 (1-1330)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
|||  
Db 297 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 356  
|||  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
|||  
Db 357 ACGTGTATCATCTGCTTCCCTGGCAGCTTTCAGTGTGATCAGTGTGTTCTTACCTC 416  
|||  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
|||



Db 417 ATCTGGCTCTTCTCTCTGTACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 476  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 477 GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 536  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 537 TCCTCAGAAGCTTTCATTAATTACATGAATGCTGCCATGCTGCACATCAACAGGGCCCTG 596  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 597 AAATCATATTCTCTCTCTCTGTGAGAGATCTGCTGACCTCTGAGCTGGCTGTC 656  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 657 TTCATGTGGTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTTCTAATTCCT 716  
QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 717 GCTGAACCTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTACCAAGACCCAGATTGAT 776  
QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 777 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAAGCAAA 836  
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db 837 CTCCTCGGAATCGCCAAAGGCGAGAA 866

## RESULT 56

US-09-729-674-19  
; Sequence 19, Application US/09729674  
; Patent No. US2001003935A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steininger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 6055-64X  
; CURRENT APPLICATION NUMBER: US/09/729,674  
; CURRENT FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 09/539,330  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 1656  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-729-674-19

## Alignment Scores:

Pred. No.:	6,26e-68	Length:	1656
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	9	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-729-674-19 (1-1656)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 165 GGGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTCTTTCGGCACC 224  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 225 AGCTGATCATCTGCTTCTCTGTCCAGCTTTCAGTGTCTCAGTGTCTCAGTGTGTTCTTACCTC 284  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 285 ATCTGGCTCTTCTCTGTCCATCAGCTTTCAGATCTCAAGTCCGTCCTCAAGCT 344  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 345 GTACAGAAGTCAGAAGAGGCCATCCATTTCAAAGCCTACCTGGACGTAGACATTACTCTG 404  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 405 TCCTCAGAAGCTTTCATTAATTACATGAATGCTGCCATGTGTCACATCAACAGGGCCCTG 464  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 465 AAATCATATTCTCTCTCTGTGAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 524  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 525 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTTTAAACGGAATCACCTTCTAATTCCT 584  
QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 585 GCTGAACCTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTCAAGACCCAGATTGAT 644  
QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 645 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAAGCAAA 704  
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
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RESULT 57  
US-10-913-553-19  
; Sequence 19, Application US/10913553  
; Publication No. US20050003491A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steininger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 6055-64X  
; CURRENT APPLICATION NUMBER: US/10/913,553  
; CURRENT FILING DATE: 2004-08-09  
; PRIOR APPLICATION NUMBER: US/09/539,330  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 1656  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-913-553-19





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Query Match: 67.08% Indels: 1
DB: 21 Gaps: 1
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QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 237 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 346
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 347 ACCTGATCATGCTGCTTCTCCCTGGCAGCTTTCAAGTGTCACTAGTGTGGTTTCTTACCTTC 406
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 407 ATCTGGCTCTCTCTCTGTCCATCAGCTTCAGGATCTACCAAGTCCGTCATCCAAGCT 466
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 467 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTTACCTGGAGCTAGACATTACTCTG 526
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 527 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCAATCAACAGGGCCCTG 586
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB 587 AAACATCATATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTC 646
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 647 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCCTTCTAATTCTT 706
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 707 GCTGAACCTGCTCATTTTCAGTGTCCGATTTGTATGAGAAGTACCAAGCCAGATTGAT 766
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 767 CACTATGTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCACGCAAAA 826
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
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; Sequence 254, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-809-391-254 (1-1766)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 237 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 296
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 297 ACCTGATCATGCTGCTTCCCTGGCAGCTTTCAAGTGTCACTAGTGTGGTTTCTTACCTTC 356
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 357 ATCTGGCTCTCTCTCTGTCCATCAGCTTCAGGATCTACCAAGTCCGTCATCCAAGCT 416
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 417 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTTACCTGGAGCTAGACATTACTCTG 476
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 477 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCAATCAACAGGGCCCTG 536
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB 537 AAACATCATATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTC 596
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 597 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCCTTCTAATTCTT 656
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DB 657 GCTGAACCTGCTCATTTTCAGTGTCCGATTTGTATGAGAAGTACCAAGCCAGATTGAT 716
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 717 CACTATGTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCACGCAAAA 776
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US-09-809-391-254
; Sequence 254, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 254
; LENGTH: 1766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-254
Alignment Scores:
Pred. No.: 6,93e-68 Length: 1766
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 10 Gaps: 1
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-809-391-254 (1-1766)
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; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

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Alignment Scores:	
Pred. No.:	6,93e-68
Score:	624.50
Percent Similarity:	81.05%
Best Local Similarity:	60.53%
Query Match:	67.08%
DB:	10
	1
	Gaps:
	1
	Indels:
	67.08%
	Mismatches:
	35
	Conservative:
	39
	Matches:
	115
	Length:
	1766

US-09-830-972-29 COPY 990 1178 (1-189) x US-09-882-171-254 (1-1766)

Qy		1	SerValValAspLeuLeuTyrTrpArgaspIleLysThrGlyValValPheGlyAla	20
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Qy		21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRile	40
Dd		347	ACGCTGATCATGCTGCTTCCCTGCCAGCTTTCAGTGTCACTAGTGTGGTTCCTTAACCTC	406
Qy		41	AlaLeuAlaLeuLeuSerValThrIleSerPhearglleTyRlysGlyVallieGlnAla	60
Dd		407	ATCCTGGCTCTTCTCTGTCAACCATCAGCTTCAGGATCTACAAGTCCGTCAATCCAAGCT	466
Qy		61	IleGlnLysSerAspGluClYHisProPhearglalyTyRLeuGluSerGluValAlaAlle	80
Dd		467	GTACAGAAGTCAGAGAAGGCCATTCCATTCAAAGCCTACTCTGGACGTGACACANTTACTCTG	526
Qy		81	SerGluGluLeuValGlnLysTyRSerAsnSerAlaLeuGlyHisValAasnCystrHille	100
Dd		527	TCTCAGAAGCTTTCATAATTACATGAATGCTGCCATGGTGACACATCAACAGGGCCCTG	586
Qy		101	LysGluLeuArgLeuPheLeuValAspAspleuValAspSerLeuLysPheAlaVal	120
Dd		587	AACACTATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGATCTCTTGAAGCTGGCTGTC	646
Qy		121	LeuMetTrpValPheThrTyRValGlyAlaLeuPheAnGlyLeuThrLeuLeulleLeu	140
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Qy		141	AlaLeuilleSerLeuPheSerValProValIleTyRGluArgHisGlnAlaGlnIleAsp	160
Dd		707	GCTGAACCTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTAGTCAAGAAGCCAGATTGAT	766
Qy		161	HisTyRLeuGluLeualaasnlYsaSnValLysaspAlaMetAlaLySilleGlnAlaLys	180
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Db      827  CTCCTCGGATCGCCAAAAAAGGCAGAA  856
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US-10-164-861-254
; Sequence 254, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted protein
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 254
; LENGTH: 1766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-164-861-254

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Alignment Scores:	
Pred. No.:	6,93e-68
Score:	624.50
Percent Similarity:	81.05%
Best Local Similarity:	60.53%
Query Match:	67.08%
DB:	17
Length:	1766
Matches:	115
Conservative:	39
Mismatches:	35
Indels:	1
Gaps:	1

US-09-830-972-29 COPY 990 1178 (1-189) x US-10-164-861-254 (1-1766)

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	Qy	21	SerLeuLeuLeuSerLeuThrValPheSerIleValSerValThraLaTrVrile	40
	Dd	347	ACGCTGAATCAGTCGTCTCCCTGGCACGCTTCAAGTGATCAGTGGTGTTTCTTACCTC	406
	Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIIeTyTLysGlyValIleGlnAla	60
	Dd	407	ATCCCTGGCTCTCTCTGTGCCAATCAGCTTCAGGATCTACAAGTCGCTCATCCAAGCT	466
	Qy	61	IleGlnIysSerAspGluGlyHiiProPheArgAlaTyTLeuGluSerGluValalaIle	80
	Dd	467	GTAAGAAGTCAGAAGAAGGCCATTCAAAGGCTACCTGGAGTAGATACTCTG	526
	Qy	81	SerGluGluLeuValGlnLytySeraasnSerAlaLeuGlyHisValasnCystThrIle	100
	Dd	527	TCCTCAGAAGCTTCCATAATTACATGAATGCTGCCATGTGCACATCAACAGGGCCCCTG	586
	Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuIlysPheaLav	120
	Dd	587	AACCTCATATTCTGTCCTCTTCGTAGAAGATCTGGTTGACTCTCTGAAGCTGGCTGTC	646
	Qy	121	LeuMetTrpValPheThrtYrvAlglyAlaLeuPheAsnGlyLeuThrLeuleulleLeu	140
	Dd	647	TTCATGTGGCTGATGACCTATGTGTGGTGCTGTTTTAAACGGTAATCACCCTCTTAATCTTT	706
	Qy	141	AlaleuilleSerLeuPheSerValprovalIletyrGluarGHiacslnaalaglinilleASP	160
	Dd	707	GCTGAACCTGCTCATTTTCAGTGTCCTCCGATGTCTATGAGAAGTACAAGACCAGATIGAT	766
	Qy	161	HistyrLeuGlyLeualaasnlYsaasnValIylsAspAlaMetaIalsilyleGlnAlalyis	180
	Dd	767	CACATATGTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGAAAAGATCCAACGAAAA	826
	Qy	181	IleProGlyLeu---LysArgIylsalagLu	189
	Dd	827	CTCCCTCGAATCGCCAAAIAAAAAAAAAAGGCAGAA	856

## RESULT 63

US-10-276-774-980  
; Sequence 980, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; PRIORITY FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIORITY FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIORITY FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 980  
; LENGTH: 1915  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-980

## Alignment Scores:

Pred. No.:	7,87e-68	Length:	1915
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	18	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-276-774-980 (1-1915)

Qy	1	SerValAlaSerLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla	20
Db	287	GGGGTGCACGATCTGATTTCTGGAGAGATGGAAGAAGACTGGGTTGTCTTTGGCACC	346
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	347	ACGCTGATCATGCTCTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGTTCTTACCTC	406
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	407	ATCTGGGCTCTCTCTCTGTACCATGATTCAGATCTACAGTCCGTTCATCCAGCT	466
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	467	GTACAGAAGTCAGAAAGAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG	526
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	527	TCCTCAGAAGCTTTCCATAAATTACATGAATGCTGCGCATGTGTCACATCAACAGGCGCCCTG	586
Qy	101	LysGluLeuArgLeuPheLeuValAlaSerLeuValAspSerLeuLysPheAlaVal	120
Db	587	AAACTCATTTTCGTCCTCTCTGGTGAAGAATCTGGTTGATCTCTTGAAGCTGGCTGTC	646
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	647	TTCATGTGGCTGATGACCTATGTTGTTGCTGTTTAAACGGAATCAACCTTCTAATCTT	706
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	707	GCTGAACCTGCTCATTTTCAGTCTCCGATTTGTCTATGAGAATACACAGCCAGATTGAT	766
Qy	161	HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	767	CACATGTTGGCTGCGCCGAGATCAGACCAAGTCAATGTTGAAAAGATCAACAGCAAA	826
Qy	181	IleProGlyLeu---LysArgLysAlaGlu	189
Db	827	CTCCCTGGATCGCCANAAAAAAGGAGNA	856

## RESULT 64

US-09-809-391-255  
; Sequence 255, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; PRIORITY FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 255  
; LENGTH: 2664  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2623)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2640)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2652)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2662)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-809-391-255

## Alignment Scores:

Pred. No.:	1,33e-67	Length:	2664
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	10	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-809-391-255 (1-2664)

Qy	1	SerValAlaSerLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla	20
Db	262	CGGGTGCACGATCTGATTTCTGGAGAGATGGAAGAAGACTGGGTTGTCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATGCTCTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGTTCTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCTGGGCTCTCTCTGTCCACCATCAGCTTCAGGATCTACAAAGTCCGTTCATCCAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAAGTCAGAAAGAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	502	TCCTCAGAAGCTTTCCATAAATTACATGAATGCTGCCATGTGTCACATCAACAGGCGCCCTG	561
Qy	101	LysGluLeuArgLeuPheLeuValAlaSerLeuValAspSerLeuLysPheAlaVal	120
Db	562	AAACTCATTTTCGTCCTCTCTGGTGAAGAATCTGGTTGATCTCTTGAAGCTGGCTGTC	621
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	622	TTCATGTGGCTGATGACCTATGTTGTTGCTGTTTAAACGGAATCAACCTTCTAATCTT	681
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160

Db 682 GCTGAAGTCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAGACCCAGATTGAT 741  
Qy 161 HistyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 742 CACTATGTTGGCATCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAAGCAAAA 801  
Qy 181 IleProGlyLeu--LysArgLysAlaGlu 189  
Db 802 CTCCTTGGATCCCAAAAAGAGGAGAA 831

RESULT 65  
US-09-882-171-255  
; Sequence 255, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
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;; PRIOR APPLICATION NUMBER: 60/048,964  
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;; PRIOR APPLICATION NUMBER: 60/057,650  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: 60/056,884  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,669  
;; PRIOR FILING DATE: 1997-09-05

Alignment Scores:  
Pred. No.: 1,338-67 Length: 2664  
Score: 624.50 Matches: 115  
Percent Similarity: 81.0% Conservative: 39  
Best Local Similarity: 60.53% Mismatches: 35  
Query Match: 67.08% Indels: 1

DB: 10 Gaps: 1  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-882-171-255 (1-2664)  
Oy 1 SerValValAspLeuLeuTyrTrpArgAspIleIysThrGlyValValPheGlyAla 20  
Db 262 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 321  
Oy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 322 ACGCTGATCATGCTGCTTTCCCTGGACGCTTTCAGTGTGCAGTGTGGTTCTTACCTC 381  
Oy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 382 ATCTGGCTCTTCTCTGTCCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 441  
Oy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 442 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTACCTGGAGCTAGACATTACTCTG 501  
Oy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 502 TCCTCAGAAGCTTTCCCATTAATACATGAATCTGCGCATGTCACATCAACAGGCCCCG 561  
Oy 101 LysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 562 AAACCTATTATTCGTCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 621  
Oy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 622 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCTTCTTAATTCTT 681  
Oy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 682 GCTGAACCTGCTCATTTTTCAGTGTCCCGATGCTCTATGAGAAGTACAAAGCCAGATTGAT 741  
Oy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
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; Sequence 255, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/10/164,861  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 255  
; LENGTH: 2664  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2623)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2640)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:

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; NAME/KEY: SITE
; LOCATION: (2652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; SEQ ID NO 6867
; LENGTH: 2768
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (2662)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-255

Alignment Scores:
Pred. No.: 1.33e-67 Length: 2664
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 17 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-164-861-255 (1-2664)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysGlyThrGlyValValPheGlyAla 20
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QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 382 ATCTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAAAGTCCGTCATCCAAAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80
Db 442 GTACAGAAGTCAGAAGAAGCCATCCATTCAAGCCCTACCTGACGCTAGACATTAATCTCTG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 502 TCCTCAGAGCTTTCATTAATACATGAATGCTGCTGCTGTCACATCAACAGGCGCCCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 562 AAATCATATTATTCGTCTCTTTCTGGTGAAGATCTGTTGACTCTCTTGAAGCTGGCTGC 621
QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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RESULT 67
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; Sequence 6867, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
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; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
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; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (2743)..(2747)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6867

Alignment Scores:
Pred. No.: 1.41e-67 Length: 2768
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 20 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-723-860-6867 (1-2768)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 320 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGGTTCTCTTTGGCACC 379
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 380 ACCTGATCATGCTGCTTCCCTGGCAGCTTTCCAGTGTATCATGTTGTGGTTCTTACCTC 439
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 440 ATCTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAAAGTCCGTCATCCAAAGCT 499
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80
Db 500 GTACAGAAGTCAGAAGAAGCCATCCATTCAAGCCCTACCTGACGCTAGACATTAATCTCTG 559
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 560 TCCTCAGAGCTTTCATTAATACATGAATGCTGCTGCTGTCACATCAACAGGCGCCCTG 619
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 620 AAATCATATTATTCGTCTCTTTCTGGTGAAGATCTGTTGACTCTCTTGAAGCTGGCTGC 679
QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 680 TTCATGTGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCAACCTTCTTAATCTT 739
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 740 GCTGAACCTGCTCATTTTTCAGTGTCCGATGTTCTATGAGAGTACAGACCCAGATTGAT 799
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 800 CACTATGTTGGCATCGCCGAGATCAGCAAGTCAATGTTGAAAGAAGTCCAAAGCAAAA 859
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 860 CTCCTCGGAATCGCCAAAAAAGGAGAA 889

RESULT 68
US-10-108-260A-449
; Sequence 449, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
```



; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.11  
; SEQ ID NO 449  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-449

Alignment Scores:  
Pred. No.: 9,3e-67 Length: 3637  
Score: 619.50 Matches: 115  
Percent Similarity: 80.53% Conservative: 38  
Best Local Similarity: 60.53% Mismatches: 36  
Query Match: 66.54% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-108-260A-449 (1-3637)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1379 TCAGTGCACGATCTGATTTCTCGAGAGATGGAAGAGACTGGGTTGTCTTTGGCACC 1438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1439 ACGCTGATCATGCTGCTTTCCCTGCGACGTTTCAGTGTTCAGTGTGTTTCTTACCTC 1498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1499 ATCTGGCTCTCTCTGTCCACATCAGCTTCAGATCTACAGTCCGTTCATCCAGCT 1558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1559 GTACAGAAGTCAGAGAAGAGCCATTTCATTCAAGCCTACCTGGAGTAGACATTACTCTG 1618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1619 TCCTCAGAAGCTTTCCATAATTACATGAATGTCGATGTCGATCAATCAACAGGCGCCCTG 1678
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1679 AACTCATATTTCGTCTCTTCTGTGAGAAGATCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1739 TTCAATGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTCTTAATCTT 1798
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGCTATGAGAAGTACAGACCCAGATTGAT 1858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1859 CACTATGTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGAAAAGATCAAGCAAAA 1918
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1919 CTCCTCGAATCGCCCAAAAAGAGGCAGAA 1948
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

## RESULT 69

US-10-159-563-443  
; Sequence 443, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159,563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133,937

; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.11  
; SEQ ID NO 443  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-443

Alignment Scores:  
Pred. No.: 9,3e-67 Length: 3637  
Score: 619.50 Matches: 115  
Percent Similarity: 80.53% Conservative: 38  
Best Local Similarity: 60.53% Mismatches: 36  
Query Match: 66.54% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-159-563-443 (1-3637)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1379 TCAGTGCACGATCTGATTTCTCGAGAGATGGAAGAGACTGGGTTGTCTTTGGCACC 1438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1439 ACGCTGATCATGCTGCTTTCCCTGCGACGTTTCAGTGTTCAGTGTGTTTCTTACCTC 1498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1499 ATCTGGCTCTCTCTGTCCACATCAGCTTCAGGATCTACAGTCCGTTCATCCAGCT 1558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1559 GTACAGAAGTCAGAGAAGAGCCATTTCATTCAAGCCTACCTGGAGTAGACATTACTCTG 1618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1619 TCCTCAGAAGCTTTCCATAATTACATGAATGTCGATGTCGATCAATCAACAGGCGCCCTG 1678
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1679 AACTCATATTTCGTCTCTTCTGTGAGAAGATCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1739 TTCAATGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTCTTAATCTT 1798
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGCTATGAGAAGTACAGACCCAGATTGAT 1858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1859 CACTATGTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGAAAAGATCAAGCAAAA 1918
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1919 CTCCTCGAATCGCCCAAAAAGAGGCAGAA 1948
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

## RESULT 70

US-09-823-245A-510  
; Sequence 510, Application US/09823245A  
; Publication No. US20020039760A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fichtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakari  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.

```
/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
/ FILE REFERENCE: GIN 6401
/ CURRENT APPLICATION NUMBER: US/09/823,245A
/ CURRENT FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/194,941
/ PRIOR FILING DATE: 2000-04-06
/ NUMBER OF SEQ ID NOS: 631
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 510
/ LENGTH: 1636
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-823-245A-510

Alignment Scores:
Pred. No.: 1,576-64 Length: 1636
Score: 597.50 Matches: 114
Percent Similarity: 80.53% Conservative: 39
Best Local Similarity: 60.00% Mismatches: 36
Query Match: 64.18% Indels: 2
DB: Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-823-245A-510 (1-1636)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
248 GCGGTCACGATCTGATTTCTGGAGAGATGTGAAGAACCTGGGGTTGCTTTGGCACC 307
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
308 ACCTGATCATGCTGCTTTC-CTGGCAGCTTTCAGTGTATCATGTTGGTTTCTTACCTC 366
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
367 ATCTGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 426
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 GTACAGAAGTCAGAAGAGGCCATCCATTCAGAGCTTACAGCTGACATGACATTAATCTCTG 486
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
487 TCTCAGAGACTTTCATATATACATGATGCTGCCATGCTGACATCAACAGGCGCTG 546
QY 101 LysGluLeuArgIlePheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
547 AAACCTCATTATTCCTCTCTCTGTTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 606
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
607 TTCATGTGGCTGATGACCTATGTGTGTGTGTTTAAACGGAATCACCTTCTTAATCTTT 666
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
667 GCTGAACCTGCTCATTTTTCAGTGTCCCGATGTCTATGAGAGTACAGACCCAGATTGAT 726
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
727 CACTATGTTGGCATCCCGCAGATCAGACCAAGTCAATGTTGAAAAGATCCCAAGCAAAA 786
QY 181 IleProGlyLeu--LysArgLysAlaGlu 189
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
787 CTCCTCGGAATCCCAAAAAAAGGCGAGAA 816

RESULT 71
US-09-960-352-5154
/ Sequence 5154, Application US/09960352
/ Patent No. US20020137139A1
/ GENERAL INFORMATION:
/ APPLICANT: Warren, Wesley C.
/ APPLICANT: Tao, Nengbing
/ APPLICANT: Byatt, John C.
/ APPLICANT: Mathialagan, Nagappan
/ TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
/ FILE REFERENCE: 16511.006/37-21(10298)C
/ CURRENT APPLICATION NUMBER: US/09/960,352
/ CURRENT FILING DATE: 2001-09-24
/ NUMBER OF SEQ ID NOS: 15112
/ SEQ ID NO 9092
/ LENGTH: 423
/ TYPE: DNA
/ ORGANISM: Bos taurus
/ OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 3,056-62 Length: 423
Score: 572.00 Matches: 115
Percent Similarity: 100.00% Conservative: 1
```

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/ TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
/ FILE REFERENCE: 16511.006/37-21(10298)C
/ CURRENT APPLICATION NUMBER: US/09/960,352
/ CURRENT FILING DATE: 2001-09-24
/ NUMBER OF SEQ ID NOS: 15112
/ SEQ ID NO 5154
/ LENGTH: 389
/ TYPE: DNA
/ ORGANISM: Bos taurus
/ OTHER INFORMATION: Clone ID: 22-LIB34-043-Q1-E1-P5
US-09-960-352-5154

Alignment Scores:
Pred. No.: 28-62 Length: 389
Score: 573.00 Matches: 117
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 61.55% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-5154 (1-389)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 GTGTGTGACCTCCTCTACTGGAGACATTAAGAACACTGGAGTGGTGTGGTGGCACC 93
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
94 TTGTTCTCTCTCTCGCTGACAGTATTACAGATTGTGAGTGTAAAGGCTGTGATCCAGGCTATC 153
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 TTGGCCCTCTCTCTGCTACTATCAGCTTTAGGATATATAGGATCTGATCCAGGCTATC 213
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 CAGAAATCTGATGAAGGCCACCCATTCAGGCAATATTTGGATCTGAAGTTCGTATATCT 273
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
274 GAGGAGTTGGTTTCAGAGTACAGCAATCTCTCTTGGTCTGATTAACGTCAACAATAAAA 333
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAla 119
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
334 GAACCTCAGACGCTCTCTTCTGATGATTTAGTTGATTTCTCTGAAGTTTGA 387

RESULT 72
US-09-960-352-9092
/ Sequence 9092, Application US/09960352
/ Patent No. US20020137139A1
/ GENERAL INFORMATION:
/ APPLICANT: Warren, Wesley C.
/ APPLICANT: Tao, Nengbing
/ APPLICANT: Byatt, John C.
/ APPLICANT: Mathialagan, Nagappan
/ TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
/ FILE REFERENCE: 16511.006/37-21(10298)C
/ CURRENT APPLICATION NUMBER: US/09/960,352
/ CURRENT FILING DATE: 2001-09-24
/ NUMBER OF SEQ ID NOS: 15112
/ SEQ ID NO 9092
/ LENGTH: 423
/ TYPE: DNA
/ ORGANISM: Bos taurus
/ OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 3,056-62 Length: 423
Score: 572.00 Matches: 115
Percent Similarity: 100.00% Conservative: 1
```

Best Local Similarity: 99.14% Mismatches: 0  
Query Match: 61.44% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-960-352-9092 (1-423)

QY 74 LeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu 93  
DB 3 TTGGAATCTGAAGTTGCTATATCTGATGATGTTGGTTCAGAACTACAGCAATTCCTCTT 62

QY 94 GlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspSerLeuVal 113  
DB 63 GGTCTGTTAACTGCACATAAAGAACTCAGACGCTCTCTTAGTTGATGATTTAGTT 122

QY 114 AspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsn 133  
DB 123 GATTTCTGAAGTTTGCAGTGTTGATGTTGGGATTTTACCTATGTTGGGCTTGTTCAT 182

QY 134 GlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerValProValIleTyrGlu 153  
DB 183 GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTCTTATTATGAA 242

QY 154 ArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAla 173  
DB 243 CGGCATCAGCGCAAAATAGATCAATCTCTGGACTTGCATAAAGAAATGTTAAAGATGCT 302

QY 174 MetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189  
DB 303 ATGGCTAAATAATCAAGCAAAAATCCCTGGATTTGAAGCGTAAAGCTGAA 350

RESULT 73

US-10-302-172-111  
; Sequence 111, Application US/10302172  
; Publication No. US20040053250A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids an  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 803\_1CNCIP  
; CURRENT APPLICATION NUMBER: US/10/302,172  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/10/225,251  
; PRIOR FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: PCT US02/05095  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 09/799,451  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 950  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 111  
; LENGTH: 3517  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (196)..(654)  
US-10-302-172-111

Alignment Scores:

Pred. No.:	Length:
4e-57	3517
Score: 543.00	Matches: 104
Percent Similarity: 69.46%	Conservative: 37
Best Local Similarity: 51.23%	Mismatches: 34
Query Match: 58.32%	Indels: 28
DB: 18	Gaps: 2

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-302-172-111 (1-3517)

QY 2 ValValAspLeuLysTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 2906 GTGCAGATCTGATTTCTTCTGGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGCACCAG 2965

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 2966 CTGATCATGCTGCTTTCCCTGGACGCTTTCAGTGTGATCAGTGGTGTCTTCTACCTCATC 3025

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 3036 CTGGCTCTTCTCTGTCCATCAGCTTCCAGATCTCAAGTCCGTTCATCCAGCTGTA 3085

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 3086 CAGAAGTCAGAGAAGGCCCATCTTCAAGCCCTACCTGGACGTAGACATTAATCTGTCTC 3145

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 3146 TCAGAACTTTCCATAATTATCATGATGCTGCCATGCTGCATCAACAGGCGCTGAAA 3205

QY 102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121  
DB 3206 CTCATTATTCCTCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTCTTC 3265

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 3266 ATGTGGCTGATGACCTATGTTGGTCTGTTTTTAAACGGAATCACCTTCTAATTTCTTGT 3325

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGln---AlaGlnIle--- 159  
DB 3326 GAACGTCTATTTTCAGTGTCCGATTTGCTATGAGAAGTACAGGATGCACGTGTGCTA 3385

QY 159 ----- 159

DB 3386 GCGCTGACGAGCAAGAGTCCACACTGAAGTATCAGAGAAGCTCCAGGGCAAAAGCAA 3445

QY 160 -----AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAla 173  
DB 3446 GAGGCACCAGACCAGATGATCACTATGTTGGCATCGCCCGCAGATCAGACCAAGTCAATT 3505

QY 174 MetAlaLys 176  
DB 3506 GTTGAAGAAG 3514

RESULT 74

US-10-660-946-4  
; Sequence 4, Application US/10660946  
; Publication No. US20040063131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/660,946  
; FILING DATE: 12-Sep-2003  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/228,213A  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/700,607  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-660-946-4
Alignment Scores:
Pred. No.: 7,63e-56 Length: 1095
Score: 526.50 Matches: 104
Percent Similarity: 72.77% Conservativeness: 35
Best Local Similarity: 54.45% Mismatches: 30
Query Match: 56.55% Indels: 22
DB: 18 Gaps: 2
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-660-946-4 (1-1095)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 329 GCGGTGCAGATCTGATTTMTGGAGAGATGTGAAGAAGACTGGGTGTCTTTGGCACC 388
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 389 ACCTGATCATGTCGTGTCCTCCCTGGCAGCTTCAGTGTCACTAGTGTGTTCTTACTTC 448
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 449 ATCTGGCTCTTCTCTGTGCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAACT 508
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 509 GTACAGAAGTCAGAAGAAGCCATCCATTCAAGCCCTACCTGGACGTAGACATTAATCTG 568
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 569 TCCTCAGAAGCTTCCATAATTACATGATGCTGCCATGTCACATCAACAGGCGCTG 628
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 629 AAACCTCATATTGCTCTCTTCTGTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGC 688
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 689 TTCATGTCGTGATGACCTATGTGTGTGCTGTTTAAACGAATCACTCCCTTCAATTCCT 748
QY 141 AlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 749 GCTGAAGTGCCTATTNAGTGTCCCGATGTGTATNAGAGTAC-----793
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 794 -----AAGGTTCCAAAGCAA 808
QY 180 sileProGlyLeu---LysArgLysAlaGlu 189
Db 809 ACTCCCTGGAATCGCCAAAAAAGGCGAA 839
RESULT 75
US-10-267-502-211
; Sequence 211, Application US/10267502
; Publication No. US20040071700A1
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; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 211
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-267-502-211
Alignment Scores:
Pred. No.: 2,31e-55 Length: 669
Score: 520.00 Matches: 96
Percent Similarity: 73.40% Conservativeness: 42
Best Local Similarity: 51.06% Mismatches: 50
Query Match: 55.85% Indels: 0
DB: 18 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-267-502-211 (1-669)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 76 GTGGAATCCCTTATCTACTGCGCGCATGTGAAGAAATCCGGCATTTGTCTTCGCGCTGC 135
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 136 CTGATCACACTGGCGCCATCTCCAGCTTCTCGGTGATCAGCGTGTTCCTCTTCTGTCG 195
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 196 CTCCTAACCTCTCTCGGCACCGTCGCTTCAGAACTCACTCAAAATCTGTGACACAGGCG 255
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 256 CAAAAGACAAACAGAGGCTCACCCCTTTAAGGATTACCTGGAGCTGGATCTGACGCTGTC 315
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 316 CACGAAAGGTACAGAACATTCGCGCGTGGCTGTGGACATATCATGATTCGATCAAGTTC 375
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 376 GAGCTGAGCGCTGTTCTTCTGTGAGGATATCATCGATTCGATCAAGTTCGCGCTCAT 435
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 436 CTGTGGGTCTTCACTTACCTACGTGGGTGCTGCTGTTCAATGGCATGACTCTGGTCTCT 495
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 496 TTTGTCCTCGCTGTTTACCTTGTCCCAAGGCTCAGAGAACACAAAGCAATCGATCGACT 555
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 556 CACTTGGATCTGGTGGCGAGCAAAATTGACAGAAATCACCAGCAAGATCCGAGTGGCAATC 615
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 616 CCCATTGGCAACAAGAACGCCGAG 639
RESULT 76
US-09-809-391-102
; Sequence 102, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
```

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; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-102

Alignment Scores:
Pred. No.:      8.58e-54      Length:      794
Score:          508.50      Matches:    102
Percent Similarity: 76.37%      Conservative: 37
Best Local Similarity: 56.04%      Mismatches: 41
Query Match:      54.62%      Indels:    3
DB:              10          Gaps:      0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-809-391-102 (1-794)

Qy      1 SerValValAspLeuLeuTyTrpArgAspIleValSerVal-ThrAlaTyIle 20
Db      254 CGGGTGCACGATCGATTTCTGGAGATGTGAAGAGCTGGGTTGTCTTTGGAC-- 311
Qy      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyIle 40
Db      312 ACGTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCACTGTGGGTTTCTTAMCT 371
Qy      40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyIleValIleGlnAla 60
Db      372 CATCTGGCTCTTCTCTGTGCACCATCATCTTCAGGATCTACAAAGTCGTCATCCCAAGC 431
Qy      60 alleGlnIleSerAspGluGlyHisProPhe-ArgAlaTyIleuSerGluValAlaIle 80
Db      432 TGTWAGAARTCAGAAAGGCCATCCCAAGCCCTACCTGAGCAGTAGACATTACTC 491
Qy      80 leSerGluGluLeuValGlnIleTyTrpSerAsnSerAlaLeuGlyHisValAsnCystrI 100
Db      492 TGTCTCAGAGCTTTCATATATACATGATGCTGCCATGTCACATCAACAGGCCCC 551
Qy      100 leIysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuIleValPheAlav 120
Db      552 TGAACATCATATTTCGTCTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTG 611
Qy      120 allLeuMetTTPValPheThrTyTrpValGlyAlaLeuPheAsnGlyLeuThrLeuIleL 140
Db      612 TCITTCATGTGCTGATGACCTATGTGTGTGCTGTTTAAACGGAATCACCTTCTAATTC 671
Qy      140 euAlaLeuIleSerLeuPheSerValProValIleTyTrpGluArgHisGlnAlaGlnIleA 160
Db      672 TTGCTGAAGTCTCATTTTTCAGTGTCCGATGCTATGAGAAGTACAGACCCAGATTG 731
Qy      160 spHisTyLeuGlyLeuAlaLeuAsnIleValSerValIleValAspAlaMetAlaIleGlnAla 180
Db      732 ATCACTATGTTGGCATGCCCGGAGATCAGACCAAGTCAATTGTTTGAAGAAGATCCCAAGCA 791
Qy      180 ys 180
Db      792 AA 793

RESULT 77
US-09-882-171-102
; Sequence 102, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
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Qy	1	SerValValAspLeuLeuTyrrTrpArgAspIleLeuLysThrGlyValValPheGlyAla	20
Db	254	GGCGTGCAGACTGATTTCTTGGAGAGATGTGAAGAAGACTGGTGTTCCTTTGGAC--	311
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrI	40
Db	312	ACGCTGATCATGCTGCTCTTCCCTGCGACGCTTTCAGTGTCACTGGTGGCTTCTTAMCT	371
Qy	40	exaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl	60
Db	372	CATCTGGCTCTCTCTCTGTCAACATCARCTTCAGGATCTACAGTCCGTCATCCAAAG	431
Qy	60	atleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI	80
Db	432	TGTWCAAGARTCAGAAAGGCCATCCAAAGGCTACCTGGAGCTAGACATTACTCT	491
Qy	80	leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI	100

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Db 492 TGTCTCTCAGAGCTTTCCATAATTACATGAATGCTGCCATGTCACATCAACAGGGCCC 551
Qy 100 leLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlav 120
Db 552 TGAACCTCATATTCTGCTCTCTTCGGTAGAAGATCTGCTGACCTCCCTTGAAGCTGGCTG 611
Qy 120 alLeuMetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeL 140
Db 612 TCTTCATGTGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCCCTTCTAATTC 671
Qy 140 euAlaLeuLeuSerLeuPheSerValProValIleTyGluArgHisGlnAlaGlnIleA 160
Db 672 TTGCTGAACTGCTCATTTTCAGTGTCCCGATGTCCTATGAGAAGTACAAAGACCCAGATTG 731
Qy 160 spHisTyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaL 180
Db 732 ATCACTATGTTGGCATCGCCGAGATCAGACCAGTCAATTGTTGAAAGAGATCCCAAGCA 791
Qy 180 Ys 180
Db 792 AA 793

RESULT 78
US-10-164-861-102
; Sequence 102, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-164-861-102

Alignment Scores:
Pred. No.: 8,58e-54 Length: 794
Score: 508.50 Matches: 102
Percent Similarity: 76.37% Conservative: 37
Best Local Similarity: 56.04% Mismatches: 41
Query Match: 54.62% Indels: 3
DB: 17 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-164-861-102 (1-794)
Qy 1 SerValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 254 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGAC-- 311
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyRil 40
Db 312 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCAATGTCAGTGTCTTAMCT 371
Qy 40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAl 60
Db 372 CATCTGCTGCTCTCTCTGTGCACCATCACTTTCAGGATCTCAACAAGTCGCTCATCAAGC 431
Qy 60 atleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyRilLeuLeuSerGluValAlaI 80
Db 432 TGTWCAGAAATCAGAAAGGCCATCCATTCGAAAGCCCTACTGAGCAGTAGACATATCTC 491
Qy 80 leSerGluLeuValGlnLysTyTrpSerAsnSerAlaLeuGlyHisValAsnCysThrI 100
Db 492 TGTCTCTCAGAGCTTTCCATAATTACATGAATGCTGCCATGTCACATCAACAGGGCCC 551

```

```

Qy 100 leLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlav 120
Db 552 TGAACCTCATATTCTGCTCTCTTCGGTAGAAGATCTGCTGACCTCCCTTGAAGCTGGCTG 611
Qy 120 alLeuMetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeL 140
Db 612 TCTTCATGTGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCCCTTCTAATTC 671
Qy 140 euAlaLeuLeuSerLeuPheSerValProValIleTyGluArgHisGlnAlaGlnIleA 160
Db 672 TTGCTGAACTGCTCATTTTCAGTGTCCCGATGTCCTATGAGAAGTACAAAGACCCAGATTG 731
Qy 160 spHisTyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaL 180
Db 732 ATCACTATGTTGGCATCGCCGAGATCAGACCAGTCAATTGTTGAAAGAGATCCCAAGCA 791
Qy 180 Ys 180
Db 792 AA 793

RESULT 79
US-10-424-599-57998
; Sequence 57998, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57998
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23384C.1
US-10-424-599-57998

Alignment Scores:
Pred. No.: 1.01e-53 Length: 878
Score: 508.50 Matches: 96
Percent Similarity: 74.47% Conservative: 44
Best Local Similarity: 51.06% Mismatches: 47
Query Match: 54.62% Indels: 1
DB: 18 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-424-599-57998 (1-878)
Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 152 GTGGAGACCTGATCTACTGCGCGGATTCGAGAAATCCGGTCCAGTGTTCGGAGGAGTA 211
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41
Db 212 CTGCTGCTTCTACTCGCTCTTACATATTTCTCTTAATCAGTGTGTAGCTTACGCTTTCA 271
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61
Db 272 CTCATCACTTGGCATAACTTTAGCGTTTGAATTTACAAAGATTAATTTGTACAAAGCAGTT 331
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyRilLeuLeuGluSerGluValAlaIleSer 81
Db 332 CAAAAGACTGCGGATGGACATCCATTCAGAAATATCTGGAACTCGATGTGTCTCTACCC 391
Qy 82 GluGluLeuValGlnLysTyTrpSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 392 CAAGAAAAGTTAAACAAATCACAGAAGTGGCCGTTGCACACATCAATGCGCGCTATTGTG 451

```





Db 114 ATGCTGCTTCCCTGCGACGCTTTTCAGTGTGCATCAGTGTGGTTTCTTACCTCATCTGGCT 173  
Qy 44 LeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63  
Db 174 CTCTCTCTGTCCACCATCAGCTTCAGGATCTCAAGTCCGTCTCATCAGCTGTACAGAAG 233  
Qy 64 SerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGlu 83  
Db 234 TCAGAAGAAGGCGCATCCATTCAAGCGCTACCTGGAGTACATCTGTCTCTCAGAA 293  
Qy 84 LeuValGlnLysTyrSerAnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeu 103  
Db 294 GCTTTCCATTAATATCATGAATGCTGCCATGCTGGTGCATCAACAGGCGCCCTGAACACTCAT 353  
Qy 104 ArgAspLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123  
Db 354 ATTCGTCTCTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTCTTCATGTGG 413  
Qy 124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIle 143  
Db 414 CTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTTCTTAATCTTGTGCTGAAC 473  
Qy 144 SerLeuPheSerVal 148  
Db 474 CTCATTTTCAGGTGC 488

## RESULT 82

US-10-242-535A-17576  
; Sequence 17576, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; PRIOR FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17576  
; LENGTH: 566  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-17576

Alignment Scores:  
Pred. No.: 1.45e-51 Length: 566  
Score: 489.00 Matches: 102  
Percent Similarity: 99.04% Conservative: 1  
Best Local Similarity: 98.08% Mismatches: 1  
Query Match: 52.52% Indels: 1  
DB: 17 Gaps: 0

US-09-830-972-29\_copy\_990\_1178 (1-189) x US-10-242-535A-17576 (1-566)

Qy 86 GlnLysTyrSerAnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArg 105  
Db 1 CAGAAGCAGCAATCTGCTCTTGG-CATGTGAAGTGCAGCATAAAGAACTCAGGCGC 59  
Qy 106 LeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 60 CTCCTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTATTCATGTGGGTATTT 119  
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeu 145

Db 120 ACCTATGTTGGTGCCTCTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTC 179  
Qy 146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165  
Db 180 TTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTTATCTAGACTT 239  
Qy 166 AlaAnLysAnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 240 GCAATAAAGATGTTAAAGATGCTATGCTTAAATCCAAGCAAAATCCCTGGATTGAAG 299  
Qy 186 ArgLysAlaGlu 189  
Db 300 CGCAAGCTGAA 311

## RESULT 83

US-10-085-783A-17576  
; Sequence 17576, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17576  
; LENGTH: 566  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-17576

Alignment Scores:  
Pred. No.: 1.45e-51 Length: 566  
Score: 489.00 Matches: 102  
Percent Similarity: 99.04% Conservative: 1  
Best Local Similarity: 98.08% Mismatches: 1  
Query Match: 52.52% Indels: 1  
DB: 18 Gaps: 0

US-09-830-972-29\_copy\_990\_1178 (1-189) x US-10-085-783A-17576 (1-566)

Qy 86 GlnLysTyrSerAnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArg 105  
Db 1 CAGAAGCAGCAATCTGCTCTTGG-CATGTGAAGTGCAGCATAAAGAACTCAGGCGC 59  
Qy 106 LeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 60 CTCCTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTATTCATGTGGGTATTT 119  
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeu 145  
Db 120 ACCTATGTTGGTGCCTCTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTC 179  
Qy 146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165  
Db 180 TTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTTATCTAGACTT 239  
Qy 166 AlaAnLysAnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 240 GCAATAAAGATGTTAAAGATGCTATGCTTAAATCCAAGCAAAATCCCTGGATTGAAG 299  
Qy 186 ArgLysAlaGlu 189  
Db 300 CGCAAGCTGAA 311



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Db 1074 CTGTTGCTGCTGCGGCACCATCTCTCTCAGGGTTTACCGCAAGTGTCTGCGGCCGCTG 1133
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 1134 CACCGGGGGATGGAGCCAAACCTTTTCCAGGCTTACCTGGATGTGGACCTCACCTGACT 1193
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 1194 CGGAGCAGACGAGAGCTTTGTCACCATGATCACCTCCGCGTGGTCTCGCGGCCACG 1253
Qy 102 GluLeuArgGluPheLeuValAspLeuValAspLeuValAspLeuValAspLeuValLeu 121
Db 1254 CAGCTGCGGCACCTTCTTCTGCTAGAACCTCTGCTGATTCCTCAAGCTGCGCCCTCCTC 1313
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 1314 TTCTACATCTTGACCTTCTGCGGTGGTCCATCTCAATGGTTTGTCTCTCATCTCGGA 1373
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 1374 GTGATGGTCTATTACCATCCCTCTGCTGACCGCAGCAGCAGCAGCAGCAGCAGCAGC 1433
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1434 TATGTGGGGTTGGTGACCAATCAGTTGAGCCACATCAAAAGCTTAAGATCCGAGCTAAATC 1493
Qy 182 ProGlyLeu-----LysArgLysAla 188
Db 1494 CAGGAGCGGAGCCCTGCGCTCTCGACGCGCAGTCTCCGGATCCAAAGCCAAAGCC 1553
Qy 189 Glu 189
Db 1554 GAA 1556

RESULT 86
US-10-723-860-3043
; Sequence 3043, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3043
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-3043

Alignment Scores:
Pred. No.: 1,128-48 Length: 2190
Score: 473.50 Matches: 95
Percent Similarity: 65.67% Conservativeness: 37
Best Local Similarity: 47.26% Mismatches: 56
Query Match: 50.86% Indels: 13
DB: 20 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-723-860-3043 (1-2190)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACAGCAGGAGCTCAGGAGTGTCTTACAGGCGCTG 1221
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACAGCAGGAGCTCAGGAGTGTCTTACAGGCGCTG 1221
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACAGCAGGAGCTCAGGAGTGTCTTACAGGCGCTG 1221
```

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Db 1222 ATGGTCTCCCTCTGCTGCTCTCTGCTGCTTACGATCGTGTGCTGCGCGCAGCTTGGCT 1281
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1282 CTGTTGCTGCTCTGCGGCACCATCTCTCTCAGGGTTTACCGCAAGTGTCTGCGGCCGCTG 1341
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 1342 CACCGGGGGATGGAGCCAAACCTTTTCCAGGCTTACCTGGATGTGGACCTCACCTGACT 1401
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 1402 CGGAGCAGACGAGACGTTTGTCCACCATGATCACCTCCGCGTGGTCTCGCGGCCACG 1461
Qy 102 GluLeuArgGluPheLeuValAspLeuValAspLeuValAspLeuValAspLeuValLeu 121
Db 1462 CAGCTGCGGCACCTTCTCTGCTAGAACCTCTGCTGATTCCTCAAGCTGCGCCCTCCTC 1521
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 1522 TTCTACATCTTGACCTTCTGCTGAGTGGTCCATCTCAATGGTTTGTCTCTCATCTCGGA 1581
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 1582 GTGATGGTCTATTACCATCCCTCTGCTGACCGCAGCAGCAGCAGCAGCAGCAGCAGC 1641
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1642 TATGTGGGGTTGGTGACCAATCAGTTGAGCCACATCAAAAGCTTAAGATCCGAGCTAAATC 1701
Qy 182 ProGlyLeu-----LysArgLysAla 188
Db 1702 CCAGGAGCGGAGCCCTGCGCTCTGACGAGCCGCGCAGTCTCCGGATCCAAAGCCAAAGCC 1761
Qy 189 Glu 189
Db 1762 GAA 1764

RESULT 87
US-10-723-860-7073
; Sequence 7073, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-7073

Alignment Scores:
Pred. No.: 1,898-48 Length: 3044
Score: 473.50 Matches: 95
Percent Similarity: 65.67% Conservativeness: 37
Best Local Similarity: 47.26% Mismatches: 56
Query Match: 50.86% Indels: 13
DB: 20 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-723-860-7073 (1-3044)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACAGCAGGAGCTCAGGAGTGTCTTACAGGCGCTG 1221
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACAGCAGGAGCTCAGGAGTGTCTTACAGGCGCTG 1221
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Db      872 GTGGCGGACCTGCTGTAAGGACACAGGAGCTCAGGAGTGTCTTCACAGCCCTG 931
Qy      22  LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      932 ATGGTCTCCTCTCTGCTGCTCTGCTGCTAGCATGCTGCTGCGCGCGCACTTGGCT 991
Qy      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      992 CTGTTGCTGCTGCGCGCACCATCTCTCTCAGGGTTTACCGAAAGTGTGCGAGCGGTG 1051
Qy      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      1052 CACCGGGGGATGGAGCCAACTTTCCAGGCTACCTGGATGTGAGTGCACCTCAGCTGACT 1111
Qy      82  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
      |||||      |||||      |||||      |||||      |||||      |||||
Db      1112 CGGAGACAGCGAAGCTTTGTCCACACAGATCACCTCCGCGTGTCTCGGCGGCCAGC 1171
Qy      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      1172 CAGCTCGCGCACCTCTCTGCTGAGAGACCTCGTGGATTCCTCAAGCTGCGCCCTCCTC 1231
Qy      122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      1232 TTCTACATCTTGACCTTGTGGGTGCATCTTCATGGTTTGACTCTTCTCATCTGGGA 1291
Qy      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      1292 GTGATTGGTCTATTACCATCCCTGCTGTACCGCGCAGCACCAGGCTCAGATCGACCAA 1351
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      1352 TATGTGGGTGTGTGACCAATCATGTTGAGCCACATCAAAAGCTAAAGATCCGAGTAAATC 1411
Qy      182 ProGlyLeu-----LysArgLysAla 188
      |||||      |||||      |||||      |||||      |||||      |||||
Db      1412 CCAGGACCGGACCTGGCTGTGCGAGCGCGAGTCTCCGATCCAAAGCAAGGCC 1471
Qy      189 Glu 189
      |||||
Db      1472 GAA 1474

RESULT 88
US-09-960-352-2205
; Sequence 2205, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2205
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (309)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 10-LIB3058-011-Q1-K1-C5
US-09-960-352-2205

Alignment Scores:
Pred. No.: 4,73e-44 Length: 431
Score: 428.00 Matches: 89
Percent Similarity: 98.89% Mismatches: 0
Best Local Similarity: 98.89% Mismatches: 1
```

```
Query Match: 45.97% Indels: 0
DB: Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-2205 (1-431)

Qy      2  ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
      |||||      |||||      |||||      |||||      |||||      |||||
Db      161 GTTGTGTGACCTCTCTCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCAGC 220
Qy      22  LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
      |||||      |||||      |||||      |||||      |||||      |||||
Db      221 TTGTTCTCTGCTCTCTGCTGACAGTATTTCACCAATTGTGAGTGTAAACGCGCTACATTGCC 280
Qy      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
      |||||      |||||      |||||      |||||      |||||      |||||
Db      281 TTGGCGCTGCTCTCTGTGACTATCAGCTNTAGGATATATAAGGGTGTGTATCCAGGCTATC 340
Qy      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      |||||      |||||      |||||      |||||      |||||      |||||
Db      341 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAAATCTGAAGTTGCTATATCT 400
Qy      82  GluGluLeuValGlnLysTyrSerAsnSer 91
      |||||      |||||      |||||      |||||      |||||      |||||
Db      401 GAGGAGTTGGTTTCAGAAAGTACAGCAATTCCT 430

RESULT 89
US-10-052-283-137
; Sequence 137, Application US/10052283
; Publication No. US20030064379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND METHOD OF USE THEREOF
; FILE REFERENCE: P2751R1C1
; CURRENT APPLICATION NUMBER: US/10/052,283
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: PCT/US00/20006
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/145,701
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 564
; SEQ ID NO 137
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-052-283-137

Alignment Scores:
Pred. No.: 8,7e-40 Length: 598
Score: 396.00 Matches: 74
Percent Similarity: 80.83% Conservative: 23
Best Local Similarity: 61.67% Mismatches: 23
Query Match: 42.53% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-052-283-137 (1-598)

Qy      1  SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      234 GCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGCACC 293
Qy      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      294 ACGCTGATCATGCTGCTTCTCCCTCGGCAGCTTTTCAGTGTCTCAGTGTGTTTCTTACCCTC 353
Qy      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
      |||||      |||||      |||||      |||||      |||||      |||||
Db      354 ATCTTGGCTCTTCTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGCTCATCCAGCT 413
Qy      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
      ::      |||||      |||||      |||||      |||||      |||||      |||||
Db      414 GTACAGAGCTCAGAGAGGCCCATTCATTCAAAGCCTACCTGGACGCTAGACATTACTCTG 473
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US-10-050-704-93
; Sequence 93, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2317)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-050-704-93

Alignment Scores:
Pred. No.: 1.84e-34 Length: 2454
Score: 361.50 Matches: 67
Percent Similarity: 77.50% Conservative: 26
Best Local Similarity: 55.83% Mismatches: 26
Query Match: 38.83% Indels: 1
DB: 14 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-050-704-93 (1-2454)
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 59 AGAGCCTACCTGGACGTAGACATTACTCTGCTCAGAAAGCTTTCCATTAATACATGAAT 118
QY 91 SerAlaLeuGlyHisValIleAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db 119 GCTGCCATGGTGCACATCAACAGGGCCCTGAACCTCATTATTCGTCCTCTTTCTGGTAGAA 178
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTyrPheThrTyrValGlyAla 130
Db 179 GATCTGGTGAACCTCCCTTGAAGCTGGCTGCTTCATGCTGCTGATGACCTATGTTGGTGCT 238
QY 131 LeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProVal 150
Db 239 GTTTTAAACGAATACACCTCTTAATCTTGTGAACTCTCACTATGTTGGCATCGCCGAGATCAGACC 298
QY 151 IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaLeuIleAsnLysVal 170
Db 299 GTCTATGAGAAGTACAGACCCAGACATTCATCACTATGTTGGCATCGCCGAGATCAGACC 358
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaGlu 189
Db 359 AAGTCAATTGTTGAAAGATCCAAAGCAAACTCCCTGGAAATCCCAAAAAAAGGCGAGAA 418

RESULT 93
US-10-798-512-93
; Sequence 93, Application US/10798512
; Publication No. US20040152164A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/798,512
; CURRENT FILING DATE: 2004-03-12
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; PRIOR APPLICATION NUMBER: US/09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2317)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-798-512-93

Alignment Scores:
Pred. No.: 1.84e-34 Length: 2454
Score: 361.50 Matches: 67
Percent Similarity: 77.50% Conservative: 26
Best Local Similarity: 55.83% Mismatches: 26
Query Match: 38.83% Indels: 1
DB: 19 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-798-512-93 (1-2454)
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 59 AGAGCCTACCTGGACGTAGACATTACTCTGCTCAGAAAGCTTTCCATTAATACATGAAT 118
QY 91 SerAlaLeuGlyHisValIleAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db 119 GCTGCCATGGTGCACATCAACAGGGCCCTGAACCTCATTATTCGTCCTCTTTCTGGTAGAA 178
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTyrPheThrTyrValGlyAla 130
Db 179 GATCTGGTGAACCTCCCTTGAAGCTGGCTGCTTCATGCTGCTGATGACCTATGTTGGTGCT 238
QY 131 LeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProVal 150
Db 239 GTTTTAAACGAATACACCTCTTAATCTTGTGAACTCTCACTATGTTGGCATCGCCGAGATCAGACC 298
QY 151 IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaLeuIleAsnLysVal 170
Db 299 GTCTATGAGAAGTACAGACCCAGACATTCATCACTATGTTGGCATCGCCGAGATCAGACC 358
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaGlu 189
Db 359 AAGTCAATTGTTGAAAGATCCAAAGCAAACTCCCTGGAAATCCCAAAAAAAGGCGAGAA 418

RESULT 94
US-09-880-107-3484
; Sequence 3484, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 3484
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 W27023
; NAME/KEY: unsure
; LOCATION: (1)..(639)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3484

Alignment Scores:
Pred. No.: 1,11e-33 Length: 639
Score: 348.00 Matches: 83
Percent Similarity: 81.73% Conservative: 2
Best Local Similarity: 79.81% Mismatches: 12
Query Match: 37.38% Indels: 8
DB: 9 Gaps: 2

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-880-107-3484 (1-639)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 233 GTTGTGACCTCTCTGCTACTGGAGACATTAAAGAGACTGGAGTGTGTTGGTCCAGC 292
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41
Db 293 CTATTCCTGCTGCTTTCATTGACAGATTACAGATTGAGCTTAACAGCTACATTGCC 352
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61
Db 353 TTGGNCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 412
Qy 62 GlnLysSer-AspGluGlyHisProPheArgAlaTyRileuGluSerGluValAlaIle-- 80
Db 413 CAGAAATCAAGATGAAGGCCACCCATTGAGGCATATCTGAGGCATATCTGAAGTGNTATTCT 472
Qy 81 ---SerGluGluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnCyth 99
Db 473 TAGGAGTGGTCANAGTCAGATCTGTCT-----GGCGANGTGAAGTCG-AC 519
Qy 99 rIleLysGlu 102
Db 520 GATAAAGGAC 529

RESULT 95
US-10-633-423-9
; Sequence 9, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; APPLICANT: Yamashita, Toshinide
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023.US900
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 60615
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-633-423-9

Alignment Scores:
Pred. No.: 1.14e-29 Length: 60615
Score: 341.00 Matches: 70
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.63% Indels: 0
DB: 19 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-633-423-9 (1-60615)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 45956 GTTGTGACCTCTCTGCTACTGGAGACATTAAAGAGACTGGAGTGTGTTGGTCCAGC 46015
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41
Db 46016 TTATTCCTGCTGCTCTCTGACAGATTGACAGTTGTCAGTGTAAACGGCTTACATTGCC 46075
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61
Db 46076 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 46135
Qy 62 GlnLysSerAspGluGlyHisProPheArg 71
Db 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165

RESULT 97
US-09-758-140-19
; Sequence 19, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene
US-09-758-140-19

Alignment Scores:
Pred. No.: 2,42e-32 Length: 198
Score: 331.00 Matches: 66
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.55% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-758-140-19 (1-198)

QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1 TTTAGGATATACAAAGGTTGTGATCCAAAGCTATCCAGAAATCAGATCAAGGCCACCCATTTC 60

QY 71 ArgAlaTyrLeuGluSerGlnValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 61 AGGGCATATCTGGAATCTGAAATCTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAAT 120

QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluPheLeuValAsp 110
Db 121 TCTGCTCTTGGTCATGTGAATCTGCAGATACAGATAAAGAACTCAGGCGCTCTTCTTAGTTGAT 180

QY 111 AspLeuValAspSerLeu 116
Db 181 GATTTAGTTGATTTCTGTG 198

RESULT 98
US-09-972-599A-19
; Sequence 19, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198

QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1 TTTAGGATATACAAAGGTTGTGATCCAAAGCTATCCAGAAATCAGATCAAGGCCACCCATTTC 60

QY 71 ArgAlaTyrLeuGluSerGlnValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 61 AGGGCATATCTGGAATCTGAAATCTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAAT 120

QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluPheLeuValAsp 110
Db 121 TCTGCTCTTGGTCATGTGAATCTGCAGATACAGATAAAGAACTCAGGCGCTCTTCTTAGTTGAT 180

QY 111 AspLeuValAspSerLeu 116
Db 181 GATTTAGTTGATTTCTGTG 198

RESULT 99
US-09-918-995-5532
; Sequence 5532, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5532
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(497)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5532

~Alignment Scores:
Pred. No.: 1,2e-31 Length: 497
Score: 330.50 Matches: 61
Percent Similarity: 81.55% Conservative: 23
Best Local Similarity: 59.22% Mismatches: 18
Query Match: 35.50% Indels: 1
DB: Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-918-995-5532 (1-497)

QY 88 TyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluPhe 107
Db 57 TACATGAATGCTGCCATGCGCACATCAACAGTCCCTGAAACTCATATTATTCCTCTTT 116
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```
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene
US-09-758-140-19

Alignment Scores:
Pred. No.: 2,42e-32 Length: 198
Score: 331.00 Matches: 66
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.55% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-758-140-19 (1-198)

QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1 TTTAGGATATACAAAGGTTGTGATCCAAAGCTATCCAGAAATCAGATCAAGGCCACCCATTTC 60

QY 71 ArgAlaTyrLeuGluSerGlnValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 61 AGGGCATATCTGGAATCTGAAATCTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAAT 120

QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluPheLeuValAsp 110
Db 121 TCTGCTCTTGGTCATGTGAATCTGCAGATACAGATAAAGAACTCAGGCGCTCTTCTTAGTTGAT 180

QY 111 AspLeuValAspSerLeu 116
Db 181 GATTTAGTTGATTTCTGTG 198

RESULT 98
US-09-972-599A-19
; Sequence 19, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198

QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1 TTTAGGATATACAAAGGTTGTGATCCAAAGCTATCCAGAAATCAGATCAAGGCCACCCATTTC 60

QY 71 ArgAlaTyrLeuGluSerGlnValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 61 AGGGCATATCTGGAATCTGAAATCTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAAT 120

QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluPheLeuValAsp 110
Db 121 TCTGCTCTTGGTCATGTGAATCTGCAGATACAGATAAAGAACTCAGGCGCTCTTCTTAGTTGAT 180

QY 111 AspLeuValAspSerLeu 116
Db 181 GATTTAGTTGATTTCTGTG 198

RESULT 99
US-09-918-995-5532
; Sequence 5532, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5532
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(497)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5532

~Alignment Scores:
Pred. No.: 1,2e-31 Length: 497
Score: 330.50 Matches: 61
Percent Similarity: 81.55% Conservative: 23
Best Local Similarity: 59.22% Mismatches: 18
Query Match: 35.50% Indels: 1
DB: Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-918-995-5532 (1-497)

QY 88 TyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluPhe 107
Db 57 TACATGAATGCTGCCATGCGCACATCAACAGTCCCTGAAACTCATATTATTCCTCTTT 116
```



QY 108 LeuValAspSerLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyr 127  
Db 117 CTGGTAGAATCTGTTGACTCTTGAAGCTGGCTGTCTTCATGTGGCTGATGACCTAT 176  
QY 128 ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 147  
Db 177 GTTGTGCTGTTTAAACGAATCACCTTCTTAATTTCTTGCTGAACCTGCTCATTTTCAGT 236  
QY 148 ValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsn 167  
Db 237 GTCCGATGCTATGAGAGTACAGACCCAGATGATCATATGTGGCATCGCCCGA 296  
QY 168 LysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArg 186  
Db 297 GATCAGACCAAGTCAATTGTTGAAAGATCCAAGCAAACTCCCTGGATCGCCAAAAA 356  
QY 187 LysAlaGlu 189  
Db 357 AAGGCAGAA 365

RESULT 100

US-09-972-599A-21  
; Sequence 21, Application US/09972599A  
; Patent No. US20020077295A1  
; GENERAL INFORMATION:  
; APPLICANT: STRITTMATTER, STEPHEN M.  
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
; FILE REFERENCE: C077 CIP US  
; CURRENT APPLICATION NUMBER: US/09/972,599A  
; CURRENT FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: PCT/US01/01041  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1120  
; OTHER INFORMATION: of human No. US20020077295A10A  
US-09-972-599A-21

Alignment Scores:  
Pred. No.: 3,24e-32 Length: 198  
Score: 330.00 Matches: 66  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 35.45% Indels: 0  
DB: Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-972-599A-21 (1-198)

QY 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71  
Db 1 AGGATATACAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGG 60  
QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91  
Db 61 GCATATCTGGAATCTGAAGTCTGCTATATCTGAGGAGTTGGTTTCAGAGTACAGTAATTCT 120  
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111  
Db 121 GCTCTTGGTTCATGTGAAGTGCACGATGAAGAACTCAGCGCCTCTTCTTGTGATGAT 180

QY 112 LeuValAspSerLeuLys 117  
Db 181 TTAGTTGATTCTCTGAAG 198  
Search completed: June 19, 2005, 07:09:22  
Job time : 509.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 06:25:42 ; Search time 2558 Seconds  
(without alignments)

2812.411 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQKIPGLKRAE 189

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/Cgn2\_1/USPTO\_spool\_p/US09830972/runat\_16062005\_153945\_19031/app\_query.fasta\_1.654  
-DB=EST -QFMT=fasgap -SUFFIX=est -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HRAPIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_ges1:\*  
9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	927	99.6	598	7	CF118424
2	927	99.6	600	9	AY404970 Homo sapi
3	927	99.6	650	6	CB215381 NISC np05
4	927	99.6	667	7	CN429712 170006000
5	927	99.6	672	7	CK977984 4109431 B
6	927	99.6	682	6	CB162885 K-EST0223
7	927	99.6	712	7	CK971318 4087182 B
8	927	99.6	743	6	CD102817 AGENCOURT
9	927	99.6	758	4	BG697436 602660623

10	927	99.6	788	1	AL533461
11	927	99.6	843	4	BG570231
12	927	99.6	849	7	CR765672
13	927	99.6	875	1	AL573494
14	927	99.6	1540	3	CR611869
15	927	99.6	1785	3	AF077050
16	924	99.2	730	1	AU297347
17	921	98.9	634	6	CB067821
18	921	98.9	670	7	CV030029
19	921	98.9	960	7	CN646472
20	921	98.9	983	7	CN803408
21	921	98.9	1031	7	CN647521
22	915	98.3	805	7	CO735185
23	915	98.3	958	4	BM801698
24	914	98.2	757	4	BG715173
25	913	98.1	924	5	BU845601
26	913	98.1	1042	7	CN805577
27	912	98.0	592	7	CN482802
28	912	98.0	871	6	CD110203
29	911	97.9	600	9	AY404972
30	911	97.9	679	4	BI149602
31	911	97.9	708	4	BI157842
32	908	97.5	779	7	CO401465
33	908	97.5	1013	7	CO4048918
34	908	97.5	1018	7	CN801888
35	905	97.2	794	1	AU080127
36	905	97.2	799	1	AU080133
37	904	97.1	695	7	CV077130
38	904	97.1	758	4	BG740561
39	904	97.1	791	7	CF977898
40	904	97.1	1081	7	CN641703
41	902	96.9	747	4	BG623462
42	900	96.7	585	7	CO259245
43	899	96.6	742	4	BT838242
44	896	96.2	3533	3	AK034902
45	894	96.0	781	4	BI079496

#### ALIGNMENTS

RESULT 1

CF118424

LOCUS

DEFINITION

CF118424  
fs543.z1 fs 103-105d fetal sheep skin library Ovis aries cdna. mRNA

sequence.

CF118424

CF118424.1 GI:33182344

EST.

KEYWORDS

SOURCE

ORGANISM

Ovis aries (sheep)

Ovis aries

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Caprinae; Ovis.

1 (bases 1 to 598)

Adelson, D.L., Cam, G.R., Desilva, U. and Franklin, I.R.

Gene expression in sheep skin and wool (hair)

Genomics 83 (1), 95-105 (2003)

Contact: Adelson, David L.

CSIRO Livestock Industries

306 Carmody Road, St Lucia QLD 4067, Australia

Tel: +61 7 3214 2700

Fax: +61 7 3214 2900

Email: li-enquiries@csiro.au.

Location/Qualifiers

1..598

/organism="Ovis aries"

/mol\_type="mRNA"

/strain="Merino"

/db\_xref="taxon:9940"

/sex="male"

/dev\_stage="103-105d pc fetus"

/lab\_host="BM25.8"

/clone\_lib="fs 103-105d fetal sheep skin library"

FEATURES  
source

/note="Organ: midflank skin; Vector: pTriplex; Site 1: EcoRI; Site 2: XbaI; Arrayed library filters screened by hybridization with labeled dinucleotide repeats. first strand synthesis XbaI-(dr)15 primed, EcoRI adaptors were ligated to cDNA before cloning. EcoRI- NotI- SalI adaptor sequence, 5'-AATTCGGCGCGGCTGAC GCGCGCGGCGAGTGG-P04-5', 5' sequencing primer 5' TCCGAGATCTGGACGAGC 3', 3' sequencing primer 5' TAATACGACTCACTATAGG 3', submitted sequences in excess of 50 bp after vector and quality clipping (phred 13) submitted to GenBank."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,74e-104 Length: 598  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CF118424 (1-598)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 32 GTTGTGACCTCTCTCTGAGAGACATTAAAGAGACTGGAGTGGTGGTGGCCAC 91  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 92 TTATTCCTGCTCTCTCACTGACAGTATTTCAGCATTTGTGAGTGTAAACGGCTACATTGCC 151  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
 DB 152 TTGGCCCTGCTCTCTGTGACTATCATCTTTAGGATATAAAGGTGTGTATCCAGGCTATC 211  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 212 CAGAAATCTGATGAGGACACCCATTCAGGCGATATTGGATCTGGAATCTGATATCT 271  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 272 GAGGAGTTGGTTTCAGAAATACAGTAAATCTGCTCTGGTCACTGTGAATGCACATAAAA 331  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121  
 DB 332 GAATCAGACGGCTCTCTTAGTGTGATGATTGATTTGATTTCTGAAAGTTGCGAGTTG 391  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 DB 392 ATGTGGGTATTTACCTATGTTGGTGGCTTGTTCATGTTCTGACACTACTAATTTGGCT 451  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 452 CTGATTTCACTCTTCAGTGTCTCTGTTATTATGAAACGGCATCAGCGCAATATAGATCAT 511  
 QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 512 TATCTAGGACTGTCGAAATAGAAATGTTAAAGATGCTATGGCTAAATATCCAGCAAAATC 571  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 572 CCTGGATTGAGCGTAAAGCTGNA 595

## RESULT 2

AY404970  
 LOCUS Homo sapiens RTN4 gene, linear GSS 16-DEC-2003  
 DEFINITION Homo sapiens RTN4 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY404970  
 VERSION AY404970.1 GI:39760944  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 600)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreria, S., Wang, G., Zheng, X.H., White, F.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302

## REFERENCE

## AUTHORS

2 (bases 1 to 600)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreria, S., Wang, G., Zheng, X.H., White, F.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.

## TITLE

## JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.

## FEATURES

## source

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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 <1..>600  
 /gene="RTN4"  
 /locus\_tag="HCM2068"

## gene

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,75e-104 Length: 600  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AY404970 (1-600)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 34 GTTGTGACCTCTCTCTGAGAGACATTAAAGAGACTGGAGTGGTGGTGGCCAC 93  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 94 CTATTCCTGCTCTCTTTCATTCAGCATTTGTGAGCGTAAACAGCTACATTGCC 153  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAAAGGTGTGTATCCAGCTATC 213  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 214 CAGAAATCAGATGAGGCGACCCATTCAGGCGATATCTGGAATCTGAAGTTGCTATATCT 273  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 274 GAGGAGTTGGTTTCAGAAATACAGTAAATCTGCTCTTGGTTCATCTGAACTGCACGATAAAG 333  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121  
 DB 334 GAATCAGGCGCTCTCTTCTAGTGTGATTTAGTGTGATTTCTGAAAGTTGCGAGTTG 393  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 DB 394 ATGTGGGTATTTACCTATGTTGGTGGCTTGTTCATGTTCTGACACTACTGATTTGGCT 453  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 454 CTCAATTCACCTCTTCAGTGTCTCTGTTATTATGAAACGGCATCAGGCGACAGATAGATCAT 513  
 QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 514 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 573

Qy 182 ProGlyLeuLysArgLysAlaGlu 189

Db 574 CCTGGATTGAAGCGCAAAAGCTGAA 597

RESULT 3

LOCUS CB215381

DEFINITION NISC\_np05dl2.y1 NICHHD\_HS\_Ut1 Homo sapiens cDNA clone IMAGE:5937070

ACCESSION CB215381

VERSION CB215381.1 GI:28263573

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 650)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
CDNA Library Preparation: CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [info@image.llnl.gov](mailto:info@image.llnl.gov)  
Plate: LLNLW13163 row: G column: 23  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1..650  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5937070"  
/sex="female"  
/tissue\_type="normal endometrium, late proliferative phase, cycle day 13"  
/lab\_host="DH10B (T1-resistant)"  
/clone\_lib="NICHHD\_HS\_Ut1"  
note="Organ: uterus; Vector: pCMV-SPORT6.1.cdb (ResGen, Invitrogen Corporation); Site 1: NotI; Site 2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (late proliferative phase, cycle day 13). Average insert size 1.9 kb. Library constructed by ResGen (Invitrogen Corporation)."

ORIGIN

Alignment Scores:

Pred. No.:	3 09e-104	Length:	650
Score:	927.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.57%	Indels:	0
DB:	6	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CB215381 (1-650)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleTysThrGlyValValPheGlyAlaSer 21

Db 19 GTTGTGACCTCCTGCTACTGAGACATTAAAGAGCTGGAGTGGTGGTGGCCAGC 78

Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 79 CTATTCTGCTGCTTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCCCTACATGCC 138

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 139 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTTGTGATCCAGCTATC 198

Qy 62 GlnlySerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 199 CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAAATCTGGAAGTTGCTATATCT 258

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

Db 259 GAGGAGTTGGTTCAAGATGACAGTAATTTCTGCTCTTGGTCACTGTGAACTGCACGATAAG 318

Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 319 GAACCTCAGGCGCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTTCAGTGTG 378

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141

Db 379 ATGTGGGTATTTACCTATGTTGGTGCCCTGTTTAAATGCTGACACTACTGATTTGGCT 438

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

Db 439 CTCAATTCACCTTCAGTGTTCTGTGTTATTTATGACGGCATCAGGCACAGATAGATCAT 498

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 499 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 558

Qy 182 ProGlyLeuLysArgLysAlaGlu 189

Db 559 CCTGGATTGAAGCGCAAAAGCTGAA 582

RESULT 4

LOCUS CN429712

DEFINITION 667 bp mRNA linear EST 16-MAY-2004

ACCESSION 1700600059220 GRN\_PRENU Homo sapiens cDNA 5', mRNA sequence.

VERSION CN429712

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 667)

AUTHORS Li Y., Xu C., Fang R., Guegler, K., Rao, M.S., Mandalam, R., Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fiek, G.J., Lebkowski, J. and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: [rbrandenberger@geron.com](mailto:rbrandenberger@geron.com)  
Insert Length: 667 Std Error: 0.00.  
Location/Qualifiers  
1..667  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/clone\_lib="GRN\_PRENU"  
note="Oligo dt primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic acid and mitogens."

ORIGIN

Alignment Scores:

Pred. No.:	3.2e-104	Length:	667
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Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservativeness: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CM429712 (1-667)

QY 2 ValValAspLeuLeuThrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 83 GTTGTGACCTCTGCTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCAGC 142  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaThrIleAla 41  
 DB 143 CTATTCTGCTGCTTTCTTACGACAGTATTGAGCATTTGAGCGTAAACAGCTACATTGCC 202  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleThrLysGlyValIleGlnAlaIle 61  
 DB 203 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCTATC 262  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaThrLeuGluSerGluValAlaIleSer 81  
 DB 263 CAGAAATCAGATCAGAGCCACCCATTCAGGGCATACTCGAATCTGAAATCTGCTATATCT 322  
 QY 82 GluGluLeuValGlnLysThrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 323 GAGGAGTTGGTTTCTGAGAGTACAGTAATCTGCTCTTGGTCTGATGAACTGCAGATAAAG 382  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 383 GAACCTCAGGCGCTCTCTTGTAGTATGATTTAGTTGATCTCTGAAATTTGAGTGTG 442  
 QY 122 MetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 DB 443 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATGCTGACACTGATGATTTGGCT 502  
 QY 142 LeuIleSerLeuPheSerValProValIleThrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 503 CTCATTTTCACTTTCAGTGTCTCTGTTATTTATTAAGAGCGCATCAGGCACAGATGATCAT 562  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 563 TATCTAGGACTTGCATAATAGATGTTTAAAGATGCTATGGCTAAATCCAGCAAAATC 622  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 623 CCTGGATTGAAGCGCAAGCTGAA 646

RESULT 5  
 CK977984 672 bp mRNA linear EST 16-MAR-2004  
 LOCUS 4109431 BARC 9BOV Bos taurus cDNA clone 9BOV37\_106 5', mRNA  
 DEFINITION sequence.  
 ACCESSION CK977984  
 VERSION CK977984.1 GI:45495958  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 672)  
 Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,  
 G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.  
 TITLE Production of EST from cDNA libraries derived from immunologically  
 activated bovine gut  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Tad S. Sonstegard  
 Bovine Functional Genomics Laboratory  
 Animal and Natural Resources Institute  
 Bldg. 200 Rn2A BARC-East, Beltsville, MD 20705, USA  
 Tel: 3015048416  
 Fax: 3015048414

Email: tads@anri.barc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 0.000925 using options -trim\_alt "-trim fasta. Vector identified  
 by cross match using options -minmatch 12 -minscore 18  
 Plate: 37 row: I column: 06  
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 High quality sequence stop: 672.

#### FEATURES

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 /tissue\_type="Pooled"  
 /dev\_stage="Multiple"  
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 /clone\_lib="BARC 9BOV"  
 /note="Organ: Abomasum; Vector: pAgen-1; Site\_1: EcoRV;  
 Site\_2: NotI; Equimolar amounts of mRNA extracted from  
 fundic and pyloric abomasums of 18 and 21 week old steers.  
 Exposure to Osteragia osteragi was initiated at 15 weeks  
 of age. fundic and pyloric abomasum"

#### ORIGIN

Alignment Scores:  
 Pred. No.: 3,24e-104 Length: 672  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservativeness: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK977984 (1-672)  
 QY 2 ValValAspLeuLeuThrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 105 GTTGTGACCTCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGCAGC 164  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaThrIleAla 41  
 DB 165 TTGTTCTGCTGCTCTGCTGACAGTATTGAGCATTTGAGTGTAAACGCTACATTGCC 224  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleThrLysGlyValIleGlnAlaIle 61  
 DB 225 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATTAAGGCTGTGATCCAGGCTATC 284  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaThrLeuGluSerGluValAlaIleSer 81  
 DB 285 CAGAAATCTGATGAGCGCCACCCATTCAGGGCATAATTTGGAATCTGAAATGCTATCT 344  
 QY 82 GluGluLeuValGlnLysThrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 345 GAGGAGTTGGTTTCTGAGAGTACAGCAATCTGCTCTTGGTCACTGTTAACTGCAATAAAA 404  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 405 GAACTCAGACGCTCTCTCTTAGTGTATGATTTAGTTGATTTCTGTAAGTTTGCAGTGTG 464  
 QY 122 MetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaIle 141  
 DB 465 ATGTGGGTATTTACCTATGTTGGTGGCTTGTCAATGGTCTGACACTACTAAATTTGGCT 524  
 QY 142 LeuIleSerLeuPheSerValProValIleThrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 525 CTGATTTTCACTTTCAGTGTCTCTGTTATTTATGACGCGCATCAGCGCAAAATGATCAT 584  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
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 QY 182 ProGlyLeuLysArgLysAlaGlu 189

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Db      645  CCTGGATTGAACGCTAAAGCTGAA 668
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RESULT 6
CB162885
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DEFINITION 5', mRNA sequence.
ACCESSION  CB162885
VERSION    CB162885.1  GI:28149011
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 682)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
          Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
          Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
          Genome Research Center
          Korea Research Institute of Bioscience & Biotechnology
          52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
          Tel: +82-42-860-4470
          Fax: +82-42-860-4409
          Email: yongsung@mail.kribb.re.kr
          Plate: 41, row: F column: 04
          High quality sequence stop: 682.
          Location/Qualifiers
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              /mol_type="mRNA"
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              /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
              /lab_host="Top10p"
              /clone_lib="L18POOLin1"
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              Site 2: NotI; The library was contributed by the Soares
              Laboratory and it was constructed as described by Bonaldo,
              M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
              6(9): 791-806. RNA was prepared from harvested cell
              culture."
ORIGIN
Alignment Scores:
Pred. No.:      3,318-104      Length:      682
Score:          927.00      Matches:    188
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    99.57%      Indels:    0
DB:             6      Gaps:      0

US-09-830-972-29_copy_990_1178 (1-189) x CB162885 (1-682)

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Db      115  GTTGTGACCTCTCTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 174
|||||
Qy      22  LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla 41
|||||
Db      175  CTATTCTCTGCTCTTTCATTGACAGTATTACAGATTGTGAGCGTAACGCTACATTGCC 234
|||||
Qy      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlLysGlyValIleGlnAlaIle 61
|||||
Db      235  TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 294
|||||
Qy      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSer 81
|||||
Db      295  CAGAAATCATGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTCTGAAGTGTGCTATATCT 354
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82  GluGluLeuValGlnLysTyrlSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
|||||
355  GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTCTTGGTTCATGTGAACGTCACGATAAG 414
|||||
Qy      102  GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db      415  GAATCTCAGGCCCTCTTCTTAGTTGATGATTAGTTGATTTCTCTGAAGTTTGCACGTGTG 474
|||||
Qy      122  MetTrpValPheThrTyrlValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
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Db      475  ATGTGGGTATTACTTAATGTTGGTGGCTTGTATATGTTCTGACACTACTGATTTGGCT 534
|||||
Qy      142  LeuLeuSerLeuPheSerValProValIleTyrlGluArgHisGlnAlaGlnIleAspHis 161
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Db      535  CTCATTTTCACTCTTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 594
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Qy      162  TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
|||||
Db      595  TATCTAGGACTTGCATAATAAGANTGTTAAAGATGCTATGGCTTAAATCCAGCAAAATC 654
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Qy      182  ProGlyLeuLysArgLysAlaGlu 189
|||||
Db      655  CTGGATTGAAGCGCAAGCTGAA 678
|||||

RESULT 7
LOCUS      CK971318
DEFINITION 4087182 BARC 9BOV Bos taurus cDNA clone 9BOV3_J07 5', mRNA
sequence.
ACCESSION  CK971318
VERSION    CK971318.1  GI:45489292
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
REFERENCE  1 (bases 1 to 712)
AUTHORS   Sonstegard, T.S., Van Taseell, C.P., Matukumalli, L.K., Harhay,
          G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
          Production of EST from cDNA libraries derived from immunologically
          activated bovine gut
          Unpublished (2004)
          Contact: Tad S. Sonstegard
          Bovine Functional Genomics Laboratory
          Animal and Natural Resources Institute
          Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
          Tel: 3015048416
          Fax: 3015048414
          Email: tads@nri.barc.usda.gov
          Single pass sequencing. Bases called and trimmed with phred
          0.000925 using options -trim_alt "-trim.fasta. Vector identified
          by cross_match using options -minmatch 12 -minscore 12
          Plate: 3 row: J column: 07
          Seq primer: CCCAGTCACGACGTTGTAAACCG
          High quality sequence stop: 712.
          Location/Qualifiers
            1..712
              /organism="Bos taurus"
              /mol_type="mRNA"
              /strain="Holstein"
              /db_xref="taxon:9913"
              /clone="9BOV3_J07"
              /sex="Male"
              /tissue_type="pooled"
              /dev_stage="Multiple"
              /lab_host="DH10B T1 phage resistant"
              /clone_lib="BARC 9BOV"
              /note="Organ: Abomasum; Vector: pagen-1; Site 1: EcoRV;
              Site 2: NotI; Equimolar amounts of mRNA extracted from
              fundic and pyloric abomasums of 18 and 21 week old steers.
              Exposure to Osteragia osteragi was initiated at 15 weeks
              of age. fundic and pyloric abomasum"

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## ORIGIN

## Alignment Scores:

Pred. No.: 3,528-104 Length: 712  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK971318 (1-712)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 18 GTTGTGACCTCTCTACTGAGAGACATTAAGAACACTGGAGTGGTGTGGTGCACG 77  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 78 TTGTTCTGCTGCTCTGCTGACAGTATTCAGCATTTGAGTGTAAAGGCTACATTGCC 137  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
DB 138 TTGGCCCTGCTCTCTGCTGACATATTAAGGCTGTGATCCAGGCTATC 197  
QY 62 GlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 198 CAGAAATCTGATGAAGCCACCCATTCAGGGCATATTTGGAATCTGAAGTGTCTATCT 257  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 258 GAGGAGTTGGTCAGAGTACAGCAATTCGTCTTGGTCATGTTAACTGCACATATAA 317  
QY 102 GluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 318 GAACCTCAGACGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 377  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 378 ATGTGGGTATTTACCTATGTTGGTGTCTTGTCAATGGTGTGACATCTACTAATTTGGCT 437  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 438 CTGATTTCACTCTCTAGTGTCTCTGTTATTAAGAAGCGCATCAGCGGCAATAGATCAT 497  
QY 162 TyrLeuGlyLeuAlaSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 498 TATCTGGACTTGCAAAATGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 557  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 558 CCTGGATTGAAGCGTAAAGCTGAA 581

## RESULT 8

CD102817

LOCUS

DEFINITION

AGENCOURT\_14009211 NIH\_MGC\_186 Homo sapiens cdna clone

IMAGE:30373271 5', mRNA sequence.

ACCESSION

CD102817

VERSION

CD102817.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 743)

NIH-MGC http://mgi.nci.nih.gov/

NATIONAL INSTITUTE OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: NDCM166 row: m column: 24  
High quality sequence stop: 617.  
Location/Qualifiers  
source  
1..743  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30373271"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_186"  
/note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: Sfil (ggcattatggcc); Site 2: Sfil (ggcgcctggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a pooled samples of tissues from Skin, meninges, duramater, pia matter and choroid plexus. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library"

## ORIGIN

## Alignment Scores:

Pred. No.: 3,748-104 Length: 743  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD102817 (1-743)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 151 GTTGTGACCTCTCTACTGAGAGACATTAAGAACACTGGAGTGGTGTGGTGCACG 210  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 211 CTATTCCTGCTCTTTCATGACAGTATTCAGCAATTCGAGGCTAACAGCTACATTCG 270  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 271 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATC 330  
QY 62 GlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 331 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTGTCTATCT 390  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 391 GAGGAGTTGGTTTCAAGATACAGTAAATTCGTCTTGGTTCATGTGAACCTGCACGATAAAG 450  
QY 102 GluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 451 GAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 510  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaIle 141  
DB 511 ATGTGGGTATTTACCTATGTTGGTGTCTTAAATGTTCTGACACTACTGATTTGGCT 570  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 571 CTCAATTCACCTCTCAGTGTCTCTGTTATTAAGAAGCGCATCAGGCGACAGATAGATCAT 630  
QY 162 TyrLeuGlyLeuAlaSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181





```

Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 99.57%              Indels: 0
DB: 1                             Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AL5333461 (1-788)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 156 GTTGTGACCTCTGCTACTGGAGAGACATTAAAGACATGGAGTGGTGTGGTGGCAGC 215
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
Db 216 CTATTCCTGCTGCTTTTCATTGACAGTATTGACGATTTGAGCGTAAACGCTCATATTGCC 275
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 276 TTGGCCCTGCTCTCTGTGACCATCAGTTTAGGATATACAGGCTGTGATCCAGCTATC 335
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 336 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTCGAAGTTGCTATATCT 395
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 396 GAGGAGTGTGTTTCTGAGAGTACAGTAATCTGCTCTGGTCATGTGAACGCGACGATAAG 455
QY 102 GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 456 GAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTGCAGGTGTTG 515
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 516 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGCTGCACACTACTGATTTGGCT 575
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 576 CTATTTCACTCTTCAGTGTCTCTGTTATTATTAAGACGGCATCAGGACAGATAGATCAT 635
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 636 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATATCCAGCAANAATC 695
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 696 CCTGGATTGAAGCGCAAAAGCTGAA 719

RESULT 11
BG570231 843 bp mRNA linear EST 10-APR-2001
LOCUS 602590632F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717662 5',
DEFINITION mRNA sequence.
ACCESSION BG570231
VERSION BG570231.1 GI:13577884
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1567 row: 0 column: 07

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High quality sequence stop: 801.
Location/Qualifiers
1. .843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4717662"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
sf11 (ggccctcgcc); Site 2: sf11 (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCAGCATG-df(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 4,48e-104 Length: 843
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BG570231 (1-843)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 2 GTTGTGACCTCTCTACTGGAGAGACATTAAAGACATGGAGTGGTGTGGTGGCAGC 61
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
Db 62 CTATTCCTGCTGCTCTTCATTGACGATTTACAGATTTGAGCGTAAACGCTCATATTGCC 121
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 122 TTGGCCCTGCTCTCTGTGACCATCAGTTTAGGATATACAGGCTGTGATCCAGCTATC 181
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 182 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTCGAAGTTGCTATATCT 241
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 242 GAGGAGTGGTTCAGAGTACAGTAATCTGCTCTTGGTCATGTAAGTGCAGGATAAG 301
QY 102 GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 302 GAATCAGGCGCTCTCTTACTGATGATTTAGTTGATTTCTCTGAAGTTGCGAGTGTG 361
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeuAla 141
Db 362 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGCTGCACACTACTGATTTGGCT 421
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 422 CTCATTTCACTCTTCAGTGTCTCTGTTATTATTAAGACGGCATCAGGACAGATAGATCAT 481
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 482 TATCTAGGACTTGCAATTAAGAAATGTTAAAGATGCTATGGCTAAATATCCAGCAANAATC 541
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 542 CCTGGATTGAAGCGCAAAAGCTGAA 565

RESULT 12
CR765672

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LOCUS CR765672 849 bp mRNA linear EST 23-SEP-2004  
 DEFINITION DKFZp469C2134 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone  
 ACCESSION CR765672  
 VERSION CR765672.1 GI:52605968  
 KEYWORDS EST.  
 SOURCE Pongo pygmaeus (orangutan)  
 ORGANISM Pongo pygmaeus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 REFERENCE 1 (bases 1 to 849)  
 AUTHORS Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,  
 Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and  
 Wiemann, S.  
 TITLE Pongo pygmaeus mRNA (Ottenwaelder, B., Obermaier, B.,  
 Deutschenbaur, S., et al.)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: MIPS  
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,  
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix  
 (Martinsried/Germany) within the cDNA sequencing consortium of the  
 German Genome Project. This clone (DKFZp469C2134) is available at  
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
 Berlin, Germany. Please contact RZPD for ordering:  
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469C2134  
 Further information about the clone and the sequencing project is  
 available at http://mips.gsf.de/projects/cdna/  
 FEATURES  
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 /dev stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="469 (synonym: pkid1)"  
 /note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.52e-104 Length: 849  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR765672 (1-849)  
 Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 150 GTTGTGACCTCTCTACTCGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCAGC 209  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 210 CTATTCTCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGTGTAAACAGCCATCATTTGCC 269  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 270 TTGGCCCTGCTTCTCTGTGACCATCATCTTTAGATATACAGGGTGTGATCAAGCTATC 329  
 Qy 62 GlnLysSerAspGluGlyYhiProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 330 CAGAAATCAGATGAGGCCACCCATTACGGCATATCTGGAATCTGGAATCTGAAGTTGCTATATCT 389  
 Qy 82 GluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 390 GAGGAGTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGTAACACTGACGATAAAG 449

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 450 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGTG 509  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 510 ATGTGGGTATTACCTATGTTGGTGCCTGTTTAAATGCTCTGACGCTACTGATTTGGCT 569  
 Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 570 CTCATTTTCACCTCTCAGTGTTCCTGTTTATTATGACGGCATCAGGCACAGATAGTATCAT 629  
 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 630 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCAAGCGCAAAATC 689  
 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 690 CCTGGATTGAAGCGCAAAAGCTGAA 713  
 RESULT 13  
 AL573494/c  
 LOCUS AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 DEFINITION clone CSODI051YB11 3-PRIME, mRNA sequence.  
 ACCESSION AL573494  
 VERSION AL573494.3 GI:46246666  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 875)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31294840.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1423.r  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?s=CSODI051CA06NF1&c=1423.r.  
 FEATURES  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="CSODI051YB11"  
 /tissue type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.72e-104 Length: 875  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x AL573494 (1-875)

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QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
      |||
Db      875 GTTGTGACCTCTGCTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 816

QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
      |||
Db      815 CTAATTCCTGCTCTTCATACACAGTATTCAGCATTTGAGCGGTAAACAGCCTACATTGCC 756

QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
      |||
Db      755 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 696

QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      |||
Db      695 CAGAAATCAGATGAAGCCACCCATTACAGGCATATCTGGAATCTGAAGTTCGTATATCT 636

QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101
      |||
Db      635 GAGGAGTTGGTCAGAAATACAGTAATTCCTCTTGGTCATGTGACTGCACGATAAG 576

QY      102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
      |||
Db      575 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTCAGGTGTTG 516

QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
      |||
Db      515 ATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAATGGTCTGACACTACTGATTTGGCT 456

QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db      455 CTCATTTCACTCTTCAGTGTCTCTGTTATTAAGACGCATCAGCACAGATAGATCAT 396

QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      395 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAAGCAAAATC 336

QY      182 ProGlyLeuLysArgLysAlaGlu 189
      |||
Db      335 CCTGGATTGAAGCGCAAGCTGAA 312

RESULT 14
CR611869
LOCUS   full-length cDNA clone CS0DN004YJ08 of Adult brain of Homo sapiens
DEFINITION (human).
ACCESSION CR611869
VERSION   CR611869.1 GI:50492676
KEYWORDS HTC; CNSLT cDNA.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL   Full-length cDNA libraries and normalization
REMARK    Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1540)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1540
/organism="Homo sapiens"

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/mol_type="mRNA"
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/clone="CS0DN004YJ08"
/tissue_type="Adult brain"
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Alignment Scores:
Pred. No.: 1.06e-103 Length: 1540
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 3 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CR611869 (1-1540)

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Db      156 GTTGTGACCTCTGCTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 215

QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
      |||
Db      216 CTAATTCCTGCTCTTCATACAGTATTCAGCATTTGAGCGGTAAACAGCCTACATTGCC 275

QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
      |||
Db      276 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 335

QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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Db      336 CAGAAATCAGATGAAGCCACCCATTACAGGCATATCTGGAATCTGAAGTTCGTATATCT 395

QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101
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Db      396 GAGGAGTTGGTCAGAAATACAGTAATTCCTCTTGGTCATGTGACTGCACGATAAG 455

QY      102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db      456 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTCAGGTGTTG 515

QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
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Db      516 ATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAATGGTCTGACACTACTGATTTGGCT 575

QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db      576 CTCATTTCACTCTTCAGTGTCTCTGTTATTAAGACGCATCAGCACAGATAGATCAT 635

QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      636 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAAGCAAAATC 695

QY      182 ProGlyLeuLysArgLysAlaGlu 189
      |||
Db      696 CCTGGATTGAAGCGCAAGCTGAA 719

RESULT 15
AF077050
LOCUS   1785 bp mRNA linear HTC 21-NOV-2002
DEFINITION Homo sapiens neuroendocrine-specific protein C homolog mRNA,
complete cds.
ACCESSION AF077050
VERSION   AF077050.1 GI:4689147
KEYWORDS HTC.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1785)
Song, H., Peng, Y., Zhou, J., Huang, Q., Dai, M., Mao, Y., Yu, Y., Xu, X.,
Luo, B., Hu, R. and Chen, J.
Human neuroendocrine-specific protein C (NSP) homolog gene
TITLE

```

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1785)  
AUTHORS Song, H.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUN-1998) Rui-Jin Hospital, Shanghai Institute of  
Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,  
Shanghai 200025, P.R. China  
FEATURES Location/Qualifiers  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1.31e-103 Length: 1785  
Score: 927.00 Matches: 168  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AF077050 (1-1785)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 247 GTTGTGACCTCCTCTGTGACCATCAGCTTAGATATACAGGGTGTGATCCAGCTATC 306  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 307 CTATTCTCGCTCTTTCATTGACGATTCAGCATTTGAGCGTAAACAGCTTACATGCC 366  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGATATACAGGGTGTGATCCAGCTATC 426  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 427 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 486  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 487 GAGGAGTGTGTTTCAAGATACAGTAAATCTGCTTTGGTCATGTAAGTCAAGCTGACGATAAG 546  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 547 GAACCTCAGCGCTCTCTTAGTTCATGATTTAGTTGATCTCTGAAAGTTGCAAGTGTG 606  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 607 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAATGGTCTGACACTACTGATTTGGCT 666  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 667 CTCATTTCACTCTCAGTGTTCCTGTATTATGAACGGCATCAGGCGACAGATAGATCAT 726  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 727 TATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 786  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 787 CTGTGATTGAAGCGCAAGCTGAA 810

## RESULT 16

AU297347

## LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Momoki Hirai

Department of Integrated Biosciences

The University of Tokyo, Graduate School of Frontier Sciences

5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan

Tel: 81-4-7136-3688

Fax: 81-4-7136-3687

Email: mhiraik@k.u-tokyo.ac.jp.

Location/Qualifiers

1..730

/organism="Pan troglodytes verus"

/mol\_type="mRNA"

/sub\_species="verus"

/db\_xref="taxon:37012"

/clone="PorA0834"

/sex="female"

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/dev\_stage="adult"

/clone\_lib="female adult cerebrum, full-length enriched

chimpanzee cDNA library"

ORIGIN

Alignment Scores:

Pred. No.: 8.59e-104 Length: 730

Score: 924.00 Matches: 187

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.47% Mismatches: 0

Query Match: 99.25% Indels: 0

DB: 1 Gaps: 0

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

DB 162 GTTGTGACCTCCTCTGTGACCATCAGCTTAGATATACAGGGTGTGATCCAGCTATC 221

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

DB 222 CTATTCTCGCTCTTTCATTGACGATTCAGCATTTGAGTGTAAACAGCTTACATGCC 281

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

DB 282 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGATATACAGGGTGTGATCCAGCTATC 341

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

DB 342 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 401

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

DB 402 GAGGAGTGTGTTCAAGATACAGTAAATCTGCTCTTGGTTCATGTAAGTCAAGCTGACGATAAG 461

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

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462 GAACCTCAGCGGCTCTCTAGTTGATGATTTAGTTGATTTCTGAAGTTTGAGTGTG 521
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122 MetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
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522 ATGTGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 581
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142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
|||||
582 CTCATTTCACTCTCTCAGTGTCTCTGTTATTTATTAACGCGCATCAGGCACAGATGATCAT 641
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162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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642 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCGAAATC 701
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182 ProGlyLeuLysArgLysAlaGlu 189
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702 CCTGGATTGAGCGCAAGCTGAA 725
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CB067821 634 bp mRNA linear EST 21-JAN-2003
ig38a06.v1 HR85 islet Homo sapiens cDNA clone IMAGE: 5' similar to
TR:09Y293 Q9Y293 FOOCEN-S. [1] ;, mRNA sequence.
CB067821
CB067821.1 GI:27812341
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 634)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Secare,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagaris,I., R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ig38a06.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 460.
Location/Qualifiers
1. .634
/organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="HR85 islet"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

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ORIGIN
Alignment Scores:
Pred. No.: 1.65e-103 Length: 634
Score: 921.00 Matches: 187
Percent Similarity: 99.47% Conservatives: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 6 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x CB067821 (1-634)
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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
|||||
Db 131 CTATTCCTGCTGCTTTCATTCAGATTCACATTTGAGCGGTGACGCTACACCTACATTGCC 190
|||||
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
|||||
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|||||
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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Db 251 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 310
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101
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Db 311 GAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTCTGTCATGTGACTGCAGATAAG 370
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QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db 371 GAACCTCAGCGGCTCTCTTCTAGTCATGATTTAGTTGATCTCTGAAGTTTGAGTGTG 430
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QY 122 MetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
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Db 551 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 610
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QY 182 ProGlyLeuLysArgLysAlaGlu 189
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Db 611 CCTGGATTGAGCGCAAGCTGAA 634
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RESULT 18
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LOCUS 9024 Full length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC014366, mRNA sequence.
CV030029
CV030029.1 GI:51488245
EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,B., Ie Feuch,C.,
Vandenhaute,J., Cusick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M.
HUMAN ORFOME Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Contact: Vidal M

```

Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739  
 Email: Marc.Vidal@dfci.harvard.edu  
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF  
 results from a PCR reaction using an MGC full-length cDNA as  
 template DNA and ORF specific primers  
 PCR Primers  
 FORWARD: ATGGACGGTCAGAGAAAATTGG  
 BACKWARD: CATTACGCTTTGGCTTCAATC  
 Insert Length: 670 Std Error: 66.00  
 Plate: 11045 row: 02 column: B  
 Seg primer: ACTGGCGCTGCTTTTACACGTCGTGACTGGGAAAAAC  
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# FEATURES source

Location/Qualifiers  
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 Donor vector. Reference : MGC (Mammalian Gene Collection)  
 Program Team, Generation and Initial Analysis of more than  
 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,  
 2002, 99(26), 16899-16903"

## ORIGIN

Alignment Scores:  
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 Score: 921.00 Matches: 187  
 Percent Similarity: 99.47% Conservative: 0  
 Best Local Similarity: 99.47% Mismatches: 1  
 Query Match: 98.93% Indels: 0  
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x CV030029 (1-670)

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 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61  
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 Db 214 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 273  
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 Db 274 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTGTGTCATGTGAATCGACCATAAAG 333  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 334 GNACTCAGCGGCTCTTCTTAGTTCATGATTAGTTGATTCTCTGAAAGTTGCAGTGTG 393  
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 Db 394 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGTGCACACTACTGATTTGGCT 453

Qy 142 LeuIleSerLeuPheSerValProValIleTyGluArgHisGlnAlaGlnIleAspHis 161  
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 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 514 TATCTAGACTTGCAATAAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAATC 573  
 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 574 CTGGATTGAAGCGCANAGCTGAA 597  
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 DEFINITION ILLUMIGEN MCQ 26335 Katze\_MMR Macaca mulatta cDNA clone IBIUM:8548  
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 (Hs.436349), mRNA sequence.  
 ACCESSION CN646472  
 VERSION CN646472.1 GI:47159915  
 KEYWORDS EST.  
 SOURCE Macaca mulatta (rhesus monkey)  
 ORGANISM Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.  
 REFERENCE 1 (bases 1 to 960)  
 AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.  
 TITLE Large-scale Rhesus Macaque cDNA Sequencing  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com  
 Sequenced on 2004.03.09. 743 Q20 bases.  
 PCR PRIMERS  
 FORWARD: CCCTCACTAAAGGGAACAAA  
 BACKWARD: CACTATAGGGCGAATTGGTA  
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 Plate: CL000173 row: H column: 11  
 Seg primer: CCCTCACTAAAGGGAACAAA  
 POLYA=No.

## FEATURES source

Location/Qualifiers  
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 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:9544"  
 /clone="IBIUM:8548"  
 /sex="Female"  
 /dev stage="adult"  
 /lab host="E. coli SOLR"  
 /clone lib="Katze\_MMR"  
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
 kit (catalog #200400) and ZAP-cDNA Gigapack III Gold  
 Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.99e-103 Length: 960  
 Score: 921.00 Matches: 186  
 Percent Similarity: 100.00% Conservative: 2  
 Best Local Similarity: 98.94% Mismatches: 0  
 Query Match: 98.93% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN646472 (1-960)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
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Db 189 CTATTCCTGCTGCTTTTCATTCAGAGTATTGAGCATTTGAGTGTAAACAGCCTACATGGC 248
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
Db 249 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 308
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 309 CAGAAATCAGATGAGAGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGGATATCT 368
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuLeuGlyHisValAsnCysThrIleLys 101
Db 369 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTTGTGTCATGTGAAGTCCAGATAAAG 428
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 429 GAACTCAGGCGCCTCTCTTAGTGTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 488
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 489 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTCAGCGCTACTGATTTGGCT 548
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 549 CTCAATTCATCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 608
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 609 TATCTAGGACTTGCAAATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAGCGAAATC 668
Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 669 CCTGGATTGAAGCGCAAGCTGAA 692

RESULT 20
CN803408 983 bp mRNA linear EST 26-MAY-2004
ILLUMIGEN MCQ 32945 Katze MMR Macaca mulatta cDNA clone
IBIUW:11396 57 similar to Bases 136 to 983 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
CN803408
CN803408.1 GI:47699384
EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 983)
AUTHORS Katze, M.G., Thomas, M., Korth, M., Tadonato, S.P. and Magness, C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.04.03. 731 Q20 bases.
PCR Primers
FORWARD: CCTCTACTAAAGGACAAACA
BACKWARD: CACTATAGGGCGAATGGGTA
Insert Length: 983 Std Error: 0.00
Plate: CL000275 Row: C Column: 03
Seq primer: CCTCTACTAAAGGACAAACA
POLY-A-No. Location/Qualifiers
1. .983
/organism="Macaca mulatta"
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/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:11396"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze MMR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN
Alignment Scores: 3.09e-103 Length: 983
Pred. No.: 921.00 Matches: 186
Score: 921.00 Conservative: 2
Percent Similarity: 100.00%
Best Local Similarity: 98.94% Mismatches: 0
Query Match: 98.93% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CN803408 (1-983)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 136 GTTGTGACCTCTCTCTACCTGGAGACATGAGAGACTGGAGTGTGTTGGTCCAGC 195
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 196 CTATTCCTGCTGCTTCATTCAGAGTATTGAGTGTGAGTGTAAACAGCCTACATGGC 255
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 256 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 315
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 316 CAGAAATCAGATGAGAGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGGATATCT 375
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuLeuGlyHisValAsnCysThrIleLys 101
Db 376 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTTGTGTCATGTGAAGTCCAGATAAAG 435
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 436 GAACTCAGGCGCCTCTCTTAGTGTGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 495
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 496 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTCAGCGCTACTGATTTGGCT 555
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 556 CTCAATTCATCTCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 615
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 616 TATCTAGGACTTGCAAATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAGCGAAATC 675
Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 676 CCTGGATTGAAGCGCAAGCTGAA 699

RESULT 21
CN647521 1031 bp mRNA linear EST 13-MAY-2004
ILLUMIGEN MCQ 28658 Katze MMR Macaca mulatta cDNA clone IBIUW:7529
5' similar to Bases 129 to 1018 highly similar to human RTN4
(Hs.436349), mRNA sequence.
CN647521
CN647521.1 GI:47160964
EST.
ACCESSION CN647521
VERSION CN647521
KEYWORDS EST.
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SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE
1 (bases 1 to 1031)
Katz, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.03.24. 773 Q20 bases.
PCR Primers
FORWARD: CCCTCACTAAGGGACAA
BACKWARD: CACTATAGGCGAATGGGTA
Insert Length: 1031 Std Error: 0.00
Plate: CL00187 row: G column: 05
Seq primer: CCCTCACTAAGGGACAA
POLYA=No.
FEATURES
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Location/Qualifiers
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBI:W7529"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katz MMER"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (catalog #200450)"
ORIGIN
Alignment Scores:
Pred. No.: 3.31e-103 Length: 1031
Score: 921.00 Matches: 186
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.94% Mismatches: 0
Query Match: 98.93% Indels: 0
DB: 7 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x CN647521 (1-1031)
QY 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 129 GTTGTGACCTCCTCTACTGGAGACATGAGAACACTGGAGTGGTGTGGTGGCCAGC 188
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrfleAla 41
DB 189 CTATTCTCTGCTCTTTCATTGACAGTATTGACATTGTGAGTGTGAACAGCTACATTGCC 248
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrfleLysGlyValIleAla 61
DB 249 TTGGCCCTGCTCTCTGTGACCATCATGCTTTAGGATATACAGGGGTGTGATCAAGCTATC 308
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrfleLysGluSerGluValAlaIleSer 81
DB 309 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGAAGTTGCCATATCT 368
QY 82 GluGluLeuValGlnLysTyrfleSerAsnSerAlaLeuGlyHisValAsnCyethrIleLys 101
DB 369 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGTTCATGTGTAACCTGACGATAAG 428
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 429 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 488

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QY 122 MetTrpValPheThrTyrfleValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 489 ATGTGGGTATTACTATGTTGGTGGCTTTGTTTAAATGCTGACCTACTGATTTGGCT 548
QY 142 LeuIleSerLeuPheSerValProValIleTyrfleArgHisGlnAlaGlnIleAspHis 161
DB 549 CTCATTTTCACTCTTTCAGTGTTCCTGTTATTATTATGAACGGCATCAGGCACAGATGATCAT 608
QY 162 TyrfleGlyLeuAlaAsnLysAsnValLysPheAlaMetAlaLysIleGlnAlaLysIle 181
DB 609 TATCTAGGACTTGCATAATAAGATGTTAAAGATGCTATGGCTAAATCAAAGCGAAATC 668
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 669 CCTGATTGAAGCGCAAGCTGAA 692
RESULT 22
CO735185
LOCUS
DEFINITION
CO735185 805 bp mRNA linear EST 29-JUL-2004
CDNA clone 10012 5', mRNA sequence.
ACCESSION
CO735185
VERSION
CO735185.1 GI:50822455
KEYWORDS
EST.
SOURCE
Spermophilus lateralis (golden-mantled ground squirrel)
ORGANISM
Spermophilus lateralis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
Spermophilus.
REFERENCE
1 (bases 1 to 805)
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Rogers, J. and Cossins, A.R.
Microarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, Spermophilus lateralis
Unpublished (2004)
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 10 row: 0 column: 12
Seq primer: pf1c T7 (5'-AATACGACTCACTATAGG-3')
High quality sequence stop: 805.
Location/Qualifiers
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/db_xref="taxon:76772"
/clone="10012"
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/tissue_type="embryo"
/dev_stage="embryonic"
/lab_host="E. coli Electromax DH10B"
/clone_lib="squirrel embryo library 1"
/notes="Vector: pF1C; Site 1: SalI GTCGAG; Site 2: BamHI
GGATCC; Normalized and subtracted cDNA library prepared
from embryos"
ORIGIN
Alignment Scores:
Pred. No.: 1.29e-102 Length: 805
Score: 915.00 Matches: 185
Percent Similarity: 99.47% Conservative: 2
Best Local Similarity: 98.40% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 7 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x CO735185 (1-805)

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QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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Db      180 GTTGTGGACCTCTCTACTCGAGACATTAAGAGACTGGAGTAGTGTGGTGGCCAGC 239
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QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
      |||
Db      240 TTATTCCTGCTGCTTTCATGACAGATTAACAGATTTGAGTGTAAACAGCCTACATGTC 299
      |||
QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
      |||
Db      300 TTGGCCCTGCTCTCTGACTATCAGCTTTAGATATATAAGGTGTGATCCAGCTATC 359
      |||
QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      |||
Db      360 CAGAAATCAGATCAGAGCCACCATTCAGGGCTTATTGGAAATCTGATGTCATATATCT 419
      |||
QY      82 GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIleLys 101
      |||
Db      420 GAGGAATTGATTACAGAAATACAGTAATCTGCTCTTGGTCATGTGAACCTGCACGATAAA 479
      |||
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
      |||
Db      480 GAACCTAGACGCTCTCTCTAGTGTGATGATTTAGTTGATTTCTAAAGTTTCGATGTTG 539
      |||
QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
      |||
Db      540 ATGTGGGTATTTACCTATGTTGGTCTGTTGTTCAATGGTCTGACACTACTGATTTTGGCT 599
      |||
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db      600 CTGATTTCACTCTTCAGTGTCTCTGTTATTAGAACGGCATCAGGCACAAATAGATCAC 659
      |||
QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      660 TATCTAGGACTTGATATAGAAATGTTAAAGATGCTATGCTAAATCCAGCAAAAT 719
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QY      182 ProGlyLeuLysArgLysAlaGlu 189
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Db      720 CCTGGATTGAAGCGCAAGCTGAA 743
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RESULT 23
BM801698      958 bp      mRNA      linear      EST 05-MAR-2002
LOCUS      AGENCOURT_6458941 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5558493
DEFINITION      5', mRNA sequence.
ACCESSION      BM801698
VERSION      BM801698.1 GI:19118521
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 958)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabbs-r@mail.nih.gov
      Tissue procurement: ATCC
      CDNA Library Preparation: Life Technologies, Inc.
      CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Agencourt Bioscience Corporation
      Clone Distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      Plate: LLAM1281 row: i column: 22
      High quality sequence start: 25
      High quality sequence stop: 579.
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        1. .958
          /organism="Homo sapiens"
          /mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:5558493"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dr primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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## ORIGIN

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Alignment Scores:
Pred. No.:      1.65e-102      Length:      958
Score:          915.00      Matches:      186
Percent Similarity: 98.94%      Conservative: 0
Best Local Similarity: 98.94%      Mismatches: 2
Query Match:      98.28%      Indels:      0
DB:              4      Gaps:      0
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US-09-830-972-29\_copy\_990\_1178 (1-189) x BM801698 (1-958)

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      |||
QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
      |||
Db      126 CTATTCCTGCTCTCTTCATGACAGTATTCAGCAATTTGTGAGCGTAAACAGCCTACATGTC 185
      |||
QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
      |||
Db      186 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATATAAGGGTGTGATCCAGCTATC 245
      |||
QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      |||
Db      246 CAGAAATCAGATCAGAGCCACCATTCAGGGCATATCTGGAAATCTGAAGTTGCTATATCT 305
      |||
QY      82 GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIleLys 101
      |||
Db      306 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACCTGCACGATAAAG 365
      |||
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
      |||
Db      366 GAACCTAGCGGCTCTCTCTAGTGTGATTTAGTGTGATTTCTGAAAGTTGCGAGTGTG 425
      |||
QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
      |||
Db      426 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATTATGGTCTGACACTACTGATTTGGCT 485
      |||
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db      486 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGCATCAGGCACAGATAGATCAT 545
      |||
QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      546 TATCTACGACTTGCAAATAAGAAATGCTAAAGATGCTATGGCTTAAATCCAGCAAAATC 605
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QY      182 ProGlyLeuLysArgLysAlaGlu 189
      |||
Db      606 CCTGGATTGAAGCGCAAGCTGAA 629
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## RESULT 24

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BM801698      757 bp      mRNA      linear      EST 08-MAY-2001
LOCUS      602675631F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4798279 5',
DEFINITION      mRNA sequence.
ACCESSION      BM801698
VERSION      BM801698.1 GI:13994106
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



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Db      244 GTTGTGACCTCTCTGTACTGGAGACATTAAGAACCTGGAGTGGTGTGGTGGCCAGC 303
QY      22  LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrileAla 41
Db      304 CTATTCTCTGCTGCTTTCAATGACAGTATTTCAGCATTTGAGCGTAACAGCCTACATTGCC 363
QY      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
Db      364 TTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 423
QY      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      424 CAGAAATCAGATGAAGCCACCCATTTCAGGCATATCTGGATCTGAAGTTCGTATATCT 483
QY      82  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      484 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTCTTGGTTCATGTAAGTGCACGATAAAG 543
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      544 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGGTGTG 603
QY      122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db      604 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAATGGTCTGCACACTACTGATTTGGCT 563
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      664 CTCATTTCATCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 723
QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      724 TATCTAGGACTTGCATAATAGATGTTNAAGATGCTATGCTGCTAANATCCAAAGCAAAATC 783
QY      182 ProGlyLeuLysArgLysAlaGlu 189
Db      784 CCTGGGATGAGCGCAAAAGCTGNA 807

CN805577      1042 bp      mRNA      linear      EST 26-MAY-2004
ILLUMIGEN MCQ 36873 Katze_MMR Macaca mulatta cDNA clone
IBIUW:12670 5' similar to Bases 138 to 1022 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
CN805577      1 GI:47701553
EST.
KEYWORDS      Macaca mulatta (rhesus monkey)
SOURCE      Macaca mulatta
ORGANISM      Macaca mulatta
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
TITLE      Cercopitheidae; Macaca.
JOURNAL      1 (bases 1 to 1042)
COMMENT      Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
ILLUMIGEN Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.12. 633 Q20 bases.
PCR Primers
FORWARD: CCTCTACTAAAGGGAACAAA
BACKWARD: CACTATAGCGCAATTGGTA
Insert Length: 1042 Std Error: 0.00
Plate: CL000243 row: C column: 03
Seq primer: CCTCTACTAAAGGGAACAAA
POLYA=Yes.
Location/Qualifiers
1. .1042
/organism="Macaca mulatta"
FEATURES
source

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/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MMR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA synthesis
kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

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## ORIGIN

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Alignment Scores:
Pred. No.:      3.3e-102      Length:      1042
Score:          913.00      Matches:    185
Percent Similarity: 99.47%      Conservative: 2
Best Local Similarity: 98.40%      Mismatches: 1
Query Match:      98.07%      Indels:      0
DB:              7          Gaps:      0

US-09-830-972-29_COPY_990_1178 (1-189) x CN805577 (1-1042)

QY      2  ValValAspLeuLeuTyrTyrPheArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      138 GTTGTGACCTCTCTCTGAGAGACATGAAGAAGACTGGAGTGGTGTGGTGGCCAGC 197
QY      22  LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrileAla 41
Db      198 CTATTCTCTGCTCTTCATTGACAGTATTCAGCATTTGAGTGTGAACAGCCTACATTGCC 257
QY      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      258 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC 317
QY      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      318 CAGAAATCAGATGAAGCGCCACCATTCAGGGCATATCTGGAATCTGAAGTTCGATATCT 377
QY      82  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      378 GAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTCTTGGTCACTGTAAGTGCACGATAAAG 437
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      438 GAACTCAGCGCCCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAAGTTTCAGGTGTG 497
QY      122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db      498 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAATGGTCTGACGCTACTGATTTGGCT 557
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      558 CTCATTTCATCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 617
QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      618 TATCTAGGACTTGCATAATAGAAATGTTAAAGATGCTATGCTGCTAAAAATCCAAAGCAAAATC 677
QY      182 ProGlyLeuLysArgLysAlaGlu 189
Db      678 CCTGGATTGAAGCGCATAGCTGAA 701

```

## RESULT 27

```

CN482802
LOCUS      CN482802
DEFINITION      Homo sapiens cDNA clone hw24h12 5', mRNA sequence. Unamplified (hw)
ACCESSION      CN482802
VERSION        CN482802.1
KEYWORDS      EST.
SOURCE        Homo sapiens (human)

```

592 bp mRNA linear EST 26-APR-2004

**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
**AUTHORS** Tsai, J. Y. and Wistow, G.  
**TITLE** Expressed sequence tag analysis of cultured primary human ocular  
 pericytes  
**JOURNAL** Unpublished (2004)  
**COMMENT** Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 24 row: h column: 12  
 Seq primer: M13Rpl reverse primer (ABI).  
**FEATURES** Location/Qualifiers  
 source 1..592  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="hw24h12"  
 /cell\_type="pericytes"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_lib="Human primary human ocular pericytes."  
 Unamplified (hw)  
 /notes="Organ: Eye; Vector: pSport1; RNA was extracted from  
 primary human pericytes in culture. A directionally cloned  
 cDNA library in the pSPORT1 vector (Invitrogen) was  
 constructed at Bioserve Biotechnology (Laurel MD)  
 essentially following the protocols of the SuperScript  
 plasmid system full details of which are contained in the  
 manufacturer's instruction manual  
 (http://www.lifetech.com/). First strand synthesis was  
 carried out using a Not I primer-adaptor  
 [5'-pGACGTAGTTCATGACGAGCGCGCC(T)15-3']. cDNA was  
 cloned in Not I/Sal I sites. EST analysis was performed at  
 the NIH Intramural Sequencing Center (NISC)."  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 1,96e-102 Length: 592  
 Score: 912.00 Matches: 185  
 Percent Similarity: 99.46% Conservative: 0  
 Best Local Similarity: 99.46% Mismatches: 1  
 Query Match: 97.96% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN482802 (1-592)  

Qy	1	SerValValAspLeuLeuTyrTrpAcqAspIleIeyIysThrGlyValValPheGlyValA	20
Db	35	TCAGTGGTTCACCTCCGTACTGAGAGACATTAAAGAAGCTGAGGTGGTTGGTGGCC	94
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	95	AGCTATTCTCTGCTCTTCATTGACAGTATTTCAGCATTTGTGAGCGTTACAGCTACATT	154
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla	60
Db	155	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAGCT	214
Qy	61	IleGlnIysSerAspGluGlyHisProPheArgNlaTyrLeuGluSerGluValAlaIle	80
Db	215	ATCCAGAAATCAGATGAAGGCCACCCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA	274
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	275	TC TGAGAGATGGTTTCAGAGATGACAGTAATTCGTCTCTTGGTCATGTGAACCTGCACGATA	334
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120

```
Query Match: 97.96% Indels: 1
DB: 6 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x CD110203 (1-871)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 187 GTTGTGACCTCTGCTACTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTGGCCAGC 246
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrIleAla 41
DB 247 CTATTCCTGCTGCTTTCATTCAGCATTTGAGCATTTGAGCGTAAACAGCTACATGTC 306
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
DB 307 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCTATC 366
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 367 CAGAAATCAGATGAAGCCACCCATTTCAGGGCATATCTGGAATCTCGAATGTCATATCT 426
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 427 GAGGAGTTGGTTCAGAACTACAGTAATTCGCTCTTGGTCATGTCGACTGCAGTAAG 486
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 487 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAATCTCGAATGTC 546
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 547 ATGTGGGATTTACCTATGTTGGTGGCTTGTGTTAAATGGTCTGACATCTACTGATTT 606
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 607 CTCAATTCATCTTCTAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATGATCAT 666
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 667 TATCTAGGACTTGCATAATGAATGTTAAAGATGCTATGCTAAATCCAAGCNAATATC 726
QY 182 ProGlyLeu-LysArgLysAlaGlu 189
DB 727 CCTGGAATGAAGCCGCAAGGCTGAA 751

RESULT 29
AY404972 600 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus RTN4 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY404972
VERSION AY404972.1 GI:39760946
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 600)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
Source 1..600
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>600
/gene="RTN4"
/locus_tag="HCM2068"
ORIGIN
Alignment Scores: 2.65e-102 Length: 600
Pred. No.: 911.00 Matches: 185
Score: 99.47% Conservative: 2
Percent Similarity: 98.40% Mismatches: 1
Best Local Similarity: 97.85% Indels: 0
Query Match: 97.96% Gaps: 0
DB: 9
US-09-830-972-29_COPY_990_1178 (1-189) x AY404972 (1-600)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 34 GTTGTGACCTCTCTGCTACTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTGGCCAGC 93
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrIleAla 41
DB 94 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGAGCATATTAAGGCTGTGATCCAAGCTATC 153
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 154 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATTAAGGCTGTGATCCAAGCTATC 213
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 214 CAGAAATCAGATGAAGCCACCCATTTCAGGGCATATTTGGAATCTGAACTGCAATATCA 273
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 274 GAGGAATGGTTCAGAAATATAGTAATCTGCTCTTGGTCATGTCGACACACATAAATA 333
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 334 GAATTGAGCGCTCTCTTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTTCAGTGTG 393
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 394 ATGTGGGATTTTACTTACGTTGGTGGCTTGTGTTCAATGGTTGACACTACTGATTTTAGCC 453
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 454 CTGATCTCACTCTTCAGTATTTCTGTTATATATGAACGGCATCAGCGCCAGATGATCAT 513
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 514 TATCTAGGACTTGCATAAAGAGCGTTAAGGATGCGATGCGCCAAATATCCAAGCAAAATC 573
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 574 CCTGGAATGAAGCCGCAAGGCTGAA 597

RESULT 30
B1149602
LOCUS B1149602
DEFINITION 602848410F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5011899 5',
mRNA sequence.
ACCESSION B1149602
VERSION B1149602.1 GI:14609603
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC <http://mgi.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11062 row: c column: 04  
High quality sequence stop: 679.

#### FEATURES

source  
1..679  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5011899"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

#### ORIGIN

Alignment Scores:  
Pred. No.: 3,17e-102 Length: 679  
Score: 911.00 Matches: 185  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.40% Mismatches: 1  
Query Match: 97.85% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1149602 (1-679)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21  
Db 37 GTTGTGTACCTCTCTGTGACTATAGGAGACATTAAGAGACTGGAGTGTGTTGGTGCCAGC 96  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrfleAla 41  
Db 97 TTATTCTGTCTGTCTGTACAGTGTTCAGCATTTGTCAGTGAACGGCTACATTGCC 156  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrflysGlyValIleGlnAlaIle 61  
Db 157 TTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCAAGCTATC 216  
Qy 62 GlnIysSerAspGluGlyHisProPheArgAlaTyrfleLeuGluSerGluValAlaIleSer 81  
Db 217 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGGAATGTCATATCA 276  
Qy 82 GluGluLeuValGlnIleTyfyrSerAsnSerAlaLeuGlyHisValAsnCyfThrIleIys 101  
Db 277 GAGGAATTTGTTTCAGAAATATAGTAATTTCTGCTCTGTGTCATGTGAACAGACATATAA 336  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuIysPheAlaValLeu 121  
Db 337 GAATTTGAGCGCTCTCTTCTAGTTCATGATTTAGTTGATTCCTTGAAGTTTGCAGTGTG 396  
Qy 122 MetTrpValPheThrTyfyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleAla 141  
Db 397 ATGTGGGTATTTACTTACGTGGTGCCCTGTTCATATGTTGACACTACTGATTTAGCC 456  
Qy 142 LeuIleSerLeuPheSerValProValIleTyfyrGluArgHisGlnAlaGlnIleAspHis 161

Db 457 CTGATCTCCTCTTTCAGTATTCTCTGTATATATGAACGGCATCAGCGCCAGATGATCAT 516  
Qy 162 TyrfleGlyLeuAlaAsnIysAsnValysAspAlaMetAlaIysIleGlnAlaIysIle 181  
Db 517 TATCTAGGACTTGCACCAAGAGTGTTAAGGATGCTGCGCAAAATCCAAAGCAAAATC 576  
Qy 182 ProGlyLeuIysArgIysAlaGlu 189  
Db 577 CCTGATTGAAGCGCCAAAGCAGAA 600  
RESULT 31  
B1157842  
LOCUS  
DEFINITION  
602923001P1 NCI\_CGAP\_Mam3 Mus musculus cDNA clone IMAGE:5062944 5',  
B1157842 mRNA sequence.  
B1157842.1 GI:14617843  
VERSION  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC <http://mgi.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1170 row: b column: 01  
High quality sequence stop: 708.  
Location/Qualifiers  
1..708  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129, C57BL/6J, FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5062944"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="10 months"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Mam3"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH  
Reference for transgenic model: Xu et al., Nature Genetics  
22, 37-43 (1999)."

ORIGIN  
Alignment Scores:  
Pred. No.: 3,36e-102 Length: 708  
Score: 911.00 Matches: 185  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.40% Mismatches: 1  
Query Match: 97.85% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1157842 (1-708)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21  
Db 59 GTTGTGACCTCTCTGTGACTGAGACATTAAGAGACTGGAGTGTGTTGGTGCCAGC 118  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrfleAla 41



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Db      119 TTATTCCTGCTGCTCTCTGACAGTGTTGAGCAATGTCAGTGTAAAGCGCTACATTGCC 178
Qy      42 LeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
Db      179 TTGGCCCTGCTCTCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 238
Qy      62 GlnLysSerAspGluHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      239 CAGAAATCAGATGAAGCCACCCATTCAGGGCATAATTTGGAATCTCAAGTTGCCATATCA 298
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      299 GAGGAATGGTTCAGAAATATAGTAATTCCTGCTTGGTCATGTCGAGCAACAATAAAA 358
Qy      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      359 GAATTCAGGCGTCTCTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGTGTG 418
Qy      122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      419 ATGTGGGTATTTACTTACCGTGTGTCCTTGTTCATATGGTTTGACACTACTGATTTTAGCT 478
Qy      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      479 CTGAATCTACTCTTCAGTATTCCTGTTATATATGAACGGCATCAGCGCGAGATGATCAT 538
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      539 TATCTAGGACTTCGAAACAAGACGGTTAAGGATGCCATGGCCAAAATCCAAAGCAAAATC 598
Qy      182 ProGlyLeuLysArgLysAlaGlu 189
Db      599 CCTGGATTGAAGCGCAAGCAGAA 622

```

## RESULT 32

```

LOCUS      CO401465
DEFINITION AGENCOURT_26749547 NIH_MGC_255 Rattus norvegicus cDNA clone
IMAGE:7317070 5', mRNA sequence.
ACCESSION  CO401465
VERSION     1
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)

```

## ORGANISM

```

Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

## REFERENCE

```

1. (bases 1 to 779)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892

```

## AUTHORS

```

Title Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
Email: cgsaps-r@mail.nih.gov

```

## JOURNAL

```

cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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## FEATURES

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Plate: L14M15373 row: 0 column: 20
High quality sequence start: 23
High quality sequence stop: 690.
Location/Qualifiers
1..779
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7317070"

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## FEATURES

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source
RESULT 33
LOCUS      CO048918
DEFINITION ILLUMIGEN_MQ0_38898 Katze WMBR Macaca mulatta cDNA clone
IBIUW:16203 5' similar to Bases 112 to 991 highly similar to human

```

```

/sex="both"
/tissue_type="Brain - Pooled from several tissues from one
or more individuals"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_255"
/note="organ: brain/CNS; Vector: pExpress-1; Site: 1:
EcoRV; Site 2: NotI; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (TRI-reagent
method). cDNA was primed using oligo-dT primer:
5'-pCAGTAGTCTTAGATCGGCGGCCGCTT-25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This primary
library is a normalized (primary library is NIH_MGC_254)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

```

## ORIGIN

```

Alignment Scores:
Pred. No.:      9,08e-102      Length:      779
Score:          908.00         Matches:    184
Percent Similarity: 98.94%     Conservative: 3
Best Local Similarity: 97.33%   Mismatches: 2
Query Match:     97.53%       Indels:     0
DB:              7           Gaps:       0

US-09-830-972-29_COPY_990_1178 (1-189) x CO401465 (1-779)

Qy      1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db      114 TCAGTTGTTGACTCTCTCTACTGGAGAGACATTAGAGACTGGAGTGGTGGTGGTGC 173
Qy      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      174 AGCTTATTCTGCTGCTGCTCTGACAGTGTTCAGCAATGTCAGTGTAAAGCGCTACATT 233
Qy      41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db      234 GCCTTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGGTGATCCAGGCT 293
Qy      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      294 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGATCTCAGTTGCTATA 353
Qy      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db      354 TCAGAGGAATTTGGTTTCAGAAATACAGTAATTCCTGCTCTTTGGTTCATGTGAACGACAATA 413
Qy      101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db      414 AAAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTTCTCCTGAGTTGCGAGTG 473
Qy      121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db      474 TTGATGTGGGTGTTTACTTATGTTGTCCTTTGATGTCATGTCACACTACTGATTTTAA 533
Qy      141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db      534 GCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCGAGATAGAT 593
Qy      161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db      594 CATTATCTAGGACTTCGAAACAAGAGTGTTAAGGATGCCATGCCCAAAATCCAAAGCAAAA 653
Qy      181 IleProGlyLeuLysArgLysAlaGlu 189
Db      654 ATCCCTGGATTGAAGCGCAAGCAGAT 680

```

## RESULT 33

```

LOCUS      CO048918
DEFINITION ILLUMIGEN_MQ0_38898 Katze WMBR Macaca mulatta cDNA clone
IBIUW:16203 5' similar to Bases 112 to 991 highly similar to human

```







Dn	641	CCTGGATTGAAGCGCAACGAGAA	664
Db	AU080133	799 bp mRNA linear EST 12-JUL-2000	
RESULT 36	AU080133	Sugano mouse brain mncb Mus musculus cDNA clone MNCb-5268	
LOCUS	AU080133	5', mRNA sequence.	
DEFINITION	AU080133	EST.	
ACCESSION	AU080133.1	GI:6084887	
VERSION	AU080133.1	mus musculus (house mouse)	
KEYWORDS	AU080133.1	Mus musculus	
SOURCE	AU080133.1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
ORGANISM	AU080133.1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	AU080133.1	1 (bases 1 to 799)	
AUTHORS	AU080133.1	Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.	
TITLE	AU080133.1	Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method	
JOURNAL	AU080133.1	Unpublished (1999)	
COMMENT	AU080133.1	Contact: Katsuyuki Hashimoto Division of Genetic Resources National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan Email: khashi@nih.go.jp URL: http://www.nih.go.jp/yoken/genbank/.	
FEATURES	AU080133.1	Location/Qualifiers	
source	AU080133.1	1..799	
	AU080133.1	/organism="Mus musculus"	
	AU080133.1	/mol_type="mRNA"	
	AU080133.1	/strain="C57BL"	
	AU080133.1	/db_xref="taxon:10090"	
	AU080133.1	/clone="MNCB-5268"	
	AU080133.1	/sex="female"	
	AU080133.1	/dev_stage="adult"	
	AU080133.1	/lab_host="TOP10"	
	AU080133.1	/notes="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer	
	AU080133.1	AGTGCCCTTTTATTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTGTGCCCTACTGG], digested and cloned into distinct DraII sites of the pME18S-FL3. XhoI sites just outside the DraII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing: 5' end primer [CTTCGTCTTAAGAAGCTGCG], 3' end primer [CGACCTGCAGCTCGAGACA]"	
ORIGIN	AU080133.1	[CGACCTGCAGCTCGAGACA]"	
Alignment Scores:	AU080133.1	Length: 799	
Pred. No.:	AU080133.1	Matches: 184	
Score:	AU080133.1	Conservative: 2	
Percent Similarity:	AU080133.1	Mismatches: 2	
Best Local Similarity:	AU080133.1	Indels: 0	
Query Match:	AU080133.1	Gaps: 1	
DB:	AU080133.1		
US-09-830-972-29_COPY_990_1178 (1-189) x AU080133 (1-799)	AU080133.1		
Qy	2	ValValAspLeuLysThrArgApilLeLyseThrGlyValValPheGlyAlaSer 21	
Db	102	GTGTGTGACCTCTGTACTGGAGACATTAGAGACTGGAGTGGTGTGGTCCAGC 161	
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIlleValSerValThrAlaTyrlleAla 41	
Db	162	TTATTCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCCCTACATGCC 221	
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArilleTyrlYseGlyValIleAlaIle 61	
Db	222	TTGGCCCTGCTCTGTGACTATCACCTTAGATATATAAGGTTGTATCCAAGCTATC 281	

Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSer 81	
Db	282	CAGAAATCAGATGAGGCCACCACCATTCAGGCGCATATTTGGAATCTCTGAAGTTGCCATATCA 341	
Qy	82	GluGluLeuValGlnLysTyrlSerAenSerAlaLeuGlyHisValAenCysThrIleLys 101	
Db	342	GAGGAATTTGGTTTCAGAAATATAGTAATCTCTGCTCTTTGGTTCATGTGAACAGCACAAATAAAA 401	
Qy	102	GluLeuArgGluLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121	
Db	402	GAATTGAGGCGTCTCTCTTAGTTGATGATTTCCTGAAAGTTTGCGAGTGTG 461	
Qy	122	MetTrpValPheThrTyrlValGlyAlaLeuPheAenGlnLysThrLeuLeuAla 141	
Db	462	ATGTGGTATTACTTACGTGGTGGTCTTGTTCATGCTTTCACACTACTGATTAGCT 521	
Qy	142	LeuIleSerLeuPheSerValProValIleTyrlGluArgHisGlnAlaGlnIleAepHis 161	
Db	522	CTGATCTCTCTTTCAGTATTCCTGTATATATATGTAACGCGCATCAGCGCAGATAGATCAT 581	
Qy	162	TyrLeuGlyLeuAlaAenLysAenValLysAspAlaMetAlaLysIleGlnAlaLysIle 181	
Db	582	TATCTAGGACTTGCAAACAGAGCGTGTAAAGATGCCCGCCAAAAATCCAACGAAAAATC 641	
Qy	182	ProGlyLeuLysArgLysAlaGlu 189	
Db	642	CCTGGATTGAAGCGCAAGCAGAA 665	
RESULT 37			
CV0077130		695 bp mRNA linear EST 25-AUG-2000	
LOCUS	CV0077130	AGENCOURT 31475102 NIH MGC 251 Rattus norvegicus cDNA clone	
DEFINITION	CV0077130	IMAGE:7388978 5', mRNA_sequence.	
ACCESSION	CV0077130	EST.	
VERSION	CV0077130.1	GI:51544161	
KEYWORDS	CV0077130.1	Rattus norvegicus (Norway rat)	
SOURCE	CV0077130.1	Rattus norvegicus	
ORGANISM	CV0077130.1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	CV0077130.1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	CV0077130.1	1 (bases 1 to 695)	
AUTHORS	CV0077130.1	NIH-MGC http://mgc.nci.nih.gov/.	
TITLE	CV0077130.1	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	CV0077130.1	Unpublished (1999)	
COMMENT	CV0077130.1	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgaphs-r@mail.nih.gov Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin CDNA Library Preparation: Open Biosystems CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1561 row: c column: 24 High quality sequence stop: 696.	
FEATURES	CV0077130.1	Location/Qualifiers	
source	CV0077130.1	1..695	
	CV0077130.1	/organism="Rattus norvegicus"	
	CV0077130.1	/mol_type="mRNA"	
	CV0077130.1	/db_xref="taxon:10116"	
	CV0077130.1</		

was primed using oligo-dT primer:  
 5'-pGACTAGTCTAGATCGGAGCGCGCCCTTT25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb  
 resulted in an average insert size of 1.6 kb. This primary  
 library is normalized (non-normalized primary library is  
 NIH MGC 250) and was constructed by Open Biosystems. Note:  
 this is a NIH\_MGC library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,42e-101 Length: 695  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.10% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CV077130 (1-695)

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Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
      |||
Db      126 GTTGTGACCTCTCTACCTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGCACG 185
      |||
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
      |||
Db      186 TTATTCCTGCTGCTGCTGACAGTTCAGCATTTGTAGTGTACGCGCCTACATTGCC 245
      |||
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
      |||
Db      246 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATAAGGGCGGTGATCCAGGCTATC 305
      |||
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      |||
Db      306 CAGAAATCAGATGAAGCCACCCATTCAGGGCAGATTTAGAAATCTGAAGTGTGATATCA 365
      |||
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
      |||
Db      366 GAGGAATGGTTCAGAAATACAGTAATTCGTCTTGGTCATGTGAAACAGCAATATAAA 425
      |||
Qy      102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
      |||
Db      426 GAACCTGAGCGGGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 485
      |||
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
      |||
Db      486 ATGTGGGTGTACTTATGTGTGTGCTTGTCAATGGTGTGACACTACTGATTTTAGCT 545
      |||
Qy      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db      546 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 605
      |||
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      606 TATCTAGGACTTGCACAAACAGAGTGTAAAGATGCCATGGCCAAAATCCAAAGCAAAATC 665
      |||
Qy      182 ProGlyLeuLysArgLysAlaGlu 189
      |||
Db      666 CTGGATTGAAGCGCAAGCAGAT 689
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## RESULT 38

BG740561  
 LOCUS BG740561 758 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602633075F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4778131 5',  
 mRNA sequence.  
 ACCESSION BG740561  
 VERSION BG740561.1 GI:14051214  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 758)  
 AUTHORS NIH-MGC <http://mge.nci.nih.gov/>.

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10633 row: f column: 20  
 High quality sequence stop: 743.  
 Location/Qualifiers  
 1..758  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4778131"  
 /lab\_host="DH108 (T1 phage-resistant)"  
 /clone\_lib="NCI\_CGAP\_Skn3"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

## FEATURES

## source

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,74e-101 Length: 758  
 Score: 904.00 Matches: 186  
 Percent Similarity: 98.41% Conservative: 0  
 Best Local Similarity: 98.41% Mismatches: 2  
 Query Match: 97.10% Indels: 1  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG740561 (1-758)

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Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
      |||
Db      130 GTTGTGACCTCTCTACCTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGCACG 189
      |||
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
      |||
Db      190 CTATTCTCTGCTCTTTCATTGACAGTATTCACATTTGAGCGTAAACAGCTACATTGCC 249
      |||
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
      |||
Db      250 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAAGGGTGTGATCCAAGCTATC 309
      |||
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
      |||
Db      310 CAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGAAGTGTGATATCT 369
      |||
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
      |||
Db      370 GAGGAGTGGTTCAGAGTACAGTAATTCGTCTTGGTTCATGTGAACGACGATTAAG 429
      |||
Qy      102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
      |||
Db      430 GAACTCAGCGGCTCTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 489
      |||
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
      |||
Db      490 ATGTGGGTATTTACCTATGTTGGTGTGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 549
      |||
Qy      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db      550 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGACAGATAGATCAT 609
      |||
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLys-AspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      610 TATCTAGGACTTGCACAAATGAAGATGTTAACAGATGCTATGGCTAAATCCAAAGCAAAAT 669
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```

QY 181 eProglyLeuLysArgLysAlaGlu 189 linear EST 24-JUN-2004  
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 Db 670 CCTGGATTGAAGCGCAAGCTGAA 694  
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 RESULT 39  
 CF977898 791 bp mRNA linear EST 24-JUN-2004  
 F26A06.048.abl.R Rat retinal ganglion cell Rattus norvegicus cDNA,  
 mRNA sequence.  
 ACCESSION CF977898  
 VERSION CF977898.1 GI:49173356  
 KEYWORDS Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 EST. Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 791)  
 Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.  
 Gene Expression Profiling of Highly Purified Rat Retinal Ganglion  
 Cells  
 Unpublished (2003)  
 Contact: Farkas RH  
 Department of Ophthalmology  
 Johns Hopkins University School of Medicine  
 600 North Wolfe Street, Baltimore, MD 21287, USA  
 Tel: 410 502 5230  
 Fax: 410 502 5382  
 Email: rfarkas@jmi.edu.  
 Location/Qualifiers  
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 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /tissue\_type="Retinal Ganglion Cells"  
 /lab\_host="DH10B"  
 /clone\_lib="Rat retinal ganglion cell"  
 /note="Organ: Eye; Vector: pDNR-LJB; Site 1: Sfil; Site 2:  
 Sfil; The library was constructed from purified rat  
 retinal ganglion cells. The Creator SMART cDNA library  
 method (Clontech) was used. EST analysis was performed on  
 the unamplified, non-normalized, non-subtracted library."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.91e-101 Length: 791  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.10% Indels: 0  
 Db: 7 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x CF977898 (1-791)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 |||||  
 Db 167 GTTGTTGACCTCCTCTACTGGAGACATTAGAGACTGGAGTGGTGTGGTGGCCAGC 226  
 |||||  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 |||||  
 Db 227 TTAATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATTGCC 286  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 |||||  
 Db 287 TTGGCCCTGCTCTCGGTGACTATCATCTTAGGATATATAGGGCGGTGATCCAGGCTATC 346  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 347 CAGAATCAGATGAAGGCCACCCTTCAGGGCATTTAGGAATCTGAAGTGTGCTATATCA 406  
 |||||  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 |||||

Db 407 GAGGAATGGTTTCAGAAATACAGTAATTTCTCTCTGTGTGATGTGAACAGCACATAA 466  
 |||||  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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 Db 467 GAACGTAGCGCGCTTTCTTCTAGTTGATGATTAGTTGATTCCCTGAAGTTTGCAGTGTG 526  
 |||||  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
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 Db 527 ATGTGGGTGTTTACTTATGTTGGTCCCTTGTCAATGCTCTCACACTACTGATTAGCT 586  
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 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
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 Db 587 CTGATCTCACCTCTCAGTATTCTCTGTTATTTATGAACGGCATCAGGTGAGATAGATCAT 646  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 647 TATCTAGACTTGCACACACAGAGTGTTAAGGATGCCATGGCCAAATCCAGCAAAATC 706  
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 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 |||||  
 Db 707 CTGTGATTGAAGCGCAAGCAGAT 730  
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 RESULT 40  
 CN641703 1081 bp mRNA linear EST 12-MAY-2004  
 LOCUS ILLUMIGEN MCQ 5216 Katze MMBR Macaca mulatta cDNA clone IBIUW:6014  
 DEFINITION 5' similar to Bases 156 to 1013 highly similar to human RTN4  
 (Hs.436349), mRNA sequence.  
 ACCESSION CN641703  
 VERSION CN641703.1 GI:47152713  
 KEYWORDS EST.  
 SOURCE Macaca mulatta (rhesus monkey)  
 ORGANISM Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.  
 1 (bases 1 to 1081)  
 Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P., and Magness,C.L.  
 Large-scale Rhesus Macaque cDNA Sequencing  
 Unpublished (2003)  
 CONTACT: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com  
 Sequenced on 2003.12.04. 735 Q20 bases.  
 PCR Primers  
 FORWARD: CCCTCACTAAAGGGAACAAA  
 BACKWARD: CACTATAGGCGAATTGGGTA  
 Insert Length: 1081 Std Error: 0.00  
 Plate: CL000043 row: H column: 10  
 Seq primer: CCCTCACTAAAGGGAACAAA  
 POLYA=Yes.  
 Location/Qualifiers  
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 /strain="Indian"  
 /db\_xref="taxon:9544"  
 /clone="IBIUW:6014"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="E. coli SOLR"  
 /clone\_lib="Katze MMBR"  
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
 kit (catalog #200400) and ZAP-CDNA Gigapack III Gold  
 Cloning Kit (catalog #200450)"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.54e-101 Length: 1081

Score: 904.00 Matches: 185  
Percent Similarity: 98.94% Conservative: 2  
Best Local Similarity: 97.88% Mismatches: 1  
Query Match: 97.10% Indels: 1  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN641703 (1-1081)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 156 GTTGTGGACCTCTCTACTTGGAGAGACATGAAGACACTGGAGTGGTGTGGTGGCCAGC 215  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
Db 216 CTATTCTCTGCTCTCTTCAATGACAGTATTACAGCAATTTGAGTGTAAACAGCCTACATGTC 275  
QY 42 LeuAlaLeuLeuSerValThrIle-SerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 276 TTGGCCCTGCTCTCTGTGACCATCANGCTTTAGGATATACAGGGGTGTGATCCAGCTAT 335  
QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 336 CCAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAATTCGCGATATC 395  
QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLeu 101  
Db 396 TGAGGAGTGGTTCAGAAATGACAGTAAATCTGCTCTTGGTCAATGTAACCTGCACGATAAA 455  
QY 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 121  
Db 456 GGAACCTCAGCGCCCTCTCTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGT 515  
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 516 GATGTGGTATTACCTATGTTGGTCCCTTGTGTTTAAATGCTGTGACGCTACTGATTTGGC 575  
QY 141 aLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
Db 576 TCTCAATTCACCTCTCAGTGTCTCTGTTATTTATGTAACCGCATCAGGCACAGATAGTCA 635  
QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 636 TTATCTAGGACTTGCAATAGATGTTAAAGATGCTATGGCTTAATCCAGCGAAT 695  
QY 181 eProGlyLeuLysArgLysAlaGlu 189  
Db 696 CCTGTGATTGAAGCGCAAGCTGAA 720

RESULT 41  
BG623462  
LOCUS 602648520F1 NIH\_MGC\_79 Homo sapiens cdna clone IMAGE:4770077 5',  
DEFINITION mRNA sequence.  
ACCESSION BG623462  
VERSION BG623462.1 GI:13674833  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 747)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LLCM1636 row: g column: 06  
High quality sequence stop: 742.  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4770077"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_79"  
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);  
Site 1: SfII (ggccgctcgcc); Site 2: SfII  
(ggcatatggcc); 5' and 3' adaptors were used in cloning  
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'  
and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGCGCCGACATG-DT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.3  
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 4,74e-101 Length: 747  
Score: 902.00 Matches: 183  
Percent Similarity: 98.39% Conservative: 0  
Best Local Similarity: 98.39% Mismatches: 3  
Query Match: 96.89% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG623462 (1-747)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 133 GTTGTGGACCTCTCTACTTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 192  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
Db 193 CTATTCTCTGCTCTCTTCAATGACAGTATTACAGCATTTGAGCGTAAACAGCCTACATGTC 252  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 253 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 312  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 313 CAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAATTCGATATCT 372  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 373 GAGGAGTGGTTCAGAAATGACAGTAAATCTCTCTTGGTCAATGCTGAACCTGCAGATAAAG 432  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 433 GAACCTCAGCGCCCTCTCTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGT 492  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 493 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGCTGTGACACTACTGATTTGGCT 552  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
Db 553 CTCATTCTACTCTTCAATGAGTGTCTGTATTTATGAACCGCATCAGGCACAGATAGTATCAT 612  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 613 TATCTAGGACTTGCAATAGATGTTTACAGATGCTCTATGTTAAATCCAGCAAAATC 672  
QY 182 ProGlyLeuLysArgLys 187  
Db 673 CCTGGATTGAAGCGCAAA 690

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RESULT 42
CO259245
LOCUS 4130644 BARC 8BOV Bos taurus cDNA clone 8BOV_51K20 5', mRNA
DEFINITION sequence.
ACCESSION CO259245
VERSION CO259245.1 GI:49144047
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 585)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and
Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANR1
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '-trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
Plate: 51 row: K column: 20
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 585.
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1.585
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_51K20"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B Tona"
/clone_lib="BARC 8BOV"
/organ="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
Not1; Site 2: EcoRI; Normalized cow cDNA intestinal mRNA
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
ORIGIN
Alignment Scores:
Pred. No.: 5,92e-101 Length: 585
Score: 900.00 Matches: 183
Percent Similarity: 99.46% Conservative: 0
Best Local Similarity: 99.46% Mismatches: 1
Query Match: 96.67% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CO259245 (1-585)

Qy 2 ValValAspLeuLeuTyrrTrrArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 32 GTTGTGTACCTCCTCTACTGGAGACATTAAGAACTGGAGTGGTCTCGGTCGCCAGC 91
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAla 41
Db 92 TTGTTCTCTGCTCTCGCTGACAGTATTACAGATTGTGAGTGTACCGGCTACATTGCC 151
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIle 61

```

```

Db 152 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 211
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81
Db 212 CAGAAATCTGATGAAGGCCACCCATTTCAGGCAATATTTGGAATCTGAAGTTGCTATATCT 271
Qy 82 GluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnCythrIleLys 101
Db 272 GAGGAGTTGGTTTCAGAAAGTACAGCAATTCCTCTCTGTGTCATGTTAACTGCACAATAAAA 331
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 332 GAATCTCAGACCCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAGCTTTGACAGTTG 391
Qy 122 MetTrpValPheThrTyrrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 392 ATGTGGGTATTACCTATGTTGGTCCCTGTGTAATGCTCTGACACTACTAATTTGGCT 451
Qy 142 LeuIleSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHis 161
Db 452 CTGATTTTCACTCTTTCAGTGTCTCTGTTTATTATGAACGGCATCAGGCGCAAAATAGATCAT 511
Qy 162 TyrrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 512 TATCTGGACCTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTAAATAATCCAAAGCAAAATC 571
Qy 182 ProGlyLeuLys 185
Db 572 CCTGGATTGAAG 583

RESULT 43
BI838242
LOCUS 603083162F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222534 5',
DEFINITION mRNA sequence.
ACCESSION BI838242
VERSION BI838242.1 GI:15949792
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11559 Row: k Column: 15
High quality sequence stop: 734.
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source
1..742
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5222534"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/organ="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics

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tracking code 025. Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 1,11e-100 Length: 742  
Score: 899.00 Matches: 185  
Percent Similarity: 98.93% Conservative: 0  
Best Local Similarity: 98.93% Mismatches: 1  
Query Match: 96.56% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1838242 (1-742)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPhe-GlyAlaSe 21  
Db 135 GTTGTTCACCTCTGCTACTGAGAGACATTAAAGACATGGAGTGGTGTGTGGTCCAG 194  
QY 21 rLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAl 41  
Db 195 CCTATTCCCTGCTCTTCATTGACATATTACAGATTTGAGCGTAAACACCTTACATTCG 254  
QY 41 aleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaI 61  
Db 255 CTTCGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGTTGTGATCCAGCTAT 314  
QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 315 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGCTATATC 374  
QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLy 101  
Db 375 TGAGGAGTGGTTCAGAAGTACAGTAATCTGCTCTTGTGTCATGTCGTAATCTGACGATAA 434  
QY 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValle 121  
Db 435 GGAACCTCAGCGGCTCTCTTAGTTCATGATTTAGTTGATCTCTGAACTTTCAGTGT 494  
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAl 141  
Db 495 GATGTGGGTATTACCTATGTGGTGGTCTGTTTAAATGCTGACACTACTGATTTTGGC 554  
QY 141 aleuLleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspH 161  
Db 555 TCTCATTTCACTCTTCAGTGTTCCTGTATTTATGAAACGCAATCAGCAGACAGATATCA 614  
QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 615 TTATCTAGGACTTGCAATAAGAAATCTTAAAGATGCTAGCTAAATCCAGCAAAAT 674  
QY 181 eProGlyLeuLysArgLys 187  
Db 675 CCCTGGATTGAAGCGCAA 693

RESULT 44  
AK034902

LOCUS  
DEFINITION  
Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430059L06 product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO PROTEIN) (FOCCN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus norvegicus], full insert sequence.

ACCESSION  
AK034902  
VERSION  
AK034902.1 GI:26084268  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1  
Carninci, P. and Hayashizaki, Y.  
TITLE  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
JOURNAL  
99279253

10349636  
2  
PUBMED  
REFERENCE  
AUTHORS  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL  
20499374  
MEDLINE  
11042159  
PUBMED  
REFERENCE  
AUTHORS  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
JOURNAL  
20530913  
MEDLINE  
11076861  
PUBMED  
REFERENCE  
AUTHORS  
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.  
TITLE  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
JOURNAL  
20530913  
MEDLINE  
11076861  
PUBMED  
REFERENCE  
AUTHORS  
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team  
TITLE  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
JOURNAL  
20530913  
MEDLINE  
11076861  
PUBMED  
REFERENCE  
AUTHORS  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, M., Tagawa, A., Takahashi, F., Takaku-Akanishi, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
TITLE  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
COMMENT  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://phantom.gsc.riken.jp/  
FEATURES  
source  
1. 3533  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:9430059L06"  
/db\_xref="taxon:10090"  
/clone="9430059L06"  
/tissue\_type="embryonic body between diaphragm region and neck"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"



/dev\_stage="12 days embryo"

misc\_feature

1. 3533  
/note="RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOMO  
PROTEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog  
[Rattus norvegicus] (SWISSPROT)Q9UK11, evidence: FASTA,  
95.8%id, 100%length, match=1068"

## ORIGIN

Alignment Scores:  
Pred. No.: 2,42e-99 Length: 3533  
Score: 896.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 2  
Best Local Similarity: 97.81% Mismatches: 2  
Query Match: 96.24% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AK034902 (1-3533)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 740 GTTGTGACCTCTCTACTGAGAGACATTAAGAAGACTGGAGTGTGTGGTCCAGC 799  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
DB 800 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTTACATTGCC 859  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 860 TTGGCCCTGCTCTCTGTGACTATCATCTTAGATATATAGGGTGTGATCCAGCTATC 919  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 920 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATTTGGAATCTGAAGTTGCCATATCA 979  
QY 82 GluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 980 GAGGAATTGGTTTCAGAAATATAGTAATCTGCTTTGTCATGTGAACAGCACATAAAA 1039  
QY 102 GluLeuArgGluLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1040 GAATGAGCGGCTCTCTTCTTGTGATGATTTAGTTGATTCCTGAAGTTTGCAGTGTG 1099  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
DB 1100 ATGTGAGTATTACTTACCTGTTGGTCCCTGTTCAATGTTTGACACTACTGATTTAGCT 1159  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 1160 CTGATCTCACTCTTCAGTATTCTCTTATATATGAACGGCATCAGGCGCAGATAGATCAT 1219  
QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1220 TATCTAGGACTTGCAAAACAGAGCGTTAAGATGCCATGGCCAAATCAAGCAAAATC 1279  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 1280 CTGGAATTGAGCGCAAGACGAA 1303

## RESULT 45

BI079496  
LOCUS BI079496 781 bp mRNA linear EST 20-JUN-2001  
DEFINITION 602876306F1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5008248 5',  
mRNA sequence.

ACCESSION BI079496

VERSION BI079496.1 GI:14497826

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC <http://mgc.nci.nih.gov/>.  
1 (bases 1 to 781)  
National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

## COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLM11052 row: k column: 01

High quality sequence stop: 773.

Location/Qualifiers

## FEATURES

source

1. 781

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N-3"

/db\_xref="taxon:10090"

/clones="IMAGE:5008248"

/tissue type="tumor, biopsy sample"

/dev stage="5 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Mam2"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

## ORIGIN

## Alignment Scores:

Pred. No.: 4,96e-100 Length: 781

Score: 894.00 Matches: 182

Percent Similarity: 98.40% Conservative: 3

Best Local Similarity: 96.81% Mismatches: 3

Query Match: 96.03% Indels: 0

DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BI079496 (1-781)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 213 GTTGTGACCTCTCTACTGAGAGACATTAAGAAGACTGGAGTGTGTGGTCCAGC 272  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
DB 273 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTTACATTGCC 332  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 333 TTGGCCCTGCTCTCTGTGACTATCATCTTAGGATATATAGGGTGTGATCCAGCTATC 392  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 393 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATTTGGAATCTGAAGTTGCCATATCA 452  
QY 82 GluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 453 GAGGAATTGGTTTCAGAAATATAGTATTCTCTCTTGTGTCATGTGAACAGCACATAAAA 512  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 513 GAATTGAGCGCTCTCTCTTAGTTGATGATTTAGTTGATTCCTCCCTGAAGTTTGCAGTGTG 572  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 573 ATGTGGGTATTACTTACCTGTTGGTCCCTTGTTCATGTTGACACTACTGATTTAGCT 632  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 633 CTGATCTCACTCTTCAGTATTCTCTTATATATGAACGGGATCAGGCCAGATCATCAT 692  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db	693	TATCTAGGACTTCGCAACAGAGCGTTAAGGATGCCATCGCCAAATCCAGCAAAAATC	752
Qy	182	ProGlyLeuLysArgLysAlaGlu 189       	
Db	753	CCTGGATTGAAGCGCAAGCAGAT 776       	
RESULT 46			
LOCUS	602678946F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811674 5',	774 bp mRNA linear EST 07-MAY-2001	
DEFINITION	mRNA sequence.		
ACCESSION	BC699274		
VERSION	BC699274.1 GI:113967408		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 774)		
AUTHORS	NIH-MGC http://mgc.nhl.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10702 row: 1 column: 11 High quality sequence stop: 774.		
FEATURES	1. .774		
source	Location/Qualifiers		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4811674"		
	/tissue_type="hippocampus"		
	/lab_host="DH10B"		
	/clone_lib="NIH MGC 95"		
	/notes="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."		
ORIGIN			
Alignment Scores:			
Pred. No.:	6,52e-100	Length:	774
Score:	893.00	Matches:	186
Percent Similarity:	98.42%	Conservative:	1
Best Local Similarity:	97.89%	Mismatches:	1
Query Match:	95.92%	Indels:	2
DB:	4	Gaps:	0
US-09-830-972-29_COPY_990_1178 (1-189) x BG699274 (1-774)			
Qy	2	ValValAspLeuLeuTyrTrpArgAspIleValLysThrGlyValValPheGlyAlaSer 21       	
Db	169	GTGTGGACCTCTCTACTGGAGAGACATTAGAGACTGGAGTGGTGTGGTCCAGC 228       	
Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41       	
Db	229	CTATTCTCGTGTCTTCAITTCAGATGATTTCAGCATTTGTCAGCGGTAAACAGCTTACATTGCC 288       	





Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 488.

## FEATURES

Source  
 1. 569  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6126776"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="PH108"  
 /clone\_lib="HR85 islet"  
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
 NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permutt Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-3692."

ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 749)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-remail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10379 row: g column: 04  
 High quality sequence stop: 745.  
 Location/Qualifiers  
 1. 749  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4505499"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## FEATURES

source  
 1. 749  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4505499"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,59e-99 Length: 749  
 Score: 886.00 Matches: 181  
 Percent Similarity: 98.90% Conservative: 2  
 Best Local Similarity: 97.31% Mismatches: 3  
 Query Match: 95.17% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG296048 (1-749)

QY 2 ValValAspLeuLeuTyrTrrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 125 GTTGTGACCTCTCTGTGACATTTAGGATATATAGGGTGTGATCCAGCTATC 184

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 185 TTATTCCTGCTGCTGCTCTGACAGTGTTCAGCATGTTCAGTGAACGCCCTACATTGCC 244

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 245 TTGGCCCTGCTCTCTGTGACATTCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 304

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 305 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 364



This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp469H1132) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

## FEATURES

source  
1..683  
/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
/clone="DKFZp469H1132"  
/tissue\_type="kidney"  
/dev\_stages="adult"  
/lab\_host="DH10B"  
/clone\_lib="469 (synonym: pkidi)"  
/note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"

## ORIGIN

Alignment Scores:  
Pred. No.: 5,35e-99 Length: 683  
Score: 885.00 Matches: 179  
Percent Similarity: 98.90% Conservative: 0  
Best Local Similarity: 98.90% Mismatches: 2  
Query Match: 95.06% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR548792 (1-683)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 140 GTTGTGACCTCTCTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 199  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 200 CTATTCTCTGCTCTTTCATTGACATGTTACAGTATTCAGCATGTGAGTGAACAGCTCATTTGCC 259  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 260 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 319  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 320 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGAAAGTTGCTATATCT 379  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 380 GAGGAGTGGTTTCAGAAGTACAGTAATCTCTGCTTGGTCATGTGAACCTGCACGATAAG 439  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 440 GNACTCAGCGCCCTCTTCTAGTCATGATTAGTTGATTCTCTGAAGTTGCACTGTG 499  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 500 ATGTGGGTATTTACCTATGTTGGTCTGTTTAATGTTGCTGCTGACCTACTGATTTGGCT 559  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 560 CTCATTTCACTCTTCAGTGCTCTGTTATTTAATGAACGGCATCAGGCACAGATAGATCAT 619  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 620 TATCTAGGACTTGCATAATGAATGTTAAAGATGCTATGGCTAAATTCNAGCGAAATC 679  
QY 182 Pro 182  
DB 680 CCT 682

## RESULT 54

## BI544917

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

603242368P1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5284672 5',  
731 bp mRNA linear EST 05-SEP-2001  
BI544917  
mRNA sequence.  
BI544917  
GI:15432229  
EST.  
BI544917.1  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11719 row: h column: 17  
High quality sequence stop: 724.

## FEATURES

## source

## 1..731

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="IMAGE:5284672"

## /tissue\_type="hippocampus"

## /lab\_host="DH10B"

## /clone\_lib="NIH\_MGC\_95"

## /note="Organ: brain; Vector: pBluescriptR (modified

## pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

## (gtcag); Oligo-dT primed using primer

## 5'-TTTTTTTTTTTTTTVN-3', size-selected for average

insert size 2.5 kb and normalized to 10<sup>5</sup>. This is a

## primary library enriched for full-length clones and

## constructed using the Cap-trapper method (Carninci, in

## preparation). Library constructed by M. Brownstein

## (NIH/NHGRI, National Institutes of Health). Note: this

## is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

1.39e-98 Length: 731  
882.00 Matches: 179  
99.44% Conservative: 0  
99.44% Mismatches: 1  
94.74% Indels: 0  
4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BI544917 (1-731)

## QY

## 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

## DB

## 191 GTTGTGACCTCTCTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 250

## QY

## 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

## DB

## 251 CTATTCTCTGCTCTTTCATTGACATGTTAGCATTTGTGAGCGTAACAGCTCATTTGCC 310

## QY

## 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

## DB

## 311 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATTAAGGGTGTGATCCAGCTATC 370

## QY

## 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81



Db 371 CAGAAATCAGATGAGCGCCACCATTCAGGCATATCTCGAATCTGATATCT 430  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrileLys 101  
 Db 431 GAGGAGTTGGTTTTCAGAAAGTACAGTAATCTCTGCTCTTGGTCAATGAACTGCACGATAAAG 490  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 491 GAACTCAGCGGCTCTCTCTAGTTGATGATTTAGTTGATCTCTGAAAGTTTCAGGTTG 550  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 551 AATGGGGTATTTACCTATGTTGGTGCTTGTGTTTAAATGGTCTGACACTACTGATTTGGCT 610  
 QY 142 LeuileSerLeuPheSerValProValileTyrGluArgHisGlnAlaGlnleAspHis 161  
 Db 611 CTCATTTCATCTCTCAGTGTCTCTGTTATTTATGAAACGGCATCAGGCACAGATAGATCAT 670  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysileGlnAlaLysile 181  
 Db 671 TATCTAGGACTTGCATAAATAGAAATGTTAAAGATGCTATGGTAAATAATCCAGCAAAATC 730

RESULT 55  
 BU503291  
 LOCUS  
 DEFINITION AGENCOURT\_8933519 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6490526  
 5', mRNA sequence.  
 ACCESSION BU503291  
 VERSION BU503291.1 GI:22809480  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 921)  
 NIH-MGC <http://imgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue procurement: The Cepko Laboratory  
 cDNA library preparation: Life Technologies, Inc.  
 cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM14040 row: h column: 15  
 High quality sequence stop: 627.  
 Location/Qualifiers  
 1..921  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6490526"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## FEATURES

source  
 Location/Qualifiers

RESULT 56  
 CO504431  
 LOCUS  
 DEFINITION GGEZCB1023A09.g chicken breast muscle - CB1 Gallus gallus cdna  
 clone GGEZCB1023A09, mRNA sequence.  
 ACCESSION CO504431  
 VERSION CO504431.1 GI:50274617  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 647)  
 Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,  
 Patricio,M., Leduc,M.C. and Coutinho,L.L.  
 Discovery of new genes expressed in the chicken breast muscle  
 Unpublished (2004)  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Helena J. Alves  
 Laboratory of Animal Biotechnology, Dep. of Animal Production  
 ESALQ - University of Sao Paulo  
 Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
 Tel: 55 19 3429 4434  
 Fax: 55 19 3429 4285  
 Email: [hjalves@esalq.usp.br](mailto:hjalves@esalq.usp.br) and [llcouth@esalq.usp.br](mailto:llcouth@esalq.usp.br)  
 PCR Primers  
 BACKWARD: T7.  
 Location/Qualifiers  
 1..647  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,93e-98 Length: 921  
 Score: 882.00 Matches: 181  
 Percent Similarity: 98.94% Conservatives: 5  
 Best Local Similarity: 96.28% Mismatches: 1  
 Query Match: 94.74% Indels: 1  
 DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BU503291 (1-921)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGTACCTCCTCTACTTGGAGAGACATTAAAGAACTGGAGTGGTGTGTGGTGCAGC 215  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerLileValSerValThrAlaTyrleAla 41  
 Db 216 TTATTCCTGCTGCTGCTGCTGACAGTTCAGCATTTGTCAGTGTAAACGGCCCTACATGTC 275  
 QY 42 LeuAlaLeuLeuSerValThrileSerPheArgLileTyrLysGlyValleleGlnAlaile 61  
 Db 276 TTGGCCCTGCTCTCTGTGACATATCAGTTTAGATATATAAGGTGTGATCCAGCTATC 335  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaileSer 81  
 Db 336 CAGAAATCAGATGAAGGGCCACCATTTCAGGGCATATTTGGAATCTCAAGTTGCCATATCA 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrileLys 101  
 Db 396 GAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTCTTGGTCATGTGAACACAGCAATAAAA 455  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAATTTGAGGGCTCTCTTCTAGTTGATGATTTAGTTGATTCCTCTGAAGTTTCAGTGTG 515  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 516 ATGTGGGTATTTACTTACGTTGGTGCCTTGTTCATATGGTTTGACACTACTGATTTTAGCT 575  
 QY 142 LeuileSerLeuPheSerValProValileTyrGluArgHisGlnAlaGlnleAspHis 161  
 Db 576 CTGATCTCATTCTTCTGATTTCTCTGATATATGAAACGGCATCAGCGGCAGATAGATCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysileGlnAlaLysile 181  
 Db 636 TATCTAGGACTTGCATAAATAGAAATGTTAAAGATGCTATGGTAAATAATCCAGCAAAATC 695  
 QY 182 Pro-GlyLeuLysArgLysAla 188  
 Db 696 CCTTGGATTAAGCGCCAAAGC 717

## RESULT 56

CO504431  
 LOCUS

DEFINITION  
 GGEZCB1023A09.g chicken breast muscle - CB1 Gallus gallus cdna  
 clone GGEZCB1023A09, mRNA sequence.

ACCESSION  
 CO504431

VERSION  
 CO504431.1 GI:50274617

KEYWORDS  
 EST.

SOURCE  
 Gallus gallus (chicken)

ORGANISM  
 Gallus gallus

REFERENCE  
 Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,  
 Patricio,M., Leduc,M.C. and Coutinho,L.L.

AUTHORS  
 Discovery of new genes expressed in the chicken breast muscle

TITLE  
 JOURNAL

COMMENT  
 Contact: Helena J. Alves  
 Laboratory of Animal Biotechnology, Dep. of Animal Production  
 ESALQ - University of Sao Paulo  
 Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
 Tel: 55 19 3429 4434  
 Fax: 55 19 3429 4285  
 Email: [hjalves@esalq.usp.br](mailto:hjalves@esalq.usp.br) and [llcouth@esalq.usp.br](mailto:llcouth@esalq.usp.br)  
 PCR Primers  
 BACKWARD: T7.  
 Location/Qualifiers  
 1..647  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"

## FEATURES

source  
 Location/Qualifiers

1..647  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"



```

/db xref="taxon:9031"
/clone="GB2CB1023A09"
/tissue_type="breast muscle"
/dev_stage="1 and 21 days old"
/lab_host="DH5 alpha"
/clone_lib="chicken breast muscle - CB1"
/Note="Vector: pSPORI1; Site 1: NotI; Site 2: SalI; This
cDNA library was constructed with the SuperScript Plasmid
System with Gateway Technology kit (Invitrogen), following
manufacturer's protocols. Plasmid DNA was purified using a
modified alkaline lysis method. Sequencing reactions were
conducted using the DYEnamic Cycle Sequencing Kit for
MegabACE (Amersham biosciences) according to the
manufacturer's recommendations. Clones were sequenced by
the 5' end with T7 primer. Sequencing reactions were
analyzed on MegabACE1000 DNA Sequencer (Amersham
biosciences). The quality and clustering of the ESTs were
analyzed using the softwares Phred/Gap3. Only EST
sequences with Phred quality greater than 20 and at least
150 bp were considered for clustering."

```

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.55e-98 Length: 647  
 Score: 881.00 Matches: 176  
 Percent Similarity: 97.34% Conservative: 7  
 Best Local Similarity: 93.62% Mismatches: 5  
 Query Match: 94.63% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x C0504431 (1-647)

```

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 54 GTGTGTGACCTCTTACTCGGACACATTAGAAGACAGGAGTGGTGTGGTCCAGC 113

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 114 TTGTTCTCTGCTCTCTAATACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTC 173

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 174 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTGTATCCAGCAATC 233

Qy 62 GlnLysSerAspGlnGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 234 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGCTGTGCT 293

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 294 GAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGTGTACATCAACGGCACAGTCAAG 353

Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 354 GAGCTGAGACGCCTCTCTCTGTCATGACCTTGGTTGATCTCTCAAGTTTGCAGTGTG 413

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 414 ATGTGGGTGTTCACTTACGTGGTCCCTGTGTTAATGTCGTGACATTTACTGATCTGCT 473

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 474 TTGATTTCTGCTTTCAGTGTCTCTGTTATTTATGAGACATCAGGCCAGATCGACCAT 533

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 534 TATTTGGGAGTAGTGAACAAGAACCTCAAGATGCGATGGCAAGATCCAAGCAAGATC 593

Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 594 CTTGGGCTGAAGCGNCAAACTGAG 617

```

RESULT 57

CK357937

LOCUS CK357937 751 bp mRNA linear EST 23-DEC-2003  
 DEFINITION AGENCOURT 17155981 NIH\_MGC\_233 Rattus norvegicus cDNA clone  
 IMAGE:7105386 5', mRNA sequence.

ACCESSION CK357937

VERSION CK357937.1 GI:40323869

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 751)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM14964 row: g column: 16

High quality sequence stop: 685.

FEATURES

source

1. 751

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

/clone="IMAGE:7105386"

/tissue\_type="heart, pooled"

/lab\_host="DH10B Tona"

/clone\_lib="NIH\_MGC\_233"

/note="Organ: heart; Vector: pExpress-1; Site 1: EcorV;  
 Site 2: NotI; RNA obtained from pooled heart tissue from a  
 mix of male and female animals at 8 wk old. Tissues were  
 snap-frozen and kept at -80C for two days before RNA  
 extraction and purification (Tri-reagent method). cDNA was  
 primed using oligo-dT primer:

5'-pCATAGTTCTAGTCGCGACGCGCCGCTT)25-3' and cloned into

the EcorV/NotI sites of pExpress-1. Size-selection &gt;1.4kb

resulted in an average insert size of 2 kb. This primary

library is not normalized (normalized primary library is

NIH\_MGC 234) and was constructed by Express Genomics

(Frederick, MD). Note: this is a NIH\_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 1.92e-98 Length: 751

Score: 881.00 Matches: 179

Percent Similarity: 97.31% Conservative: 2

Best Local Similarity: 96.24% Mismatches: 5

Query Match: 94.63% Indels: 0

DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK357937 (1-751)

```

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 159 GTTGTGACCTCTCTACTGGAGAGACATTAGAAGACTGGAGTGGTGTGGTCCAGC 218

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 219 TTATTTCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTACGTGAACGGCTTACATGCC 278

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

```

Db 279 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAGGGCGGTGATCCAGGCTATC 338  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLysSer 81  
 Db 339 CAGAAATCAGATCAGAGCCACCCATTCAGGCGCATATTTAGAAATCTCAAGTTGCTATATCA 398  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 399 GAGGAATTCGGTTTCAGAAATACAGTAATCTGCTCTTTGGTCATGTGAACAGCAATATAAA 458  
 QY 102 GluLeuArgGluLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 459 GAACTGAGCGGGTTTCTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGGTGTTG 518  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 519 ATGTGGGTGTTACTTATGTGTGGTCTGTTCAATGGTCTGACACTACTGATTTTAGCT 578  
 QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 579 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 638  
 QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 639 TATCTAGGACTTGCAACAGAGTGTTAAGATGCCATGGCCANNATCCAGCAAAATC 698  
 QY 182 ProGlyLeuLysArgLys 187  
 Db 699 CCTGGATTGAAGCGCAAG 716

RESULT 58  
 CN219472 821 bp mRNA linear EST 08-APR-2004  
 LOCUS WLA006H01.ab1 WLBRAIN Gallus gallus cdna 5', mRNA sequence.  
 DEFINITION CN219472  
 VERSION CN219472.1 GI:46298814  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 821)

REFERENCE  
 Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and  
 Lundberg, J.  
 EST analysis of brain and testis cdna libraries from White Leghorn  
 and Red Jungle Fowl  
 Unpublished (2004)  
 CONTACT: Peter Savolainen  
 Department of Biotechnology  
 Royal Institute of Technology, KTH  
 SE-106 91 Stockholm, SWEDEN  
 Tel.: +46 (0)8 5537 8481  
 Fax: +46 (0)8 5537 8335  
 Email: Peter.Savolainen@biotech.kth.se

Seq primer: M13 reverse primer.  
 Location/Qualifiers  
 1..821

FEATURES  
 source  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn"  
 /db\_xref="taxon:9031"  
 /sex="female"  
 /lab\_host="ElectroMAX DH10B (Invitrogen)"  
 /clone\_lib="WLBRAIN"  
 /notes="Organ: brain; Vector: pSPORT-1; Site 1: Hind III;  
 Site 2: EcoRI; The cdna libraries were created with the  
 Superscript Plasmid System (Invitrogen)."  
 ORIGIN

Alignment Scores:  
 Pred. No.: 2,9e-98 Length: 821  
 Score: 880.00 Matches: 176

Percent Similarity: 97.85% Conservative: 6  
 Best Local Similarity: 94.62% Mismatches: 4  
 Query Match: 7 Indels: 0  
 DB: Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN219472 (1-821)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 177 GTTGTGTGACCTCTTACTTGGCGAGACATTAAAGACAGAGGAGTGGTGTGGTGCAGC 236  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 237 TTGTCTCTGCTCTCTCATTAACAGTTCAGCATCGTGAGCGTGACACCTTACATTCGC 296  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLys 61  
 Db 297 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGGAGTTATCCAGGCAATC 356  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLysSer 81  
 Db 357 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTTGAGTCTGATGTGCTGTCT 416  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 417 GAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTGTGTCATCAACGGCAGTCAAG 476  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 477 GAGCTGAGAGCGCTCTCTTCCTGCTGATGACTTGGTTGATTCTCTGAAGTTTCAGTGTG 536  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 537 ATGTGGGTGTTCACTTACCTGCTGCTTGTATTAATGGTCTGACATTTACTGATCTGGCT 596  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 597 TTGATTTCTGCTGTTCTGAGTGTCTCTGTTATTATGAGACATCAGGCCAGATCGACCAT 656  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 657 TATTTGGGACTAGTGAACAAAGACGTCAAAGATGCGATGGCAAGATCCCAAGCAAGATC 716  
 QY 182 ProGlyLeuLysArgLys 187  
 Db 717 CCTGGCTGAAGCGCAAA 734

RESULT 59  
 CK305449 736 bp mRNA linear EST 01-MAR-2004  
 LOCUS SB02029A2B02.f1 normalized Keck-Tegu Library SB02 Taeniopygia  
 DEFINITION guttata cdna clone SB02029A2B02.f1 5, mRNA sequence.  
 CK305449  
 ACCESSION CK305449  
 VERSION CK305449.1 GI:44815023  
 KEYWORDS EST  
 SOURCE Taeniopygia guttata  
 ORGANISM Taeniopygia guttata

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
 Estrilidinae; Taeniopygia.  
 1 (bases 1 to 736)

TITLE Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M.,  
 Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.  
 and Liu, L.  
 The Songbird Neurogenomics Initiative: An Evolving Public Resource  
 for Study of Genes, Brain, and Behavior  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: David F. Clayton  
 University of Illinois  
 B107 CUSL, 601 S. Goodwin, Urbana, IL 61801, USA  
 Tel: 217 244 3668  
 Fax: 217 244 1648  
 Email: dclayton@uiuc.edu

Base Calling/Quality Scores: PHRED from Washington University Genome Center.

Vector Trimming: Cross\_match from Washington University Genome Center. PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script. This sequence is vector free and at least 200 bp in length. Funded by PHS grant # R01 NS045264, 'Songbird Neurogenomics Initiative.'

FEATURES	SOURCE
----------	--------

## ORIGIN

**Alignment Scores:**

Pred. No.:	7,78e-98	Length:	736
Score:	876.00	Matches:	175
Percent Similarity:	96.81%	Conservative:	7
Best Local Similarity:	93.09%	Mismatches:	6
Query Match:	94.09%	Indels:	0
DB:	7	Gaps:	0

US-09-830-972-29 COPY 990 1178 (1-189) x CK305449 (1-736)

Qy	2	ValValAspLeuLeuTyTrpArgaspIleLysIysThrGlyValValPheGlyAlaSer	21
Db	125	GTGTGTGACCTCTCTTTCTGGCGAGACATTAAAGAAGACCGGGGTGGTGTGGAGCCAG	184
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla	41
Db	185	TTGTTCCTGCTGCTCTCTATTAACTAGTGTTCAGCATCGTAGTGTACAGCGCTCAATTGCC	244
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAlaIle	61
Db	245	CTGGCCCTGCTCTGTCTCACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC	304
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrlenGluSerGluValAlaIleSer	81
Db	305	CAGAAGTCTGATGAGGGGCACCCCTTCAGGCGCTTACCTGAGCTCGGATGTGGCGGTGTCG	364
Qy	82	GluGluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValenCysThrIleLys	101
Db	365	GAGGAGCTCATCCAGAAGTACAGCAACGTCTGTCTGGGCCACCTGTAACCGCACCTGCCG	424
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	425	GAGCTGGCGGGCTCTTCTCTGTGATGACCTGTGGGATTCCTCAAGTTCGCAAGTATTG	484
Qy	122	MetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla	141
Db	485	ATGTGGTTTTTCATTACGTGGTGCCCTTGTTCAATGGTCTGACATTACTGATCTCGGCT	544
Qy	142	LeuIleSerLeuPheSerValProValIleTyrlenGluArgHisGlnAlaGlnIleAspHis	161

Score: 876.00 Matches: 175  
 Percent Similarity: 96.81% Conservative: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 94.09% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK303615 (1-765)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 119 GTTGTGGACCTCTTCTTCTGGGAGACATTAAGAAGACCGGGTGTGTGGAGCCAGC 178  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 179 TTGTTCTCTGCTCTCTATTAACAGTGTTCAGCATCTGTGAGTGTTCACAGCTACATTCGC 238  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 239 CTGGCCCTGCTCTCTGTCCACATCAGCTTTAGGATATACAGGAGTATTCAGGCAATC 298  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 299 CAGAAGTCTGATGAGGGCCACCCCTTCAGGGCTTACCTGAGCTCGGATGTGGCCGTGTCG 358  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 359 GAGGAGCTCATCCAGAGTACAGCAACGCTGCTGGGCCACGTCGTAACCGCACCGTCCCG 418  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 419 GAGCTCGGGCGCTCTTCTCTGCGAGACCTGTGGATTCCTCAAGTTCGAGATTG 478  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 479 ATGTGTTTTTCACTTACGTTGGTGGCTTGTTCATGTGCTGACATTTACTGATCTGGCT 538  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 539 TTGATTTCGCTCTTCAGTGTCTCTGTATTTATGAGACATCAGGCCCAATTCGACCAT 598  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 599 TACCTGGGACTGTGTAACAGAACGTCGAAGATGCCATGGCAAGATCCAGCAAGATC 658  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 659 CCTGGGTTGAAGCGCAAACTGAA 682

## RESULT 61

CK306874 793 bp mRNA linear EST 01-MAR-2004  
 LOCUS SB02042A1A11.f1 normalized Keck-Tagu Library SB02 Taeniopygia  
 DEFINITION guttata cDNA clone SB02042A1A11.f1 5, mRNA sequence.

ACCESSION CK306874  
 VERSION CK306874.1 GI:44816448  
 KEYWORDS EST.

## SOURCE

ORGANISM Taeniopygia guttata  
 Taeniopygia guttata  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
 Estrildinae; Taeniopygia.

## REFERENCE

AUTHORS Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,  
 Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.  
 and Liu,L.

TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource  
 for Study of Genes, Brain, and Behavior

## JOURNAL

COMMENT Unpublished (2004)  
 Contact: David F. Clayton  
 University of Illinois  
 B107 CLSU, 601 S. Goodwin,  
 Tel: 217 244 3668  
 Fax: 217 244 1648

Email: dclayton@uiuc.edu  
 Base Calling/Quality Scores: PHRED from Washington University  
 Genome Center.  
 Vector Trimming: Cross match from Washington University Genome  
 Center PHRAP suite. Low quality bases (Phred score < 20) were  
 trimmed from both ends of the sequence by an in-house script.  
 This sequence is vector free and at least 200 bp in length. Funded  
 by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'

## PCR Primers

FORWARD: TAATACGACTCACTATAGG(T7)

BACKWARD: ATTAACCTCTACTAAAG(T3)

Insert Length: 793 Std Error: 0.00

Place: SB02042A1 row: A column: 11

Seq primer: TAATACGACTCACTATAGG (T7)

High quality sequence stop: 793.

## FEATURES

source

1..793  
 /organism="Taeniopygia guttata"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:59729"  
 /clone="SB02042A1A11.f1"  
 /tissue\_type="brain"  
 /dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,  
 and adult (pooled)"  
 /lab\_host="DH108"  
 /clone\_lib="normalized Keck-Tagu Library SB02"  
 /note="Organ: brain; Vector: pBS II SK(+); Site\_1:  
 EORI(5' side of insert); Site\_2: NotI (3' side of  
 insert); The library was constructed and normalized as  
 described by Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 (1996), Genome Research 6(9): 791-806. An identifying tag  
 was added at the 3' during cDNA synthesis:  
 insertAAAAAAAAAAAAAAAAAATCGCA."

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,668-98 Length: 793  
 Score: 876.00 Matches: 175  
 Percent Similarity: 96.81% Conservative: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 94.09% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK306874 (1-793)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 89 GTTGTGGACCTCTTCTTCTGGCGAGACATTAAGAAGACCGGGTGTGTGGAGCCAGC 148  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 149 TTGTTCTCTGCTCTCTATTAACAGTGTTCAGCATCTGTGAGTGTTCACAGCTACATTCGC 208  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 209 CTGGCCCTGCTCTCTGTCCATCAGCTTTAGATATACAGGAGTATTCAGGCAATC 268  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 269 CAGAAGTCTGATGAGGGCCACCCCTTCAGGGCTTACCTGGACTCGGATGTGGCCGTGTCG 328  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 329 GAGGAGCTCATCCAGAAGTACAGCAACGTCGTGCTGGGCCACGTCGAACCGCACCGTCCCG 398  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 389 GAGCTCGGGCGCTCTTCTCTCGATGACCTTGGTGATTCCTCAAGTTCGAGATTG 448  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 449 ATGTGTTTTTCACTTACGTTGGTGGCTTGTTCATGTGCTGACATTTACTGATCTCGCT 508

QY 142 LeuileSerLeuPheSerValProValIleTyArgHisGlnAlaGlnIleAspHis 161  
 |||||  
 Db 509 TTGATTTTCGCTCTTCAGTCTTCTGTTATTTATGAGACATCAGGCCCAATCGACCAT 568  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 569 TACCTGGGACTTGTGTAACAAAGAACGTCAAAGATGCGCAAGATCCAAAGCAAGATC 628  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 |||||  
 Db 629 CTGCGTTGAAGCGCAAACTGAA 652  
 |||||

## RESULT 62

CK304164

LOCUS

DEFINITION

SB02022B2C10.f1 normalized Keck-Tagu Library SB02 Taeniopygia

guttata cDNA clone SB02022B2C10.f1 5, mRNA sequence.

ACCESSION

CK304164

VERSION

1

KEYWORDS

EST.

SOURCE

ORGANISM

Taeniopygia guttata

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;

Estrilidae; Taeniopygia.

1 (bases 1 to 852)

Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M.,

Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.

and Liu, L.

The Songbird Neurogenomics Initiative: An Evolving Public Resource

for Study of Genes, Brain, and Behavior

Unpublished (2004)

Contact: David F. Clayton

University of Illinois

B107 CUSL, 601 S. Goodwin, Urbana, IL 61801, USA

Tel: 217 244 3658

Fax: 217 244 1648

Email: dclayton@uiuc.edu

Base Calling/Quality Scores: PHRED from Washington University

Genome Center.

Vector Trimming: Cross\_match from Washington University Genome

Center PHRAP suite. Low quality bases (Phred score &lt; 20) were

trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded

by PHS grant # R01 NS045264, 'Songbird Neurogenomics Initiative.'

PCR Primers

FORWARD: TAATACGACTCACTATAGG (T7)

BACKWARD: ATTAACCTCACTAAG (T3)

Insert Length: 852 Std Error: 0.00

Plate: SB02022B2 row: C column: 10

Seq primer: TAATACGACTCACTATAGG (T7)

High quality sequence stop: 852.

Location/Qualifiers

1..852

/organism="Taeniopygia guttata"

/mol\_type="mRNA"

/db\_xref="taxon:59729"

/clone="SB02022B2C10.f1"

/tissue\_type="brain"

/dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,

and adult (pooled)"

/lab\_host="DH10B"

/clone\_lib="normalized Keck-Tagu Library SB02"

/note="Organ: brain; Vector: pBS II SK(+); Site: 1:

Score(5', side of insert); Site: 2: NotI (3' side of

insert); The library was constructed and normalized as

described by Bonaldo, M.F., Lennon, G. and Soares, M.B.

(1996). Genome Research 6(9): 791-806. An identifying tag

was added at the 3' during cDNA synthesis:

insertAAAAAAAAAAAAAAAAATGGCA."

ORIGIN

Alignment Scores:

Pred. No.: 9,59e-98 Length: 852  
 Score: 876.00 Matches: 175  
 Percent Similarity: 96.81% Conservative: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 94.09% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK304164 (1-852)

QY 2 ValValAspLeuLeuTyTrpArgAspIleLysValThrGlyValValPheGlyAlaSer 21  
 |||||  
 Db 109 GTTGTGACCTCTCTTCTGCGAGACATTAAGAAAGACCGGGGTGTGTTCGAGCCAGC 168  
 |||||  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAla 41  
 |||||  
 Db 169 TTGTTCTCGTCTCTCTATTAAACAGTGTTCAGCATCGTGAGTGTACAGCCTACATTGCC 228  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAla 61  
 |||||  
 Db 229 CTGGCCCTGCTCTCTGTCCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCAATC 288  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisPropheArgAlaTyLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 289 CAGAAAGTCTGATGAGGGCCACCCCTTCAGGGCTTACCTGGAGCTCGGATGTGGCCGTGTCG 348  
 |||||  
 QY 82 GluGluLeuValGlnLysTyTrpSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 |||||  
 Db 349 GAGGAGCTCATCCAGAGTACAGCAGCTGTGCTGGGCCACGTAAGCGGACCGTCCGG 408  
 |||||  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 409 GAGCTGGCGGCTCTCTCTCGTCGATGACCTGGTGGATTCCCTCAAGTTCGACGATTATG 468  
 |||||  
 QY 122 MetTrpValPheThrTyTrpValGlyAlaLeuPheAlaGlyLeuThrLeuLeuIleAla 141  
 |||||  
 Db 469 ATGTGGTTTTTCACTTACGTTGGTGGCTGTTCATATGCTGTGACATTTACTGATCTGGCT 528  
 |||||  
 QY 142 LeuIleSerLeuPheSerValProValIleTyArgHisGlnAlaGlnIleAspHis 161  
 |||||  
 Db 529 TTGATTCGCTCTTCAGTGTCTCTGTTATTTATGAGACATCAGGCCCAATTCACCAT 588  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 589 TACCTGGGACTTGTGAACAAAGACGTCAAAGATGCGTAAAGATCCAAAGCAAGATC 648  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 |||||  
 Db 649 CTGGGTTGAAGCGCAAACTGAA 672  
 |||||

## RESULT 63

BG109465

LOCUS

DEFINITION

602280543F1 NIH\_MGC\_86 Homo sapiens cDNA clone IMAGE:4368011 5',

mRNA sequence.

ACCESSION

BG109465

VERSION

BG109465.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

Homo sapiens

REFERENCE

1 (bases 1 to 819)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: LLAMI0021 row: f column: 12  
 High quality sequence stop: 647.  
 Location/Qualifiers  
 1. .819

## FEATURES

source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4368011"  
 /tissue\_type="osteosarcoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 86"  
 /note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.533 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.05e-97 Length: 819  
 Score: 875.50 Matches: 185  
 Percent Similarity: 97.88% Conservativeness: 0  
 Best Local Similarity: 97.88% Mismatches: 3  
 Query Match: 94.04% Indels: 2  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG109465 (1-819)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 19 GTTGTGACCTCTCTGCTGACGACATTAAGACACTGGAGTGGTGTGGTGGCAGC 78  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValLeuAla 41  
 Db 79 CTATTCTCTGCTCTTCACTGACAGTATTGACGATTTGAGCGTAAACGGTGTGATCCAGTATGC 138  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
 Db 139 TTGGCCCTGCTCTCTGACCATTCAGCTTTAGGATATACAGGGTGTGATCCAGTATGC 198  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 199 CAGAAATCAGATGAGGCCACCCATTCAGGCGATATCTGGATCTGAGTGGTATATCT 258  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 259 GAGGAGTTGGTTCAGAAATACAGTAATTTCTGCTCTTGGTCAATGTAACGATGCAATAAG 318  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 319 GAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAGTGGCAGG--TTG 376  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 377 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGGTCTGACACTACTGATTTGGCT 436  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 437 CTCAATTTCACTCTTCAGTGTCTCTGTTATTATTAAGCGCATCAGGCACAGATAGATCAT 496  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla-LysIle 181  
 Db 497 TATCTAGGACTTGCATAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAT 556  
 QY 181 eProGlyLeuLysArgLysAlaGlu 189  
 Db 557 CCCTGATTGACGGCAAAAGCTGAA 581

RESULT 64  
 CO503803 685 bp mRNA linear EST 13-JUL-2004  
 LOCUS  
 DEFINITION GGEZCB1022G02.g chicken breast muscle - CB1 Gallus gallus cdna

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

clone GGEZCB1022G02, mRNA sequence.

CO503803

CO503803.1 GI:50273989

EST.

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

1 (bases 1 to 685)

Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,  
 Patricio,M., Leduc,M.C. and Coutinho,L.L.

Discovery of new genes expressed in the chicken breast muscle

Unpublished (2004)

Contact: Helena J. Alves

Laboratory of Animal Biotechnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434

Fax: 55 19 3429 4285

Email: hjalves@esalq.usp.br and llicoutin@esalq.usp.br

PCR Primers

BACKWARD: T7.

Location/Qualifiers

1. 685

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="GGEZCB1022G02"

/tissue\_type="breast muscle"

/dev\_stage="1 and 21 days old"

/lab\_host="DH5 alpha"

/clone\_lib="chicken breast muscle - CB1"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This  
 cDNA library was constructed with the SuperScript Plasmid  
 System with Gateway Technology kit (Invitrogen), following a  
 manufacture's protocols. Plasmid DNA was purified using a  
 modified alkaline lysis method. Sequencing reactions were  
 conducted using the Dynamic Cycle Sequencing Kit for  
 MegabACE (Amersham Biosciences) according to the  
 manufacturer's recommendations. Clones were sequenced by  
 the 5' end with T7 primer. Sequencing reactions were  
 analyzed on MegaBACE1000 DNA Sequencer (Amersham  
 Biosciences). The quality and clustering of the ESTs were  
 analyzed using the softwares Phred/Cap3. Only EST  
 sequences with Phred quality greater than 20 and at least  
 150 bp were considered for clustering."

## ORIGIN

Alignment Scores:

Pred. No.: 9.34e-98 Length: 685  
 Score: 875.00 Matches: 175  
 Percent Similarity: 96.81% Conservativeness: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 93.98% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CO503803 (1-685)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 72 GTTGTGACCTCTCTTACTGGCGAGCATTAAGACAGAGTGGTGTGGTGGCAGC 131  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValLeuAla 41  
 Db 132 TTGTTCTCTGCTCTCTCTATTAAACAGTGTTCAGCATCTGAGCGTGCAGCTTACATTGCC 191  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
 Db 192 TTGGCCCTGCTCTTCTGTGACCATCAGCTTTAGGATATACAGGAGTATTCAGGCAATC 251  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 252 CAAAGTCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCTGATGTAGCTGTCT 311  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 312 GAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGCATCATCAAGCGACAGTCAAG 371  
 QY 102 GluLeuAArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 372 GAGCTGAGACGCTCTCTCTCGTATGATGCTTGTGATTTCTCTGAAGTTTGCAGTGTG 431  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLysLeuAla 141  
 Db 432 ATGTGGGTGTTACACTAGCTTGGTGGCTTGTATTAATGGTCTGACATTACTGATCTGCT 491  
 QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 492 TTGATTTGCTGTTTCAGTGTCTCTGTTATTATGAGACATCAGGCCCATGACCAT 551  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 552 TATTTGGGACTAGTGAACAAGAAGCTCCAAGATGGATGGCCCAAGATCCAGCCCAAGATC 611  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 612 CTTGGGCTGAAGCGCAAACTGAG 635

RESULT 65  
 COS81452  
 LOCUS ILLUMIGEN MCQ\_47216 Katze\_MMLV Macaca mulatta cDNA clone  
 DEFINITION IBTUM:17799 5' similar to Bases 83 to 959 highly similar to human  
 RTN4 (Hs.436349), mRNA sequence.  
 ACCESSION COS81452  
 VERSION COS81452.1 GI:50412806  
 KEYWORDS EST.  
 SOURCE Macaca mulatta (rhesus monkey)  
 ORGANISM Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.  
 REFERENCE 1 (bases 1 to 960)  
 Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.  
 Large-scale Rhesus Macaque cDNA Sequencing  
 Unpublished (2003)  
 CONTACT: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com  
 Sequenced on 2004.06.24. 532 020 bases. Library Preparation: Prof.  
 Michael Katze Lab at University of Washington DNA Sequencing:  
 Illumigen Biosciences Inc. For further information, see  
 http://www.macaque.org

PCR Primers  
 FORWARD: CCTCACTAAAGGGAACAAA  
 BACKWARD: CACTATAGCGGATTCGGTA  
 Insert Length: 960. Std Error: 0.00  
 Plate: CL000396 row: H column: 08  
 Seq primer: CCTCACTAAAGGGAACAAA  
 POLYA=Yes.

# FEATURES

Location/Qualifiers  
 1..960  
 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
 /strain="Indian"  
 /db\_xref="taxon:9544"  
 /clone="IBTUM:17799"  
 /sex="female"  
 /dev\_stages="adult"  
 /lab\_host="Electromax DH10B"  
 /clone\_lib="Katze\_MMLV"  
 /note="Organ: liver; Vector: pDONR 222; Site\_1: BsrG I;

Site 2: BsrG I; Created from CloneMiner cDNA Library  
 Construction kit (catalog #18249-029)"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.51e-97 Length: 960  
 Score: 875.00 Matches: 180  
 Percent Similarity: 97.34% Conservative: 3  
 Best Local Similarity: 95.74% Mismatches: 4  
 Query Match: 93.98% Indels: 1  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x COS81452 (1-960)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysIleValValPheGlyAlaSerLeu 22  
 Db 84 GTTGACCTCTCTAGTGGAGAGACTTGAAGAAATATGGAGTGGTGTGGCCAGCTA 143  
 QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 144 TTCCTGCTCTTCTTGCACAGTATTACAGATTGTGAGTGTAAACAGCTACATTGCCCTG 203  
 QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 204 GCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGCTATCCAG 263  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 264 AAATCAGATGAGGCCACCCATTGAGGCATATCTGGAAATCTGAAGTTGGCATATCTGAG 323  
 QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
 Db 324 GAGTTGGTTCAAGAGTACAGTAATTTCTGCTCTTGTCTCATGTGAACTGCACGATAAAGGAA 383  
 QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 384 CTCAGGGCCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAAGTTTGCAGTGTGTGATG 443  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142  
 Db 444 TGGGTATTACTATGTTGGTGGCTTGTATTGTTAATGTTGACGCTACTGATTTGGCTCTC 503  
 QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 Db 504 ATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATGATCATTTAT 563  
 QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 564 CTAGGACTTGCAAAATAAGAATGTTAAAGATGCTATGGCTAAATATCCAGCGAAAAATCCC 623  
 QY 182 oGlyLeuLysArgLysAlaGlu 189  
 Db 624 TGGATTGAAGCGCAAGCTGAA 645

# RESULT 66

CDS111521

LOCUS

DEFINITION

AGENCY:14353136 NIH\_MGC\_187 Homo sapiens cDNA clone

IMAGE:30405928 5', mRNA sequence.

CDS111521

VERSION

CD511521.1 GI:31443239

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 758)

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH



Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM193 row: n column: 17

High quality sequence stop: 614.

Location/Qualifiers

#### FEATURES

source

1..758

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30405928"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_187"

/note="Organ: Blood vessels - aorta, basilar and artery;

Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2:

SfiI (ggcgctcgccg); 5' and 3' adaptors were used in

cloning as follows: 5' adaptor sequence:

5'-CACGCCATTATGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGCGCGGACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.4 kb

(range 0.5-4.0 kb). 14/15 colonies contained inserts by

PCR. This library was enriched for full-length clones and

was constructed by Clontech Laboratories (Palo Alto, CA).

Note: this is a NIH\_MGC Library."

#### ORIGIN

##### Alignment Scores:

Pred. No.: 1.25e-97 Length: 758  
Score: 874.50 Matches: 182  
Percent Similarity: 98.39% Conservative: 1  
Best Local Similarity: 97.85% Mismatches: 1  
Query Match: 93.93% Indels: 2  
DB: 6 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD511521 (1-758)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 148 GTTGTGACCTCTGTACTGGAGAGACATTAAAGACATGGAGTGTGTGGTGGCCAGC 207  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
DB 208 CTATTCTCTGCTTTCATGACAGTATTCAGCATTTGTGAGCGTACACGCTACATTGCC 267  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
DB 268 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAAGCTATC 327  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 328 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGAAGTTGCTATATCT 387  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 388 GAGGAGTTGGTTCAGAGTACAGTAAATCTGCTCTTGGTCACTGATGACTGCACGATAAG 447  
QY 102 GluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 448 GAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTCAGTGTG 507  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB 508 ATGTGGGTATTTACCTATGTGTGTGCTGCTTTAAATGGTCTGACACTCTGATTTTGGCT 567  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 568 CTCATTTCATCTTCAGTGTCTCTGTTATTATGACGGCATCAGGCACAGATAGATCAT 627

QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet-AlaLysIleGlnAlaLysIle 181  
DB 628 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGGTAAATCAAAGCAAAA 687  
QY 181 ePro--GlyLeuLys 185  
DB 688 TCCCTCGGGAATTGAAA 703

#### RESULT 67

BG427864

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

EST.

GI:13334370

NIH-MGC

http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1367 row: f column: 13

High quality sequence stop: 712.

Location/Qualifiers

1..713

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4614924"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_75"

/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:

SfiI (ggcgctcgccg); Site 2: SfiI (ggccattatggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGCGCGGACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.65

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH\_MGC Library."

#### ORIGIN

##### Alignment Scores:

Pred. No.: 1.32e-97 Length: 713  
Score: 874.00 Matches: 182  
Percent Similarity: 97.85% Conservative: 0  
Best Local Similarity: 97.85% Mismatches: 4  
Query Match: 93.88% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG427864 (1-713)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 146 GTTGTGACCTCTCTGCTGAGAGACATTAAAGACATGGAGTGTGTGGTGGCCAGC 205  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
DB 206 CTATTCTCTGCTTTCATTTGACAGTATTCAGCATTTGTGAGCGTACACGCTACATTGCC 265



QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 266 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTATC 325  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 326 CAGAAATCAGATGAAGGCCACCAATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 385  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysPheThrIleLys 101  
 Db 386 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGGTCAATGTAAGCTGCACGATAAG 445  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 446 GAATCAGCGGCTCTCTCTAGTTAGATTTAGTTGATCTCTGAGGTTGTCAGTGTG 505  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 506 ATGTGGGTATTTACCTATGTTGGTGC-CTGTTTAATAGTCTGCACACTACTGATTTGGCT 564  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 565 CTCATTTCACTCTTCAGTGTCTCTGTCATTTATGAACGGCATCAGGCAAGATAGATCAT 624  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 625 TATCTAGAGCTTGCAANTAGAAATGTTACAGATGCTAATGGTAAATCCAGCAAAATC 684  
 QY 182 ProGlyLeuLysArgLys 187  
 Db 685 CTGGATTGAAGCGCAAG 702

RESULT 68  
 BG400408  
 LOCUS  
 DEFINITION 602464428F1 NIH\_MGC\_75.Homo sapiens cDNA clone IMAGE:4592670 5',  
 mRNA sequence.  
 ACCESSION BG400408  
 VERSION BG400408.1 GI:13293856  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 905)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
 http://image.llnl.gov  
 Plate: LLCW1331 row: g column: 07  
 High quality sequence stop: 708.  
 Location/Qualifiers  
 1..905  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4592670"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_75"  
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggccctcgccg); Site 2: SfiI (ggccattggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCCATATGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A,

## FEATURES

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,46e-97 Length: 905  
 Score: 873.00 Matches: 182  
 Percent Similarity: 96.84% Conservative: 2  
 Best Local Similarity: 95.79% Mismatches: 4  
 Query Match: 93.77% Indels: 2  
 DB: 4 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG400408 (1-905)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 153 GTTGTGGACCTCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCAGC 212  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 213 CTATTTCCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTAACAGCCTACATTGCC 272  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 273 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTATC 332  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 333 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 392  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 393 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGGTCAATGTAAGCTGCACGATAAG 452  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 453 GAATCAGCGGCTCTCTCTAGTTAGATTTAGTTGATTTCTGAAAGTTGCAATGTG 512  
 QY 122 Met-TrpValPheThrTyrValGlyAlaLeuPheAsn-GlyLeuThrLeuLeuIleAla 141  
 Db 513 ATCGTGGGTATTTACCTATGTTGGTGCCTGTTTACTGGTCTGACACTACTGATTGGG 572  
 QY 141 LaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspH 161  
 Db 573 CTCTCATTTCACTCTTCACTGTTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATC 632  
 QY 161 LeTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 633 ATTATCTAGGACTTGCAANTAGAAATGTTAAGATGCTATGGTAAATCCAGCAAAA 692  
 QY 181 LeProGlyLeuLysArgLysAlaGlu 189  
 Db 693 TCCCTGGATTGAAGCGCAAGTTGAA 718  
 RESULT 69  
 BU364240  
 LOCUS  
 DEFINITION BU36585074F1 CSECHN72 Gallus gallus cDNA clone ChEST539d19 5', mRNA  
 sequence.  
 ACCESSION BU364240  
 VERSION BU364240.1 GI:25872241  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 820)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

C, or G and N = A, C, G, or T). Average insert size 1.65  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392

COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

Location/Qualifiers

1..820

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Compton Line 151"

/db\_xref="taxon:9031"

/clone="CHES7539d19"

/sex="female"

/tissue\_type="cerebrum"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSECHN72"

/note="Organ: brain; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Alignment Scores:  
Pred. No.: 2,85e-97 Length: 820  
Score: 872.00 Matches: 177  
Percent Similarity: 96.83% Conservative: 6  
Best Local Similarity: 93.65% Mismatches: 5  
Query Match: 93.66% Indels: 1  
DB: Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BU364240 (1-820)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 156 GTTGTGACCTCTTACTGGCGAGACATTAAAGACAGGAGTGTGTGGTGGCCAGC 215  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 216 TTGTTCTGCTGCTCTCTATTAAACAGTGTTCAGCATGTCGAGCGTGACGTTACATTC 275  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 276 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGTATTCAGGCAATC 335  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 336 CAAAGTCCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCTGATGCTAGTGTCT 395  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 396 GAAGAGCTGATTACAGAAATACACAGTGTGTGCTTGGTCACATCAACGGCAGTCAAG 455  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 456 GAGCTGAGAGCGCTCTTCTCTGTTGATGACTTGTGTTGATCTCTGAAGTTTCAGTGTG 515

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleuLeuAla 141  
Db 516 ATGTGGGTGTTTCACTTACGTTGGTCTGTTTAAATGGTCTGACATTACTGATGGCT 575  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 576 TTGATTTGCTGTTCTCAGTGTCTCTGTTATTATGAGACATCAGGCCAGATCGACCAT 635  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 636 TATTTGGGACAGTAGTGAACAAGACCTCAAGATGCGATGGCAAGATCCACCAAGATC 695  
QY 182 Pro-GlyLeuLysArgLysAlaGlu 189  
Db 696 CCTGGGCTGGAAGCGCAAACTGAG 720

## RESULT 70

CA322433

LOCUS

CA322433

DEFINITION

UI-M-FX0-ckk-n-21-0-UI.r1 NIH\_BMAP\_FX0 Mus musculus cDNA clone

IMAGE:6820918 5', mRNA sequence.

CA322433

ACCESSION

CA322433

VERSION

CA322433.1

KEYWORDS

EST.

Mus musculus (house mouse)

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/

1 (bases 1 to 817)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..817

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CS7BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:6820918"

/tissue\_type="whole brain"

/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_FX0"

/note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR I;

Site\_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is ACCGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

## ORIGIN

```
Alignment Scores:
Pred. No.: 5,01e-97 Length: 817
Score: 870.00 Matches: 185
Percent Similarity: 97.40% Conservative: 2
Best Local Similarity: 96.35% Mismatches: 2
Query Match: 93.45% Indels: 3
DB: 6 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CA322433 (1-817)

QY 1 SerValValAspLeuLeu-TyrTrp-ArgAspIleIysIysThrGlyValValPheGlyA 20
DB 41 TCAGTTGTGGCTCTCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAAGGCTTAC 100
QY 20 laSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrI 40
DB 101 CCAGCTTATCTCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAAGGCTTAC 160
QY 40 leAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnA 60
DB 161 TTGCCCTTGGCCCTGCTCTCTGCTGCTATCAGCTTTAGGATATATAAGGGTGTGATCCA 220
QY 60 laIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaI 80
DB 221 CTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCC 280
QY 80 leSerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI 100
DB 281 TATCAGAGGAATGGTTTCAGAAATATAGTAATTCCTGCTTGGTTCATGTGAACACACA 340
QY 100 leYleGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuIysPheAlaV 120
DB 341 TAAAGAAATTTAGAGCGTCTCTCTTAGTTGATGATTTAGTTCCCTGAGTTTGCAG 400
QY 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnClyLeuThrLeuLeuIleL 140
DB 401 TGTTCATGTGGTATTTACTTACGTTGGTGGCTCTTCAATGGTTTGCACACTACTGATTT 460
QY 140 euAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA 160
DB 461 TAGCTCTGATCTCCTCTTCAGTATTCCTGTTATATATGACCGCATCAGGGCCAGATAG 520
QY 160 ePHisTyrLeuGlyLeuAlaAsnIysAsnValIysAspAlaMetAlaIysIleGlnAlaL 180
DB 521 ATCATTAATCTAGGACTTGCACCAAGAGCGTTTAAGGATGCCATGCCAAATCCCAAGCA 580
QY 180 yeIlePro-GlyLeuIysArgIysAlaGlu 189
DB 581 AAATCCCTGGGATTGAAGCCANAGCAGAA 610

RESULT 71
CD623552/c 659 bp mRNA linear EST 12-JAN-2004
LOCUS 5608673H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD623552
ACCESSION CD623552
VERSION CD623552.1 GI:40271817
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
source 1..659
```

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/notice="Vector: pDrive Cloning Vector"
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## ORIGIN

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Alignment Scores:
Pred. No.: 4.9e-97 Length: 659
Score: 869.00 Matches: 177
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.44% Mismatches: 0
Query Match: 93.34% Indels: 0
DB: 6 Gaps: 0
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD623552 (1-659)

```
QY 12 LysIysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 31
DB 654 AGGAAGACTGGAGTGGTGTGGTGCCAGCCTATTCTCTGCTGCTTTTCATTGACAGTATTC 595
QY 32 SerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPhe 51
DB 594 AGCATTTGTGAGCGTAACAGCCTACATTCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT 535
QY 52 ArgIleTyrIysGlyValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArg 71
DB 534 AGGATATACAGAGGTGTGATCCNAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGG 475
QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnIysTyrSerAsnSer 91
DB 474 GCATATCTGGAATCTGAAGTTGCTATATCTCAGGAGTTGGTTTCAGAGTACAGTAATTC 415
QY 92 AlaLeuGlyHisValAsnCysThrIleIysGluLeuArgArgLeuPheLeuValAspPhe 111
DB 414 GCTCTTGTGTCATGAACTGCACGATAAAGAACTCAGCGGCTCTTCTTAGTTGATGAT 355
QY 112 LeuValAspSerLeuIysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
DB 354 TTAGTTGATCTCTGAGTTTGCAGTGTTCAGTGGGTATTTACCTATGTTGGTGCCTTG 295
QY 132 PheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIle 151
DB 294 TTTAATGTCCTGACACTACTGATTTGGCTCTCATTTTCACCTTTCAGTGTCTCTGTTATT 235
QY 152 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnIysAsnValIys 171
DB 234 TATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAAATTAAGAATGTAAA 175
QY 172 AspAlaMetAlaIysIleGlnAlaIysIleProGlyLeuIysArgIysAlaGlu 189
DB 174 GATGCTATGGCTAAAATCCAGCAAAATACCTGGATTGAAGGCCAAGCTGAA 121
```

## RESULT 72

```
CD623553
LOCUS 5608673J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD623553
ACCESSION CD623553
VERSION CD623553.1 GI:40271818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 660)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
```

Email: gfu@incyte.com

## FEATURES

Location/Qualifiers  
 1..660  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /notes="Vector: pDrive Cloning Vector"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,91e-97 Length: 660  
 Score: 869.00 Matches: 177  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.44% Mismatches: 0  
 Query Match: 93.34% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD623553 (1-660)

QY 12 LysLeuThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPhe 31  
 :::  
 Db 6 AGGAGACTCGAGTGTGTGGTGGCCAGCTATTCCTGCTGCTTTTCATTGACAGTATTC 65  
 QY 32 SerLeuValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPhe 51  
 :::  
 Db 66 AGCATTTGTGAGCGTAACAGCTACATTTGCTTTGGCCCTCTCTGTGTGACCATGACTTT 125  
 QY 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71  
 :::  
 Db 126 AGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATCAGGCCACCCATTCAGG 185  
 QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91  
 :::  
 Db 186 GCATATCTGGAATCTCAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAATGACAGTATTC 245  
 QY 92 AlaLeuGlyHisValAsnCystrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111  
 :::  
 Db 246 GCTCTTGGTCATGTGAACATGACGATAAAGGAACATCAGGGCCCTCTTCTTAGTTGATGAT 305  
 QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeu 131  
 :::  
 Db 306 TTATTTGATTCCTGAAGTTTGACGTTGGTGGGTATTTACCTATGTTGTTGCTTTG 365  
 QY 132 PheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerValProValIle 151  
 :::  
 Db 366 TTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTTCATCTCTTCAAGTGTTCCTGTTAT 425  
 QY 152 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLys 171  
 :::  
 Db 426 TATGAACGGCATCAGGCACAGATAGATCATTTCTAGGACTTGCATAATGAAGATGTTAA 485  
 QY 172 AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189  
 :::  
 Db 486 GATGCTATGGCTAAATCCAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 539

## RESULT 73

## BI872386

LOCUS 603397035F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5400584 5',  
 DEFINITION mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1201 row: f column: 09

High quality sequence stop: 754.

Location/Qualifiers

## FEATURES

source

1..857  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5400584"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.26e-96 Length: 857  
 Score: 867.00 Matches: 184  
 Percent Similarity: 97.89% Conservative: 2  
 Best Local Similarity: 96.84% Mismatches: 1  
 Query Match: 93.13% Indels: 3  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BI872386 (1-857)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 :::  
 Db 130 GTTGTGTGACCTCTCTGCTGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 189  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 :::  
 Db 190 TTATTTCTGCTGCTCTCTGACAGTTCAGCATTTGTGAGTGTAAAGCGCTACATTGCC 249  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 :::  
 Db 250 TTGGGCCCTGCTCTCTGTGACTATCATGCTTTAGGATATATAAGGGGTGTGATCCAAGCTATC 309  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 :::  
 Db 310 CAGAAATCAGATCAAGGCCACCATTCAAGGCATATTGGAAATCTGAAGTTGCCATATCA 369  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101  
 :::  
 Db 370 GAGGAATGGTTTCAGAAATATAGTAATCTGCTCTTGGTTCATGTGAACAGCACATAAAA 429  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 :::  
 Db 430 GAAATGAGCGCTCTCTCTTAGTATTTAGTTAGTTCTCCCTCAAGTTTCAGGTGTG 489  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 :::  
 Db 490 ATGTGGGTATTTACTTACCTTGCTGCTTGTTCATGTTTTCAGTCTACTGATTTTAGCT 549  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 :::  
 Db 550 CTGATCTCACTCTTCAGTATTCCTGTATATATGAACGGCATCAGCGCGCAGATAGATCAT 609  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla-LysIleGlnAla-LysI 181  
 :::  
 Db 610 TATCTAGGACTTGCAGAACAGAGCGTTAGGATGCCATCGCCAAATATCCAGCAAAAAA 669  
 QY 181 leProGlyLeu-LysArgLysAla 188

```

Db      670 TCCCTGGATTGAGCGCAAGCA 693
|||||
RESULT 74
BU949473
LOCUS
DEFINITION
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
EST.
BU949473.1 GI:24200824
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 609)
AUTHORS
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE
Endocrine Pancreas Consortium
JOURNAL
Unpublished (2000)
COMMENT
Other ESTs: in67h09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 471.
FEATURES
source
1..609
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127360"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI, Site_2: XhoI; cDNA made by oligo-dT priming. ~1kb. 5'
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
ORIGIN
Alignment Scores:
Pred. No.: 1,376-96 Length: 609
Score: 865.00 Matches: 177
Percent Similarity: 98.33% Conservative: 0
Best Local Similarity: 98.33% Mismatches: 3
Query Match: 92.91% Indels: 0
DB: 5 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x BU949473 (1-609)
Qy 10 AspileLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThr 29
Db 1 GACATTAAAGAGATTGGAGTGGTGTGGTGGCCAGCCTATTCTCTCTTCATTGACA 60

```

```

Qy 30 ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIle 49
Db 61 GTATTACGATTGTGAGCGTAACGCTACATTGCTTGGCCCTGCTCTCTGTGACCATC 120
Qy 50 SerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro 69
Db 121 AGCTTTAGGATATACAAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGCCACCCA 180
Qy 70 PheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSer 89
Db 181 TTCAGGGCATATCTGGAATCTGAAAGTTCATATCTGAGGAGTTGGTTCAGAACTACTGT 240
Qy 90 AsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuVal 109
Db 241 AATTCTGCTCTTGGTCATGCACTGCACGATAAAGGAACCTCAGCGGCTCTTCTTAGTT 300
Qy 110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTrrpValPheThrTyrValGly 129
Db 301 GATGATTTAGTTGATTCTCTGAAGTTTGACAGTTGTGATGGGTATTTACCTATGTTGGT 360
Qy 130 AlaLeuPheArgGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
Db 361 GCCTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTCTCT 420
Qy 150 ValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn 169
Db 421 GTTATTTATGACCGCATCAGCAGATAGATCATTTATCTAGGACTTGCATAATAGAAAT 480
Qy 170 ValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189
Db 481 GTTAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 540

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RESULT 75
BE733819
LOCUS
DEFINITION
601569133F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843729 5',
mRNA sequence.
ACCESSION
BE733819
VERSION
BE733819.1 GI:10147721
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 716)
NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM539 row: a column: 10
High quality sequence stop: 716.
FEATURES
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3843729"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by

```



Db 643 TTATCTAGGACTTGCATAAATAAGAACTTTCACAGATCTTAATGGTAAATAATCCAGCAAAA 702

Qy 181 leProGlyLeuLysArgLysAlaGlu 189

Db 703 TCCTGGATTGAAGCCCAAGCTGAC 728

## RESULT 77

BI394814

LOCUS

DEFINITION

ppin.pk009.15 Normalized Chicken Pituitary/Hypothalamus/Pineal Library Gallus gallus cDNA clone ppin.pk009.15 5' similar to gi|5902016.ref|NP\_008939.1| reticulon 4; neuroendocrine-specific protein c like (foocen) [Homo sapiens] gi|13637055.ref|XP\_002439.3| neuroendocrine-specific protein C like (foocen) [Homo sapiens] gb|AAD27783.1|AF077050\_1 (AF077050) neuroendocri, mRNA sequence.

ACCESSION

BI394814

VERSION

BI394814.1

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE

Porter,T.E. and Cogburn,L.A.

ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA

Library USDA/IFAPS Animal Genome Project

Unpublished (2001)

Contact: Larry A. Cogburn

University of Delaware

Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-1335

Fax: 302-831-2822

Email: cogburn@udel.edu, www.chickest.udel.edu.

Location/Qualifiers

1..646

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Commercial broiler chicken"

/db\_xref="taxon:9031"

/clone="ppin.pk009.15"

/sex="Male and Female"

/tissue type="Pituitary Gland/Hypothalamus/Pineal Gland"

/dev stage="Embryonic (d12,d14,d19); post-hatch

/lab host="E. Coli EMDH10B"

/clone\_lib="Normalized Chicken

Pituitary/Hypothalamus/Pineal Library"

/note="Vector: pCMVSPORT6; Library made from equivalent

pools of total RNA isolated from each tissue at different

ages. Single pass sequencing from 5'-end"

ORIGIN

Alignment Scores:

Pred. No.: 2,646-96 Length: 646

Score: 863.00 Matches: 174

Percent Similarity: 95.74% Conservative: 6

Best Local Similarity: 92.55% Mismatches: 8

Query Match: 92.70% Indels: 0

DB: 4 Gaps: 0

US-09-830-972-29\_copy\_990\_1178 (1-189) x BI394814 (1-646)

Qy 2 ValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

Db 51 GTTGTGACCTCTTCTTACGAGACATTAAAGACAGAGGAGTGTGTTGGTCCAGC 110

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 111 TTGTTCTCTGCTCTCTTACAGTGTTCAGCATCGTGGAGCGTACAGCTTACATGCC 170

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 171 TTGGCCCTGCTTTTCTGTGACCATCAGCTTTAGGATATATACAGGAGGAGTTATCCAGGCAATC 230

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerClnuValAlaIleSer 81

Db 231 CAAAAGTCCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCTGATAGCTGTGTCT 290

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

Db 291 GAAGAGCTGATTACAAATACAGCAGTGTGTGCTTGGTCACATCAACGGCACAGTCAAG 350

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 351 GAGCTGAGACGCTCTTCTGCTGATGACCTTGTGTTGATCTCTCAAGTTTCAGTGTG 410

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141

Db 411 ATGTGGGTGTTCACTTACGTTGGTGCCTTGTTTAATGGTCTGACATTACTTGATCTGGCT 470

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

Db 471 TTGATTCGCTGTTTCAGTGTTCCTGTTTATTTATGAGACATCAGGCCAGATCCACCAN 530

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysPheAlaMetAlaLysIleGlnAlaLysIle 181

Db 531 TATTGGGACTTNTGAACAAGAACGTCAAAGATGCGATGGCAAGATCCAAAGCAAGATC 590

Qy 182 ProGlyLeuLysArgLysAlaGlu 189

Db 591 CCNNNCTGAAGCGCNCNNACTGAG 614

RESULT 78

BUI39629

LOCUS

DEFINITION

BUI39629

VERSION

BUI39629.1

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE

Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,

Fong,W.T., Pickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

22335534

PUBMED

12445392

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1..1028

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="White Leghorn, Hisex"

/db\_xref="taxon:9031"

/clone="CHEST117m23"

/dev stage="16 day embryo"

/lab host="DH10B"

/clone lib="CHEOCHL24"

/note="Organ: brain; Vector: pBluescript II KS(+); Site 1:

EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)

[Stratagene] vector to accommodate cDNA produced with the

T-trimmed protocol [Construction of uni-directionally

cloned cDNA libraries from messenger RNA for improved 3'



end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggcgcgtgagcccgatccgaaaaag] [5'aattcttttttcggatccgggctgacgc]

## ORIGIN

Alignment Scores:  
Pred. No.: 5,13e-96 Length: 1028  
Score: 863.00 Matches: 178  
Percent Similarity: 96.34% Conservative: 6  
Best Local Similarity: 93.19% Mismatches: 5  
Query Match: 92.70% Indels: 2  
DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BUI39629 (1-1028)

```
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
|||
Db 186 TCAGTTGTTGACCTCTTACTGGCGAGACATTAAAGACAGGAGTGTGTGGTGC 245
|||
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
|||
Db 246 AGCTTGTCTCTGCTCTCATTAACAGTTCAGCATCGTGAGCGTGACAGTTACATT 305
|||
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
|||
Db 306 GCCTTGGCCCTGTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCA 365
|||
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
|||
Db 366 ATCCAAAGTCCGATGAAGGCCATCCATTAGGCGCTTACTTGAGTCTGATGAGTGTG 425
|||
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
|||
Db 426 TCTGAGAGCTGATTACAGAAATACACAGCTGTGTGTCACATCAACGCCACAGTC 485
|||
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
|||
Db 486 AAGGAGCTGAGAGCGCTCTCTCTGTTGATGACTTGTGTTGATTTCTGAAGTTTGCA 545
|||
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
|||
Db 546 TTGATGGGTGTCTACTTACGTGTGTGCTGTTGTTAATGCTTGATCTGATGACTG 605
|||
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
|||
Db 606 GCTTTGATTTCGCTGTTTCAGTGTTCCTGTTATTTATGAGACATCAGGCCAGATCGAC 665
|||
QY 161 HisTyrLeuGlyLeuAlaLeuLysAsnValLysAspAlaMetAla-LysIleGlnAlaLys 180
|||
Db 666 CATTATTGGGACTAGTGAACAGAACGTCNAAGATGCGATGCGCAAAAGATCCAAAGCAA 725
|||
QY 180 stlePro-GlyLeuLysArgLysAlaGlu 189
|||
Db 726 GATCCCTGGCTTGAAGCGCAAAACTGAG 754
|||
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RESULT 79

CD000871

LOCUS

DEFINITION

IMAGE:30321390 5', mRNA sequence.

ACCESSION

CD000871

VERSION

CD000871.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 735)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM120 row: 1 column: 07

High quality sequence stop: 530.

## FEATURES

source

1..735

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30321390"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_186"

/note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: Sfil

(ggccattggcc); Site 2: Sfil (ggcgcctcgcc); Library is

oligo-dr primed and directionally cloned. cDNA was

prepared from a pooled samples of tissues from Skin,

meninges, duramater, pia matter and choroid plexus. 5'

and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGGCGGCCGACATG-dt(30)BN-3'

(where B = A, C, G or T). Average

insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC

Library"

## ORIGIN

Alignment Scores:

Pred. No.: 5,63e-96 Length: 735

Score: 861.00 Matches: 180

Percent Similarity: 98.36% Conservative: 0

Best Local Similarity: 98.36% Mismatches: 1

Query Match: 92.48% Indels: 2

DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD000871 (1-735)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

|||

Db 189 GTTGTGACCTCTCTACTGGAGAGACATTAAAGACACTGGAGTGTGTGGTGCAGC 248

|||

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

|||

Db 249 CTTATTCCTGCTCTTTCATTGACATTTACAGCATTTGGAGCGTAACACGCTACATTGCC 308

|||

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

|||

Db 309 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGTATC 368

|||

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

|||

Db 369 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 428

|||

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

|||

Db 429 GAGGAGTTGGTTTCAGAAATACAGTAAATCTCTCTTGGTCATGTGAACGTCACGATAAAG 488

|||

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

|||

Db 489 GAATCAGCGCGCTCTTCTTAGTGTAGTATTAGTTGATTTCTCTGAAGTTTCAGAGTTTG 548

|||

QY 122 MetTrpValPheThrTyrVal-GlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl 141

|||

Db 549 ATGTGGGTATTACCTATGTTTGGTGCCTTGTTTAATGCTGTCGACACTACTGATTTTGGC 608

|||



QY 141 aleulleSerLeuPheSer-ValProValIleTyrGluArgHisGlnAlaGlnIleAspH 161  
 Db 609 TCTCATTTCACTCTTCAGTGGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATC 668  
 QY 161 iSTyLeuGlyLeuAlaAsnLysAenValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 669 ATTATCTAGGACTTCCCAATAAAATGTTAAAGATGCTATGGCTAAATCCAGCCAAA 728  
 QY 181 lePro 182  
 Db 729 TCCCT 733  
 RESULT 80  
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 LOCUS 4125836 BARC 8BOV Bos taurus cDNA clone 8BOV\_41013 5', mRNA  
 DEFINITION  
 ACCESSION CN791158.1 GI:47687138  
 VERSION  
 KEYWORDS  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 677)  
 Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and  
 Matukumalli,L.K.  
 Construction and Analysis of a cDNA Library Generated From  
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle  
 Unpublished (2004)  
 JOURNAL Contact: Richard G. Baumann  
 COMMENT Bovine Functional Genomics Lab  
 ANRI  
 BLDG 162: BARC-EAST, Beltsville, MD 20705, USA  
 Tel: 3015048604  
 Fax: 3015048744  
 Email: rbaumann@anri.barc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 0.000925 using options -trim\_alt '- -trim\_fasta. Vector identified  
 by cross\_match using options -minmatch 12 -minscore 18  
 Plate: 41 row: 0 column: 13  
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 High quality sequence stop: 677.  
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 /strain="Holstein"  
 /db\_xref="taxon:9913"  
 /clone="8BOV 41013"  
 /sex="Female"  
 /tissue\_type="Epithelial, Muscle"  
 /dev\_stage="Lactating, Neonatal"  
 /lab\_host="DH10B TonA"  
 /clone\_lib="BARC 8BOV"  
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:  
 NotI; Site 2: EcoRI; Normalized cow cDNA intestinal  
 library in pCMVSPORT6.1, constructed from equimolar mRNA  
 pools derived from 5 sources, 4 lactating neonatal, 1  
 neonatal intestinal 4/5 Lactating, Proximal Duodenum,  
 Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal  
 Duodenum, Jejunum, Distal Ileum"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 8.86e-96 Length: 677  
 Score: 859.00 Matches: 174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 92.27% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN791158 (1-677)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGGACCTCCCTCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCACG 215  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 216 TTGTTCTGCTGCTCTGCTGCACAGATTTCAGCATTGTGAGTGTAAACGGCTTACATTGCC 275  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 335  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAGAAATCTGATGAAGCCACCAATTCAGGCGATATTGGGAATCTGAAGTTGCTATATCT 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCythrIleLys 101  
 Db 396 GAGGAGTTGGTTTCAGAGTACAGCAATTCCTCTCTTGGTTCATGTTAACTGCACATAAAA 455  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAATCTCAGACGCCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTTGTG 515  
 QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 516 ATGTGGGTATTACTATGTTGGGCGCTTGTTCATGTCGTGACACTACTAATTTGGCT 575  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 576 CTGATTTCACTCTTCAGTGTTCCTGTTATTATTGAACGGCATCAGGCCCAATAGATCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 175  
 Db 636 TATCTGGACTTGCAATAAGATGTTAAAGATGCTATGGCT 677  
 RESULT 81  
 BUI38907  
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 DEFINITION  
 ACCESSION BUI38907  
 VERSION BUI38907.1 GI:25353139  
 KEYWORDS  
 EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 759)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Ford,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 JOURNAL 2235534  
 MEDLINE 12445392  
 PUBMED  
 COMMENT  
 Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612089930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..759  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="ChEST115a3"  
 FEATURES  
 source

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/dev stage="16 day embryo"
/lab_host="DH10B"
/clone_lib="CSQCHL24"
/Note="Organ: Brain; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol. (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcgctgcagcccgagccgagaaaaag]
[5'aattcttttttcggatccg999ctgcagc]
```

ORIGIN

Alignment Scores:  
Pred. No.: 1-85e-95 Length: 759  
Score: 857.00 Matches: 176  
Percent Similarity: 96.81% Conservative: 6  
Best Local Similarity: 93.62% Mismatches: 6  
Query Match: 92.05% Indels: 1  
DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BUI38907 (1-759)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspLysLysThrGlyValValPheGlyAlaSer 21
DB 137 GTTGTGACCTCTTACTGGCGAGACATTAAAGACAGGAGTGTGTTGGTGCAGC 196
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 197 TTGTTCTCTGCTCATTAACAGTGTTCAGCATCTGAGCGTGACCTTACATGTC 256
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 257 TTGGCCCTGCTTCTCTGACCATCAGCTTTAGGATATACAGGAGTTATCCAGGCAATC 316
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 317 CAAAGTCGCGATGAGGCCATCCATTAGGCGCTTACTGGAGTCTGATGAGTGTGCT 376
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 377 GAAGAGCTGATTCAGAAATACAGCAGTGTGCTTGGTCACATCAACCGCAGTCAAG 436
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 437 GAGCTGAGCGCTCTTCCTCGTTGATGACTTGGTTGATCTCTGAAGTTTGCAGTGTG 496
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 497 ATGTGGGTGTCACTTACGTGTGCTGCTGTTTAATGCTGCATTAATGCTGCTGCT 556
QY 142 LeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 557 TTGATTCGCTGTCTAGTGTCTCTGTTATTTATGAGAGACATCAGGCCGAGATCGACCA 616
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 617 TATTTCGGACTAGTGACAGAACGTCGTCATGATGCGATGGCAAGATCCAGCAAGATC 675
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 676 CTTGGGCTGAAGCGCAAACTGAG 699
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RESULT 82

CR771568  
LOCUS CR771568 684 bp mRNA linear EST 23-SEP-2004  
DEFINITION DKFZp469C23377 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone  
ACCESSION DKFZp469C23377 5', mRNA sequence.  
VERSION CR771568  
KEYWORDS CR771568.1 GI:52614841 EST.

SOURCE ORGANISM

Pongo pygmaeus (orangutan)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
1 (bases 1 to 684)  
AUTHORS Ottenwaelder, B., Obermaier, B., Deutschenbaue, S., Schaipp, A.,  
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and  
Wiemann, S.  
TITLE Pongo pygmaeus mRNA (Ottenwaelder, B., Obermaier, B.,  
Deutschenbaue, S., et al.)  
JOURNAL Unpublished (2004)  
COMMENT Contact: MIPS

FEATURES

location/Qualifiers  
1..684  
/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
/clone="DKFZp469C2337"  
/tissue\_type="kidney"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="469 (synonym: pkid1)"  
/note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"

ORIGIN

Alignment Scores:  
Pred. No.: 3-75e-95 Length: 684  
Score: 854.00 Matches: 173  
Percent Similarity: 99.43% Conservative: 0  
Best Local Similarity: 99.43% Mismatches: 1  
Query Match: 91.73% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR771568 (1-684)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspLysLysThrGlyValValPheGlyAlaSer 21
DB 162 GTTNTGACCTCTCTCTACCTGGAGACATTAAGAGACTGGAGTGGTGTGGTGCAGC 221
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 222 CTATTCTGCTGCTTTCATTGACAGTATTTCAGCATTTGAGTGTGAACACCTTACAT 281
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 282 TTGGCCCTGCTTCTCTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCTATC 341
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 342 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAACTGAGTGTGATATCT 401
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 402 GAGGAGTTGTTTTCAGAAATGACAGTAACTTCTCTTGTGTCATGTGAACCTGCAGATAAG 461
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 462 GAACCTCAGCGCTCTCTTCTTGTGATGATTTAGTGTGATTTCTGAAGTTTGCAGTGTG 521
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
```

```

Db      522 ATGTGGTATTACCTATGTTGGTGGCTGTTTAAATGGTCTGACGCTACTGATTTGGCT 581
Qy      142 LeuileSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      582 CTCATTTCATCTCTTCTGAGTCTCTGTTATTATGAGCGGCATCAGGCACAGATAGATCAT 641
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 175
Db      642 TATCTAGGACTTGCAGAAATGAAGATGTTAAAGATGCTATGGCT 683

RESULT 83
BU848611      813 bp      mRNA      linear      EST 16-OCT-2002
LOCUS      AGENCOURT_10276498 NIH_MGC_144 Mus musculus cDNA clone
DEFINITION      IMAGE:6596409 5', mRNA sequence.
ACCESSION      BU848611
VERSION      BU848611.1 GI:24033573
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2825 row: p column: 09
High quality sequence stop: 160.
FEATURES
source      1. 813
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /clone="IMAGE:6596409"
            /lab_host="DH10B (T1-phage-resistant)"
            /clone_lib="NIH_MGC_144"
            /note="Organ: Brain; Vector: pDNR-LIB; Site_1: SfiI
            (ggccatcgcc); Site_2: SfiI (ggccgcctcgcc); cDNA made
            by oligo-dT priming and directionally cloned. 5' and 3'
            adaptors were used in cloning as follows:
            5'-AAGCAGTGTATCAACGAGCGGCGGCGCATGCGCGGG-3' and
            5'-ATTCTAGAGCGGCGGCGGCGGCGCATG-DT(30)NN-3'. Full-length
            enriched library was constructed using the Clontech
            Creator SMART kit and size-selected to contain the 0.2-0.5
            kb size fraction (other fractions present in NIH_MGC_143).
            Library created in the laboratory of M. Brownstein (NIH,
            NIH). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      4.8e-95      Length:      813
Score:          854.00      Matches:    179
Percent Similarity: 95.79%      Conservative: 3
Best Local Similarity: 94.21%      Mismatches: 6
Query Match:    91.73%      Indels:     2
Db:             5          Gaps:         0

US-09-830-972-29_COPY_990_1178 (1-189) x BU848611 (1-813)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      159 GTTGTGACCTCCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 218
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

```

```

Db      219 TTATTCCTGCTGCTGCTCTCAGCAGTGTTCAGCATTTGTCAGTGTAAACGCCCTACATTCGC 278
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      279 TTGGCCCTGCTCTCTGTGACTATCAGCTTTTAGGATATATAAGGGTGTGTATCAAGCTATC 338
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      339 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATTTGGAATCTGAAGTTGCCATATCA 398
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      399 GAGGAATTTGGTTTCAGAAATATAGTAATTTCTCTTGTGTCATGTGAACAGCAATAAATA 458
Qy      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      459 GAATTTAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGTGTG 518
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      519 ATGTGGGTATTACTTACGTTGGTGGCTTGTTCATGTTGACACTACTGATTTAGCT 578
Qy      142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      579 CTGATCTCCTCTTCTGATTTCTGTTATATATGAACGCGCATCAGGCGCAGATAGATCAT 638
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet-AlaLysIleGlnAlaIle 181
Db      639 TATCTAGGACTTGCAGAAACAGAGCGGTAAAGATGCCATGCCGNNCAAAATCCAGCAAAAAT 698
Qy      181 eProGlyLeu-LysArgLysAlaGlu 189
Db      699 CCTTGGATTGANGCGGCAAAACAGNA 724

RESULT 84
BU847877      614 bp      mRNA      linear      EST 05-SEP-2001
LOCUS      603192073P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5263026 5',
DEFINITION      mRNA sequence.
ACCESSION      BU847877
VERSION      BU847877.1 GI:15435189
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11663 row: b column: 19
High quality sequence stop: 614.
FEATURES
source      1. 614
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5263026"
            /tissue_type="hippocampus"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_95"
            /note="Organ: brain; Vector: pBluescriptR (modified)

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pbluescript KS+); Site 1: BamHI; Site 2: Sall-XhoI (gtcag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores: 7.56e-95 Length: 614  
 Pred. No.: 851.00 Matches: 174  
 Score: 851.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.41% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1547877 (1-614)

QY 16 ValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35  
 Db 7 GTGGTGTGGTGGCCAGCCTATTTCCTGCTGCTTCATTGACAGTATTTCAGCATTTGTGAGC 66

QY 36 ValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrls 55  
 Db 67 GTAACAGCCTACATTCCTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAG 126

QY 56 GlyValIleGlnAlaIleGlnIlySerAspGluGlyHisProPheArgAlaTyrlsGlu 75  
 Db 127 GGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGA 186

QY 76 SerGluValAlaIleSerGluGluLeuValGlnIlySerSerAsnSerAlaLeuGlyHis 95  
 Db 187 TCTGAAGTTGCTATATCTCAGGAGTTGGTTCAGAACTACAGTAATTTCTGCTCTGTCAT 246

QY 96 ValAsnCysThrIleIlySerGluLeuArgLeuPheLeuValAspSerValAspSer 115  
 Db 247 GTGAACCTGCACGATAAAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCT 306

QY 116 LeuIlyPheAlaValLeuMetTrpValPheThrTyrlValGlyAlaLeuPheArgGlyLeu 135  
 Db 307 CTGAAGTTTGCAGTGTGAGTGGGATTTACCTATGTTGGCCCTGTTTAAATGTCATG 366

QY 136 ThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIleTyrlGluArgHis 155  
 Db 367 ACACACTACTGATTTTGGCTCTCATTTCTCAGTGTTCCTGTTATTTATGAACGGCAT 426

QY 156 GlnAlaGlnIleAspHisTyrlsGlyLeuAlaAsnIlyAsnValIlyAspAlaMetAla 175  
 Db 427 CAGGCACAGATGATCATTTATCTAGGACTTGCAGAAATGAAGATGTTAAAGATGCTATGGCT 486

QY 176 LysIleGlnAlaIlyProGlyLeuIlyAspGlyAlaGlu 189  
 Db 487 AAATCCAGCAAAAATCCCTGATTTGAAGCCGCAAGCTGAA 528

## RESULT 85

CN429726 708 bp mRNA linear EST 16-MAY-2004  
 LOCUS 1700059934467 GRN\_PRENU Homo sapiens cDNA 5', mRNA sequence.

## DEFINITION

CN429726

## ACCESSION

CN429726.1 GI:47417320

## VERSION

EST.

## KEYWORDS

Source

## ORGANISM

Homo sapiens (human)

## REFERENCE

1. (bases 1 to 708)  
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Mura, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. W.

## TITLE

Transcriptome characterization elucidates signaling networks that

JOURNAL  
COMMENT

control human ES cell growth and differentiation  
 Nat. Biotechnol. 22 (6), 707-716 (2004)  
 Contact: Brandenberger R  
 Regenerative Medicine  
 Gen Corporation  
 230 Constitution Drive, Menlo Park, CA 94025, USA  
 Tel: 650 473 8658  
 Fax: 650 473 7760  
 Email: rbrandenberger@gen.com  
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## FEATURES

## Source

1..708  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="embryonic stem cell, retinoic acid and  
 mitogen-treated hES cell line H7"  
 /clone\_lib="GRN PRENU"  
 /note="oligo dT primed, full-length enriched cDNA library  
 from hES cell line H7 (p29) maintained in feeder-free  
 conditions. Embryoid bodies were generated in the presence  
 of all-trans retinoic acid and mitogens."

## ORIGIN

Alignment Scores: 9.27e-95 Length: 708  
 Pred. No.: 851.00 Matches: 174  
 Score: 851.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.41% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN429726 (1-708)

QY 16 ValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35

Db 1 GTGGTGTGGTGGCCAGCCTATTTCCTGCTGCTTCATTGACAGTATTTCAGCATTTGTGAGC 60

QY 36 ValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrls 55

Db 61 GTAACAGCCTACATTCCTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAG 120

QY 56 GlyValIleGlnAlaIleGlnIlySerAspGluGlyHisProPheArgAlaTyrlsGlu 75

Db 121 GGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGA 180

QY 76 SerGluValAlaIleSerGluGluLeuValGlnIlySerSerAsnSerAlaLeuGlyHis 95

Db 181 TCTGAAGTTGCTATATCTCAGGAGTTGGTTCAGAACTACAGTAATTTCTGCTCTGTCAT 240

QY 96 ValAsnCysThrIleIlySerGluLeuArgLeuPheLeuValAspSerValAspSer 115

Db 241 GTGAACCTGCACGATAAAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCT 300

QY 116 LeuIlyPheAlaValLeuMetTrpValPheThrTyrlValGlyAlaLeuPheArgGlyLeu 135

Db 301 CTGAAGTTTGCAGTGTGATGTTGGGATTTACCTATGTTGGTCCCTGTTTAAATGTCATG 360

QY 136 ThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIleTyrlGluArgHis 155

Db 361 ACACACTACTGATTTTGGCTCTCATTTCTCAGTGTTCCTGTTATTTATGAACGGCAT 420

QY 156 GlnAlaGlnIleAspHisTyrlsGlyLeuAlaAsnIlyAsnValIlyAspAlaMetAla 175

Db 421 CAGGCACAGATGATCATTTATCTAGGACTTGCAGAAATGAAGATGTTAAAGATGCTATGGCT 480

QY 176 LysIleGlnAlaIlyProGlyLeuIlyAspGlyAlaGlu 189

Db 481 AAATCCAGCAAAAATCCCTGATTTGAAGCCGCAAGCTGAA 522

## RESULT 86

BG568630

## LOCUS

BG568630 755 bp mRNA linear EST 10-APR-2001

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DEFINITION 602587637F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716393 5',
mRNA sequence.
ACCESSION BG568630
VERSION BG568630.1 GI:13576283
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 755)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1564 row: j column: 10
High quality sequence stop: 719.
Location/Qualifiers
1..755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4716393"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 76"
/note="organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES
source
BG428512 906 bp mRNA linear EST 14-MAR-2001
LOCUS 602501030F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614679 5',
mRNA sequence.
ACCESSION BG428512
VERSION BG428512.1 GI:13335018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1366 row: l column: 08
High quality sequence stop: 730.
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4614679"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1.32e-94 Length: 906
Score: 851.00 Matches: 184
Percent Similarity: 96.86% Conservative: 2
Best Local Similarity: 95.81% Mismatches: 3
Query Match: 91.41% Indels: 4
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BG568630 (1-755)

Qy 2 ValValAspLeuLeuTyrTriArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 178 GTTGTGACCTCCTGTACTGGAGACATTAAGACATGGAGCTGGTGTGTGGTCCAGC 237
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 238 CTATTCTCTGCTCTTTCATTGACAGTATTGACATTTGTGAGCGTAAACAGCTACATTGCC 297
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 298 TTGGCCCTGCTCTGTGACCATCATGCTTTAGGATATACAGGGGTGTCATCAAGCTATC 357
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 358 CAGAATATAGATGAAGGCCACCCATTACAGGCATATCTGGATCTGAAGTTGCTATATCT 417
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnGlyThrIleLys 101
Db 418 GAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTGTGGGTCTATGTGAACTGCACGATAAG 477

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Qy 102 GluLeuArgAqLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 478 GAATCAGCGCCCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 537
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 538 ATGTGGGTATTTACATGTTGGTGGCTTGTATATGAGCGCATCAGGCACAGATGATCAT 596
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 597 CTCATTTTCACCTCTTCAGTGTTCCTGTTATTTATGAACGCGCATCAGGCACAGATGATCAT 656
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAla-MetAlaLysIleGlnAla--Lys 180
Db 657 TATCTAGACCTTGCATATGAATGATTTACAGATGCTAATGTTAAATCCAAAGCAAAA 716
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 717 ATCCCTGGATTGAAGCGCAAAAGTAA 743

RESULT 87
BG428512 906 bp mRNA linear EST 14-MAR-2001
LOCUS 602501030F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614679 5',
mRNA sequence.
ACCESSION BG428512
VERSION BG428512.1 GI:13335018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1366 row: l column: 08
High quality sequence stop: 730.
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4614679"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1.32e-94 Length: 906
Score: 851.00 Matches: 184
Percent Similarity: 96.86% Conservative: 0
Best Local Similarity: 98.40% Mismatches: 2

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Query Match:	91.41%	Indels:	3
DB:	4	Gaps:	0
US-09-830-972-29_COPY_990_1178 (1-189) x BG428512 (1-906)			
Qy	2	ValValAspLeuLeuTyrTripArgAspIleLeuValysThrGlyValValPheGlyAlaSer	21
Db	103	GTGTGTGACCTCCCTGCTGCTGAGAGACATTAAGAAGACTGAGAGTGCTGTGGTGCCACG	162
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	163	CTATTCTCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACGCTTACATTGCC	222
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	223	TTGGCCCTGCTCTCTGTGACCATTGACCTTTAGGATATACAGGGTGATCCAGCTATTC	282
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	283	CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT	342
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	343	GAGAGATTGGTTTCAGAGTACAGTAATTCCTCTCTGGTCATGAGTGCACGATAAAG	402
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	403	GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG	462
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	463	ATGTGGGTATTACCTATGTTGGTGCCCTGTTTAAAGTCTGACACTCTGATTTTGGT-	521
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGlu-ArgHisGlnAlaGlnIleAspHis	161
Db	522	CTCATTTTCACTCTTCAGTGTTCCTGTTATTTATGAACCGGCATCAGGCACAGATAGTCA	581
Qy	161	sTyrLeuGlyLeuAlaLeuLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	582	TTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGT-AAATTCACAGCAAAAT	640
Qy	181	eProGlyLeuLysArgLys	187
Db	641	CCCTGGATTGAAGCGCAAA	659

RESULT 88				
BU109449				
LOCUS	BU109449	915 bp	mRNA	linear EST 25-NOV-2002
DEFINITION	603126259f1 CSEQCHL13	Gallus gallus	cDNA clone	CHEST95f15 5', mRNA sequence.

ACCESSION	BUI09449	
VERSION	BUI09449.1	GI:25312699
KEYWORDS	EST.	
SOURCE	Gallus gallus (chicken)	
ORGANISM	Gallus gallus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	

REFERENCE 1 (bases 1 to 915)  
 AUTHOR Boardman, P. E.; Sanz-Ezquerro, J.; Overton, I. M.; Burt, D. W.; Bo  
 Fong, W. T.; Tickle, C.; Brown, W. R. A.; Wilson, S. A. and Hubbard,  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

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FEATURES             Location/Qualifiers
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         /organism="Gallus gallus"
         /mol_type="mRNA"
         /strain="White Leghorn, Hisex"
         /db_xref="taxon:9031"
         /clone="ChEST95f15"
         /dev_stage="22"
         /lab_host="DH10B"
         /clone_lib="CSECHL13"
         /note="Organ: limbs; Vector: pBluescript II KS(+); Site.1: EcoRI; Site.2: NotI; Modification of pBluescript II KS(+): [Stratagene] vector to accommodate cDNA produced with the T-timed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgacgcccgatcgcgaataaaag] [5'aattcttcttttcgaaccgacctcacgc]"

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## ORIGIN

Alignment Scores:	
Pred. No.:	1.78e-94
Score:	850.00
Percent Similarity:	96.33%
Best Local Similarity:	92.59%
Query Match:	91.30%
DB:	5
Length:	175
Matches:	175
Conservative:	7
Mismatches:	7
Indels:	1
Gaps:	0

US-09-830-972-29 COPY 990 1178 (1-189) x BU109449 (1-915)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla	20
Db	127	CGCGTGTGTGACCTCCCTTAACTGCGGAGACATTAAAGAACAGGAGTGGTGTGGTGCC	186
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	187	AGCTTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGGCTGACAGCTTACATT	246
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	247	GCCTTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAGGAGATTATCCAGGCA	306
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerCluValAlaIle	80
Db	307	ATCCAAAGTCCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCGTAGTAGCTGTG	366
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	367	TCTGAGAGCTGATTCCAGAAATACAGCAGTGTGTGCTTGGTCACATCAACGGCACAGTC	426
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	427	AAGGAGCTGAGACGCCCTCTCTCGTTGATGACTTGGTGTGATTCTCTGAAGTT-GCAGTG	485
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	486	TTGATGTGGGTGTTCATTACGTCTGGTGCCCTGTGTTAATGGTCTGACATTACTGTACTG	545
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	546	GCCTTGATTTCCGCTGTTCCAGTGTCTCTGTTATTTATGAGAGACATCAGGCCCAGATCGAC	605
Qy	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	606	CATTATTGGGGACTAGTGAAACAAGAACGTCAAAGATGCGATGGCAAAAGATCCAAGCAAAG	665
Qy	181	IleProGlyLeuLysArgLysAlaGlu	189
Db	666	ATCCCTGGGCTGAAGCGCAAAATTGAG	692

BQ807975  
LOCUS NISC\_Kk12d10.v1 NCI CGAP Brn72 Macaca mulatta cDNA clone EST 31-JUL-2002  
DEFINITION IMAGE:5331139.5', mRNA sequence.  
ACCESSION BQ807975  
VERSION BQ807975.1 GI:22032184  
KEYWORDS EST.  
SOURCE Macaca mulatta (rhesus monkey)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
REFERENCE 1 (bases 1 to 619)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
CDNA Library Preparation: cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
Plate: LLAM11840 row: H column: 20  
Seq primer: M13RP1 reverse primer (ABI).  
LOCATION/Qualifiers  
FEATURES  
source  
1..619  
/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/db\_xref="taxon:9544"  
/clone="IMAGE:5331139"  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NCI CGAP Brn72"  
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: Not I; Site 2: EcoRV; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.2 kb. Constructed by Invitrogen. Note: this is a NCI\_CGAP Library."

ALIGNMENT Scores:  
Pred. No.: 1.35e-94 Length: 619  
Score: 849.00 Matches: 171  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.84% Mismatches: 0  
Query Match: 91.19% Indels: 0  
DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BQ807975 (1-619)

Qy 2 ValValAspLeuLeuTyrrpArgAspIleYsThrGlyValValPheGlyAlaSer 21  
Db 100 GTTGTGACCTCCTCTACTGGAGACATGAAGAGCTGGAGTGGTGTGGTCCAGC 159  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrileAla 41  
Db 160 CTATTTCCTGCTGCTTTTCATTGACATATTAGCATTTGTGAGTGTAAACAGCCTACATTGCC 219  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIle 61  
Db 220 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAGCTATC 279  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81  
Db 280 CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTCGATATCT 339  
Qy 82 GluGluLeuValGlnLysTyrrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 340 GAGGAGTGTGGTTTCAGAGTACAGTAATTCCTGCTCTGTGTCATGTGAACTGCACGATAAG 399

Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 400 GAACCTCAGCGCCCTCTCTTCTAGTTAGTATTTAGTTAGTTCTCTGAAGTTTCAGTGTG 459  
Qy 122 MetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
Db 460 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATATGCTGACCTACTGATTTGGCT 519  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHis 161  
Db 520 CTCATTTTCACCTCTTCAGGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATATCAT 579  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174  
Db 580 TATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATG 618  
RESULT 90  
CR771272 644 bp mRNA linear EST 23-SEP-2004  
LOCUS DKFZP469F2235.r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone  
DEFINITION DKFZP469F2235.5', mRNA sequence.  
ACCESSION CR771272  
VERSION CR771272.1 GI:52614545  
KEYWORDS EST.  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.  
REFERENCE 1 (bases 1 to 644)  
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
TITLE Pongo pygmaeus mRNA (Poustka, A., Albert, R., Moosmayer, P., et al.)  
JOURNAL Unpublished (2004)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZP469F2235  
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.  
FEATURES  
source  
1..644  
/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
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/tissue\_type="kidney"  
/dev\_stages="adult"  
/lab\_host="DH10B"  
/clone\_lib="469 (synonym: pkid1)"  
/note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"

ALIGNMENT Scores:  
Pred. No.: 1.91e-94 Length: 644  
Score: 848.00 Matches: 172  
Percent Similarity: 97.73% Conservative: 0  
Best Local Similarity: 97.73% Mismatches: 4  
Query Match: 91.08% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR771272 (1-644)

Qy 2 ValValAspLeuLeuTyrrpArgAspIleYsThrGlyValValPheGlyAlaSer 21  
Db 115 GTTGTGACCTCCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 174  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrileAla 41



```

Db      175 CTATTCTGCTGCTTTTCATTGACAGTATTACAGATTTGAGTGTAAACAGCCTACATTGCC 234
QY      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
        |||||
Db      235 TTGGCCCTGCTTTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 294
QY      62  GlnIleSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
        |||||
Db      295 CAGAAATCAGATGAAGCCACCATTCAGGGCATATCTGGAATCTCGAATGCTATATCT 354
QY      82  GluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
        |||||
Db      355 GAGGAGTTGNNTCAGAGTACAGTAATTTCTGCTTTGGTCATGTGACTGCAGTAAG 414
QY      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
        |||||
Db      415 GAATTCANGCGCNCCTCTTAGTTGATGATTTAGTTGATTTCTGGAATTTGAGTGTG 474
QY      122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141
        |||||
Db      475 ATGTGGGTATTTACCTATGTTGGTGCCTTTGTTAATGGTCTGACGCTACTGATTTTGGCT 534
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
        |||||
Db      535 CTCAATTCATCTCTCAGTGTTCCTCGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 594
QY      162 TyrLeuGlyLeuAlaAsnIleValIleValIleValIleValIleValIleValIle 177
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Db      595 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGCTGCTAAATATC 642

RESULT 91
BG696431 991 bp mRNA linear EST 07-MAY-2001
LOCUS 602659532F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802911 5',
DEFINITION mRNA sequence.
ACCESSION BG696431
VERSION BG696431.1 GI:13961567
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-r@mail.nih.gov
        Tissue Procurement: James Cleaver, M.D.
        cDNA Library Preparation: Life Technologies, Inc.
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
        Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: L14M10697 row: 0 column: 08
        High quality sequence stop: 763.
        Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
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                /lab_host="PH10B (T1 phage-resistant)"
                /clone_lib="NCI CGAP Skn3"
                /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.5kb. Library constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."

FEATURES
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        /organism="Homo sapiens"
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        /clone_lib="NCI CGAP Skn3"
        /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
        Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
        Average insert size 1.5kb. Library constructed by Life
        Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 6.25e-94 Length: 991

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Score: 846.00 Matches: 181
Percent Similarity: 97.33% Conservative: 1
Best Local Similarity: 96.79% Mismatches: 3
Query Match: 90.87% Indels: 3
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BG696431 (1-991)

QY      4  AspLeuLeuTyrTrpArgAspIleIleIleIleIleIleIleIleIleIleIleIleIle 23
        |||||
Db      216 GACCTCTCTGCTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGCCTATTTC 275
QY      24  LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43
        |||||
Db      276 CTGCTGCTTTTCATTGACAGTATTCAGCATTTGAGCGTAAACAGCCTACATGCTTGGCC 335
QY      44  -LeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIleGlnly 63
        |||||
Db      336 CTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAA 395
QY      63  sSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluG1 83
        |||||
Db      396 ATCAGATGAAGCCACCCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCTGAGGA 455
QY      83  uLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleIleGluLe 103
        |||||
Db      456 GTAGGTTTCAGAAAGTACAGTAATTCGCTCTTGGTCATGTAAGTGCACCATTAAGAACT 515
QY      103 uArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTr 123
        |||||
Db      516 CAGGCGCCTCTTCTAGTTGATGATTTAGTTCTCTGAAAGTTTGCAAGTTTGATGTG 575
QY      123 pValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuAla 143
        |||||
Db      576 GGTATTTACATATGTTGGTGCCTTGTAAATGGTCTGACACTACTGAT-TTGGCTCTCAT 634
QY      143 eSerLeuPheSerValProValIleTyrGluArgHisGlnAla-GlnIleAspHisTyrL 163
        |||||
Db      635 TTCACCTTTCAGTGTTCCTGTTATTATGACGGCATCAGGCAACAGATGATCATATTTC 694
QY      163 euGlyLeuAlaAsnIleValIleValIleValIleValIleValIleValIleValIle 183
        |||||
Db      . 695 TAGGACTTGCATTAAGATGTCATAAGATGCTATGGTAAATCCAAAGCAAAATCCCTG 754
QY      183 llyLeuLysArgLysAla 188
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Db      755 GATTGAAGCGCAAAAGC 771

RESULT 92
BG696431 815 bp mRNA linear EST 05-SEP-2001
LOCUS 603189563F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261007 5',
DEFINITION mRNA sequence.
ACCESSION BG696431
VERSION BG696431.1 GI:15435924
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-r@mail.nih.gov
        Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
        cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
        Toshinuki and Piero Carninci (RIKEN)
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov  
 Plate: LLAM11657 row: n column: 16  
 High quality sequence stop: 757.

# FEATURES

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 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5261007"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_95"

/note="Organ: Brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,45e-94 Length: 815  
 Score: 845.50 Matches: 183  
 Percent Similarity: 96.32% Conservative: 0  
 Best Local Similarity: 96.32% Mismatches: 5  
 Query Match: 90.82% Indels: 3  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1548612 (1-815)

QY 2 ValValAspLeuLeuThrValPheSerLeuValPheGlyAlaSer 21  
 Db 169 GTTGTGACCTCTCTGACCATCAGTTAGGATATACAGGGTGTATCCAGCTATC 348  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValPheSerLeuValPheAla 41  
 Db 229 CTAATTCCTGCTCTTCAATGACATATTACAGATTGTGAGCGTAACAGCTTACATGCC 288  
 QY 42 LeuAlaLeuLeuSerValThrPheSerLeuValPheSerLeuValPheGlyAlaSer 61  
 Db 289 TTGGCCCTGCTCTGACCATCAGTTAGGATATACAGGGTGTATCCAGCTATC 348  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaThrLeuGluSerGluValAlaLeuSer 81  
 Db 349 CAGAAATCAGATGAAGGCCACCGATTTCAGGCGCATATCTGGAATCTGAAAGTTGCTATATCT 408  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrLeuLys 101  
 Db 409 GAGGAGTTGGTTTCAAGATGACAGTAATTTCTGCTTGTGTGATGTAACCTGCACGATAAG 468  
 QY 102 GluLeuArgArgLeuPheLeuValAsp-AspLeuValAspSerLeuLysPheAlaValle 121  
 Db 469 GAACCTAGCCCTCTTCTAGTACATGATTAGTCTGTAAGTTGAGTGT 528  
 QY 121 uMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 529 GATGGGGTATTACATATTGTTGGTCCCTTGTATTATGTAACGGCATCAGGATAGATC 588  
 QY 141 aleuileSerLeuPheSer-ValProValIleTyrGluArgHisGlnAlaGlnIleAspH 161  
 Db 589 TCTCATTTTCACTTTTCACTGTTCTCTGTTATTATGTAACGGCATCAGGATAGATC 648  
 QY 161 isTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 649 ATTATCTAAGACTGC--AATAGATGTTAGGATGCTATGTTAAATATCCAGCAAAA 706  
 QY 181 leProGlyLeuLysArgLysAlaGlu 189  
 Db 707 TCCCTGGATTGAAGGCCAAAGTTGAA 732

## RESULT 93

AV702687  
 LOCUS AV702687 719 bp mRNA linear EST 08-OCT-2000  
 DEFINITION AV702687 ADB Homo sapiens cDNA clone ADBBB01 5', mRNA sequence.  
 ACCESSION AV702687  
 VERSION AV702687.1 GI:10719017  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 719)  
 AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,  
 Xiao, H., Xu, X., Li, N., Qian, B., Liu, P., Qu, J., Gao, X., Cheng, Z.,  
 Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,  
 Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.  
 Homo sapiens cDNA ADB clones  
 Unpublished (2000)  
 CONTACT: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919(ex.45)  
 Fax: 86-21-50801922  
 Email: hanzgchgc.sh.cn  
 This clone is available at CHGC in Shanghai.

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1..719

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="ADBBB01"

## /tissue\_type="Adrenal gland"

## /dev\_stage="Adult"

## /lab\_host="SOLR"

## /clone\_lib="ADB"

## /note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

## Alignment Scores:

## Pred. No.: 6,99e-94 Length: 719

## Score: 844.00 Matches: 176

## Percent Similarity: 97.78% Conservative: 0

## Best Local Similarity: 97.78% Mismatches: 3

## Query Match: 90.66% Indels: 1

## DB: 1 Gaps: 0

## US-09-830-972-29\_COPY\_990\_1178 (1-189) x AV702687 (1-719)

## QY 11 lleylsystrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30

## Db 1 ATTAAGAAGACTGGAGTGTGTGGTGCCAGCTATTCTCTGCTGCTTTCATTGACAGTA 60

## QY 31 PheSerileValSerValThrAlaThrileAlaLeuAlaLeuSerValThrileSer 50

## Db 61 TTCAGCATTTGGAGCGTAACAGCTTACATTCTGGCCCTGCTCTGTGACCAATCAGC 120

## QY 51 PheArgileTyrLysGlyValileGlnAlaileGlnLysSerAspGluGlyHisProPhe 70

## Db 121 TTTAGGATATACAGGGTGTGATCCAGTATCCAGAAATCAGATGAAGCCACCAATTC 180

## QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluValAlaLeuValGlnLysTyrSerAsn 90

## Db 181 AGGGCATATCTGGAAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAGTACAGTAAT 240

## QY 91 SerAlaLeuGlyHisValAsnCysThrileLysGluLeuArgLeuPheLeuValAsp 110

## Db 241 TCTGCTCTGTGTCATGGAACCTGCACCAATAAAGAACTCAGCGGCTCTTCTTAGTTGAT 300

## QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrValGlyAla 130

Db 301 GATTAGTTGATCTCTGAGTTTGCAGTTGTGAGTTGGTATTACCTATCTTGGTGCC 360  
 QY 131 LeuPheAsnGlyLeuThrLeuLeuLeuLeuAlaLeuLeuSerLeuPheSerValProVal 150  
 Db 361 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCACTGTTCTGTT 420  
 QY 151 IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnVal 170  
 Db 421 ATTATGAACGGCATCAGCAGACAGATAGATCATTTATCTAGGACTTGCAAATAAGATGTT 480  
 QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIlePro-GlyLeuLysArgLysAlaGlu 189  
 Db 481 AAGATGCTATGCTTAATATCCAGCAAAATATCTTGGATTGAAGCGCANAGCTGAA 538

RESULT 94  
 CK791443  
 LOCUS BULL16200 826 bp mRNA linear EST 25-FEB-2004  
 DEFINITION AGENCOURT 18667576 NIH\_MGC 230 Mus musculus cDNA clone  
 IMAGE:30848940 5', mRNA sequence.

ACCESSION CK791443  
 VERSION CK791443.1 GI:42803439  
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1. (bases 1 to 826)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

Tissue Procurement: Shioiko Kimura/Atsushi Yamada, (NCI, CCR)

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM156 row: a column: 13

High quality sequence stop: 680.

Location/Qualifiers

1. .826

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:30848940"

/tissue\_type="Pooled thyroids from 5 mice"

/lab\_host="DH10B Tona"

/clone\_lib="NIH\_MGC 230"

/notes="Organ: thyroid; Vector: pExpress-1; Site: 1: NotI;

Site: 2: NotI; RNA obtained from 5 normal wild-type mice

thyroid. cDNA was primed using oligo-dT primer:

5'-pGACTAGTTCTAGATCGGCGCGCC(T)25-3' and cloned into

the EcoRV/NotI sites of pExpress-1. Size-selection 1.4 kb

resulted in an average insert size of 1.2 kb. Normalized

version of this library is NIH\_MGC189library constructed

by Express Genomics (Frederick, MD). Note: this is a

NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1 74e-93 Length: 826

Score: 841.50 Matches: 177

Percent Similarity: 98.36% Conservative: 3

Best Local Similarity: 96.72% Mismatches: 2

Query Match: 90.39% Indels: 2

DB: 7 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK791443 (1-826)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 171 GTTGTGGACCTCTGTTACTGGAGACACATTAAAGAGATGGAGTGGTGTGGTCCAGC 230  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 231 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATTGCC 290  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 291 TTGGCCCTCTCTCTGTCATCTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGTATC 350  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 351 CAGAAATCAGATGAAGGCCACCCATTTCAGGGGCATATTTGGAATCTGAAATTCCTCCATATCA 410  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 411 GAGGAATTTGGTTCAGAAATATAGTAATTTCTGCTCTTGGTTCATGTGAACAGCACAATAAA 470  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuPheAlaValLeu 121  
 Db 471 GAATTGAGGGCTCTCTCTTCTAGTTGATTTAGTTGATTCCTCAAGTTTCAGTGTGTG 530  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleAla 141  
 Db 531 ATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATAGTTTGCACACTACTGATTTTAGT 590  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 591 CTGATCTCACTCTTCAGTATTCCTGTTATATATGAACGGCATCAGCGCAGATAGATCAT 650  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 651 TATCTAGGACTTGC-AACAAGAGCGTTAAGGATGCGTGGCCCAAAATCCAG---CAAATC 706

182 ProGlyLeu 184  
 707 CCTGGATTG 715

RESULT 95  
 BULL16200 961 bp mRNA linear EST 25-NOV-2002  
 LOCUS 603002628F1 CSEQCHL15 Gallus gallus cDNA clone Chest1198 5', mRNA  
 DEFINITION sequence.

ACCESSION BULL16200

VERSION BULL16200.1 GI:25322885

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

## ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 961)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE 22335534

PUBMED 12445392

COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).

Location/Qualifiers

1. .961

/organism="Gallus gallus"

/mol\_type="mRNA"

## FEATURES

source

```

/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST11g8"
/sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSPQCHL15"
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) t-stragenel vector to accommodate cDNA produced with the t-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites (5'ggccgctgcagcccgagatccgaaaaaag) (5'aattcttttttcggatccgggctgcagc)"

```

## ORIGIN

Alignment Scores:  
 Pred. No.: 3 83e-93 Length: 961  
 Score: 839.50 Matches: 175  
 Percent Similarity: 96.28% Conservative: 6  
 Best Local Similarity: 93.09% Mismatches: 7  
 Query Match: 90.17% Indels: 2  
 DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BULL16200 (1-961)

```

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 175 GTTGTGGACCTCTTACTGGCGACATTAAGAAGACAGGAGTGTGTGGTCCAGC 234
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 235 TTGTTCCCTGCTCTCTCAATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC 294
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 295 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCAATC 354
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 355 CAAAGATCCGATGAAGGCCATCCATTAGGCGCTTACTTGGAGTCTGTAGTGTGTCT 414
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 415 GAAGAGCTGATTACAGAAATACAGCAGTGTGTGCTTGGTTCATCAACGGCAGCTCAAG 474
QY 102 GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 475 GAGCTGACGCGCTTCTCTGTTGATGACTTGGTGTGATCTCTGAAGTTGCGAGTGTG 534
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141
DB 535 ATGGGGGTTCACCTTACGTTGGTCCCTGTTTATGCTGCTGACATTACTGATGCT 594
QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 595 TTGATTTCCGCTTTCAGTGTTCCTGTTATTTATGAGACATCAAGCCCGAGATCCACCAT 654
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 655 TATTGGGAGCTAGTGAAACAGAACTCAAGATGCGATGGC-AAAGATCAAGCAAGAT- 712
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 713 CCTGGCTGAAGCGCAAACTGAG 736

```

RESULT 96

BG698881

LOCUS

665 bp mRNA linear EST 07-MAY-2001

## DEFINITION

602703292F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:480455 5', mRNA sequence.

## ACCESSION

BG698881

## VERSION

BG698881.1 GI:13966613

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 665)  
 NIH-MGC http://mgs.nci.nih.gov/.

## AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

## TITLE

Unpublished (1999)

## JOURNAL

Contact: Robert Strausberg, Ph.D.

## COMMENT

Email: cgapbs-remail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM10691 row: h column: 24

High quality sequence stop: 662.

## FEATURES

Location/Qualifiers

1..665

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:480455"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.61e-93 Length: 665  
 Score: 839.00 Matches: 179  
 Percent Similarity: 98.90% Conservative: 0  
 Best Local Similarity: 98.90% Mismatches: 2  
 Query Match: 90.12% Indels: 2  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG698881 (1-665)

```

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 123 GTTGTGGACCTCTTACTGGCGACATTAAGAAGACAGTGTGTGGTCCAGC 182
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 183 CTATTCTCGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCCTACATTGCC 242
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 243 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCAAGCTATC 302
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 303 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGATCTGAAGTTGCTATATCT 362
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 363 GAGGAGTGGTTCAGAAAGTACAGTAATCTCTCTTGGTTCATGTGAACCTGCACGATAAG 422
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 423 GAATCAGGGCGCTCTTCTTTAGTTGATGATTGATTCCTCTCTGAAGTTTGCAGTGTG 482
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141

```

```

Db      483  ATGTGGTATTTACCTATGTTGGTCTGTTGTTAAATGGTCTGACACTACTGAT-TTGGCT 541
      |||
Qy      142  LeuileSerLeuPheSerValProValileTyrgluAghHieGlnAlaGlnileAspHis 161
      |||
Db      542  CTCATTTCACCTCTTCAGTGTCTCTGTTATTATGAACGCGCATCAGCACAGATAGATCAT 601
      |||
Qy      162  TyrLeuGlyLeuAlaAsnLysHsnValLysAspAlaMetAlaLysileGlnAlaLyslle 181
      |||
Db      602  TATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGT-AAATCCAAAGCAAAATC 660
      |||
Qy      182  Pro 182
      |||
Db      661  CCT 663

CO505196      669 bp      mRNA      linear      EST 13-JUL-2004
GGEZEB1026A09.g embryo breast muscle - EB1 Gallus gallus cDNA clone
GGEZEB1026A09, mRNA sequence.
CO505196
CO505196.1 GI:50275382
EST.
Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 669)
Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,
Patricio,M., Leduc,M.C. and Coutinho,L.L.
Discovery of new genes expressed in the chicken breast muscle
Unpublished (2004)
Contact: Helena J. Alves
Laboratory of Animal Biotechnology, Dep. of Animal Production
ESALQ - University of Sao Paulo
Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
Fax: 55 19 3429 4285
Email: hjalves@esalq.usp.br and llicoutin@esalq.usp.br
PCR Primers
BACKWARD: T7
Location/Qualifiers
1..669
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="GGEZEB1026A09"
/tissue_type="breast muscle"
/dev_stage="embryos with 9 and 17 days old"
/lab_host="DH5 alpha"
/clone_lib="embryo breast muscle - EB1"
notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This
cDNA library was constructed with the SuperScript Plasmid
System with Gateway Technology kit (Invitrogen), following
manufacturer's protocols. Plasmid DNA was purified using a
modified alkaline lysis method. Sequencing reactions were
conducted using the DYEnamic Cycle Sequencing Kit for
MegABACE (Amersham Biosciences) according to the
manufacturer's recommendations. Clones were sequenced by
the 5' end with T7 primer. Sequencing reactions were
analyzed on MegABACE1000 DNA Sequencer (Amersham
Biosciences). The quality and clustering of the ESTs were
analyzed using the softwares Phred/cap3. Only EST
sequences with phred quality greater than 20 and at least
150 bp were considered for clustering."

ORIGIN
Alignment Scores:
Pred. No.: 2.63e-93 Length: 669
Score: 839.00 Matches: 175
Percent Similarity: 96.28% Conservative: 6
Best Local Similarity: 93.09% Mismatches: 6

FEATURES
source
RESULT 98
LOCUS      CN429705
DEFINITION      676 bp. mRNA linear EST 16-MAY-2004
ACCESSION      CN429705
VERSION      CN429705.1 GI:47417299
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 676 Std Error: 0.00.
Location/Qualifiers
1..676
source

```

```

Query Match:      90.12%      Indels:      2
DB:              7          Gaps:      0

US-09-830-972-29_COPY_990_1178 (1-189) x CO505196 (1-669)

Qy      3  ValAspLeuLeuTyrrTip-AtgAspIleLysLysThrGlyValValPheGlyAlaSerLe 22
      |||
Db      43  GTTGACCTCTCTTACTGNCGAGACATTAAGAAAGACAGGAGTGGTGT-TGGTCCAGCTT 101
      |||
Qy      22  uPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAlaLe 42
      |||
Db      102  GTTCTCTGCTCTCTCATTAACAGTGTTCAGCATCTGAGCGTGCAGAGCTTACATTGCCCTT 161
      |||
Qy      42  uAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIleGl 62
      |||
Db      162  GGCCCTGCTCTTCTGTGACCATCAGCTTTAGGATATACAAAGGAGTATTATCCAGGCAATCCA 221
      |||
Qy      62  nLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSerGl 82
      |||
Db      222  AAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTTGGAGTCTGATGTAGTGTGTCTGA 281
      |||
Qy      82  uGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGl 102
      |||
Db      282  AGAGCTGATTTCAGAAATACAGCAGTGTCTGCTGCATCAACAGCGCACAGTCAAGCA 341
      |||
Qy      102  uLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMe 122
      |||
Db      342  GCTGAGACGCTCTTCCTCGTTGATGACCTGGTGTGATTCTCTGAAAGTTTGCAGTGTGAT 401
      |||
Qy      122  tTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLe 142
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Db      402  GTGGGTGTTCACTTACGTTGGTGGCTTGTGTTAATGGTCTGACATCTACTGATGATGCTT 461
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Db      462  GATTTCTGCTGTTTCAGTGTCTCTGCTGTTATTATGAGAGACATCAGGCCACATCGACCATTA 521
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Qy      162  rLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysileGlnAlaLyslleBr 182
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RESULT 98
LOCUS      CN429705
DEFINITION      676 bp. mRNA linear EST 16-MAY-2004
ACCESSION      CN429705
VERSION      CN429705.1 GI:47417299
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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Location/Qualifiers
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source

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## ORIGIN

Alignment Scores:	
Pred. No.:	3.55e-93
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Percent Similarity:	99.42%
Best Local Similarity:	99.42%
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Length:	676
Matches:	172
Conservative:	0
Mismatches:	1
Indels:	0
Gaps:	0

US-09-830-972-29 COPY 990 1178 (1-189) X CN429705 (1-676)

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37	ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGly	56
67	ACAGCCTACATTGGCTTGGCCCTCTCTGTGTGACCATCAGCTTTTAGGATATATACAAGGCT	126
57	ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer	76
127	GTGATCCAAAGCTATCCAGAAATCAGATGAAGCCACCCATTCAAGGCATATCTGGAAATCT	186
77	GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal	96
187	GAAGTTTGCTATATCTCAGGAGTGTGTTTCAGAAGTACAGTAATTCCTCTCTTGGTCATGTG	246
97	AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu	116
247	AACTCGACGATAAAGGAACCTCAGCGGCGCTCTCTTCTAGTTGATGATTAGTTGATTCCTG	306
117	LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr	136
307	AAGTTTGAGTGTGTGATGGGTATTTACCTATGTTGGTGCCCTGTGTTTAATGGTCTGACA	366
137	LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln	156
367	CTACTGATTTTGGCTCTCATTTCACTCTTCAAGTGTTCTCTGTTATTATTAAACGGCATCAG	426
157	AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys	176
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DEFINITION	G603138816F1 CSEQCHL15 Gallus gallus cDNA clone CHEST12704 5', mRNA sequence.
ACCESSION	BUI16870
VERSION	BUI16870.1 GI:25324153
KEYWORDS	EST.
SOURCE	Gallus gallus (chicken).
ORGANISM	Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE	1 (bases 1 to 934)
AUTHORS	Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,

TITLE	JOURN	MEDLIN	PUBME	COMMENT
1	2	3	4	5

Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392

1241552  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).

## FEATURES

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DB	232	TTGTTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC	291
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
DB	292	TTGGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATCAAGGAGTTATCCAGGCATC	351
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
DB	352	CAAAAGTCCGATGAAGGCCATCCATTTAGGCGTACTTGGAGTCTCATGTAGCTGTGTCT	411
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QY	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla	141

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RESULT 100  
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 LOCUS AGENCOURT 13665211 NIH\_MGC\_184 Homo sapiens cDNA clone  
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 CB956475  
 VERSION CB956475.1 GI:30212592  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 735)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-rc@mail.nih.gov](mailto:cgabbs-rc@mail.nih.gov)  
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Cloned through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDCM153 row: n column: 11  
 High quality sequence stop: 619.  
 Location/Qualifiers

## FEATURES

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 adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CAGGCCATATGCCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCCGCGCCGATG-3' (30)BN-3' (where B = A,  
 C, or G and N = A, C, or T). Average insert size 1.38  
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
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 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

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US-09-830-972-29\_COPY\_990\_1178 (1-189) x CB956475 (1-735)

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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
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 Db 369 CAGAAATCAGATGAAGGCCACCAATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 428  
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Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
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 Db 429 GAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTCTCTGTGGTCATGTGAACCTGCACGATAAAG 488  
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Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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Qy 162 TyrLeuGlyLeuAlaAsn-LysAsn-ValLysAspAlaMetAla---LysIleGlnAla 180  
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Search completed: June 19, 2005, 10:16:59  
 Job time : 2580 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:29:05 ; Search time 24.5171 Seconds  
(without alignments)  
2960.058 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
Sequence: 1 SVDDLWYRDIKKTGVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1  
US-09-789-386-2  
; Sequence 2, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2

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Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVNDAMAKIOAK 1183
QY 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192

RESULT 2
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

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Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
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QY 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192

RESULT 3
US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
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; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAV 120
Db 1064 IQKSDGHPFRAYLESEVAISELQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAV 1123
QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVNDAMAKIOAK 180
Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVNDAMAKIOAK 1183
QY 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192

RESULT 4
US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAV 120
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Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
QY 121 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
Db 1124 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192

## RESULT 5

US-10-060-036-71  
; Sequence 71, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yugu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-060-036-71

Query Match 100.0%; Score 931; DB 14; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 120  
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
QY 121 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
Db 1124 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192

## RESULT 6

US-10-267-502-429  
; Sequence 429, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Galant, Ron  
; APPLICANT: Kim, Jaeseob  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 429  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-267-502-429

Query Match 100.0%; Score 931; DB 15; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 120  
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
QY 121 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
Db 1124 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192

## RESULT 7

US-10-327-213-9  
; Sequence 9, Application US/10327213  
; Publication No. US20040121341A1  
; GENERAL INFORMATION:  
; APPLICANT: FILBIN, MARIE T.  
; APPLICANT: DOMENICONI, MARCO  
; APPLICANT: CAO, ZIXUAN  
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)  
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION  
; FILE REFERENCE: CUNY/003  
; CURRENT APPLICATION NUMBER: US/10/327,213  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-327-213-9

Query Match 100.0%; Score 931; DB 16; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 120  
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
QY 121 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
Db 1124 LMWVFTYVGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192

## RESULT 8

US-10-466-258-9  
; Sequence 9, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW

	Query Match	100.0%	Score 931;	DB 16;	Length 1192;
	Best Local Similarity	100.0%;	Pred. No. 1.1e-83;		
	.Matches 189;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SVDDLWYRDIKKTGVVFGASLFLLSVTWFSIVSVTAYTALALSVTISPRIYKGVIOA	60		
Db	1004	SVDDLWYRDIKKTGVVFGASLFLLSVTWFSIVSVTAYTALALSVTISPRIYKGVIOA	1063		
Qy	61	IQKSDGEHPFRAYLESEVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV	120		

Query Match	99.6%;	Score 927;	DB 9;	Length 199;
Best Local Similarity	100.0%;	Pred. No. 2.9e-84;		
Matches 188;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTSFRIYKGVIOAI	61	
Db	12	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTSFRIYKGVIOAI	71	
Qy	62	QKSDGHPFRAYILESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVSLKPAVL	121	
Db	72	QKSDGHPFRAYILESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVSLKPAVL	131	
Qy	122	MWFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGANKNVKDMAKIOAKI	181	
Db	132	MWFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGANKNVKDMAKIOAKI	191	
Qy	182	PGLKRKAE	189	
Db	192	PGLKRKAE	199	

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RESULT 11
US-10-660-946-1
; Sequence 1, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
;; STREET: 3174 Porter Drive  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: U.S.  
;; ZIP: 94304  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 1.5  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/660,946  
;; FILING DATE: 12-Sep-2003  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/228,213A  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: 08/700,607  
;; FILING DATE: <Unknown>  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0114 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-855-0555  
;; TELEFAX: 415-845-4166  
;;  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 199 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; IMMEDIATE SOURCE:  
;; LIBRARY: <Unknown>  
;; CLONE: Consensus  
;;  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-660-946-1  
  
Query Match 99.6%; Score 927; DB 15; Length 199;  
Best Local Similarity 100.0%; Pred. No. 2.9e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71  
  
Qy 62 QKSDEGHPFRAYLESEVAISELQKYSNSALGHVNCITIKELRRLFLVDDDLVDSLKFAVL 121  
Db 72 QKSDEGHPFRAYLESEVAISELQKYSNSALGHVNCITIKELRRLFLVDDDLVDSLKFAVL 131  
  
Qy 122 MWVFTYVGALFNGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKVKNVQKAMAKIOAKI 181  
Db 132 MWVFTYVGALFNGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKVKNVQKAMAKIOAKI 191  
  
Qy 182 PGLKRAE 189  
Db 192 PGLKRAE 199  
  
RESULT 12  
US-10-810-653-25  
; Sequence 25, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A

;; CURRENT APPLICATION NUMBER: US/10/810,653  
;; CURRENT FILING DATE: 2004-03-29  
;; PRIOR APPLICATION NUMBER: US/09/893,348  
;; PRIOR FILING DATE: 2001-06-28  
;; PRIOR APPLICATION NUMBER: US 09/314,161  
;; PRIOR FILING DATE: 1999-05-19  
;; PRIOR APPLICATION NUMBER: US 09/218,277  
;; PRIOR FILING DATE: 1998-12-22  
;; PRIOR APPLICATION NUMBER: PCT/US98/14715  
;; PRIOR FILING DATE: 1998-07-21  
;; PRIOR APPLICATION NUMBER: IL 124500  
;; PRIOR FILING DATE: 1998-05-19  
;; NUMBER OF SEQ ID NOS: 29  
;; SOFTWARE: Patent in version 3.1  
;; SEQ ID NO 25  
;; LENGTH: 199  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-810-653-25  
  
Query Match 99.6%; Score 927; DB 16; Length 199;  
Best Local Similarity 100.0%; Pred. No. 2.9e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71  
  
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Db 132 MWVFTYVGALFNGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKVKNVQKAMAKIOAKI 191  
  
Qy 182 PGLKRAE 189  
Db 192 PGLKRAE 199  
  
RESULT 13  
US-09-789-386-6  
; Sequence 6, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-6  
  
Query Match 99.6%; Score 927; DB 9; Length 373;  
Best Local Similarity 100.0%; Pred. No. 6.4e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 245

QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 121  
DB 246 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 305  
QY 122 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 181  
DB 306 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 365  
QY 182 PGLKRAE 189  
DB 366 PGLKRAE 373

RESULT 14  
US-09-765-205-6  
; Sequence 6, Application US/09765205  
; Patent No. US20020034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: human  
US-09-765-205-6

Query Match 99.6%; Score 927; DB 9; Length 373;  
Best Local Similarity 100.0%; Pred. No. 6.4e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VDILLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 186 VDILLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 245  
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 121  
DB 246 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 305  
QY 122 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 181  
DB 306 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 365  
QY 182 PGLKRAE 189  
DB 366 PGLKRAE 373

RESULT 15  
US-09-893-348-24  
; Sequence 24, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-893-348-24

Query Match 99.6%; Score 927; DB 9; Length 373;  
Best Local Similarity 100.0%; Pred. No. 6.4e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 245  
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 121  
DB 246 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAYL 305  
QY 122 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 181  
DB 306 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 365  
QY 182 PGLKRAE 189  
DB 366 PGLKRAE 373

Search completed: June 16, 2005, 13:04:04  
Job time : 24.5171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 27.2927 Seconds  
(without alignments)  
2678.292 Million call updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
Sequence: 1 SWVDLLYWRDIKTKGVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	100.0	893	3 AAY95012	Aay95012 Human sec
2	931	100.0	983	6 ABU11573	Abu11573 Human MDD
3	931	100.0	1178	3 AAY71311	Aay71311 Human neu
4	931	100.0	1192	3 AAY56967	Aay56967 Human MAG
5	931	100.0	1192	4 AAB82349	Aab82349 Human NOG
6	931	100.0	1192	4 AAU04591	Aau04591 Human NOG
7	931	100.0	1192	5 ABG30938	Abg30938 Human NOG
8	931	100.0	1192	5 ABP68600	Abp68600 Human pan
9	931	100.0	1192	5 ABB81078	Abb81078 Human neu
10	931	100.0	1192	6 ABR59667	Abr59667 Human NOG
11	931	100.0	1192	8 ADO08103	Ado08103 Human pol
12	931	100.0	1192	8 ADO26400	Ado26400 Human tru
13	931	100.0	1192	8 ADP45551	Adp45551 Human NOG
14	931	100.0	1192	8 ADP67234	Adp67234 Human NOG
15	931	100.0	1192	8 ADR11366	Adr11366 Human NOG
16	928	99.7	200	4 AAB64514	Aab64514 Human sec
17	927	99.6	199	2 AAU53947	Aau53947 Human NSP
18	927	99.6	199	2 AAW78313	Aaw78313 Fragment
19	927	99.6	199	3 AAB12805	Aab12805 Human NSP
20	927	99.6	199	4 AAB82348	Aab82348 Human NOG
21	927	99.6	199	5 ABB81080	Abb81080 Human neu
22	927	99.6	199	8 ADP67236	Adp67236 Human NOG
23	927	99.6	373	3 AAY53624	Aay53624 A bone ma
24	927	99.6	373	3 AAY56969	Aay56969 Human MAG
25	927	99.6	373	3 AAB24242	Aab24242 Human NOG

ALIGNMENTS

RESULT 1  
AAY95012  
ID AAY95012 standard; protein; 893 AA.  
XX AC AAY95012;  
XX XX  
DT 19-JUN-2000 (first entry)  
DE Human secreted protein vb22\_1, SEQ ID NO:64.  
XX XX

Human; secreted protein; cancer; tumour; cardiovascular disorder;  
blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
neurodegenerative disease; asthma; contraceptive.

OS Homo sapiens.

XX WO200011015-A1.  
XX XX

PD 02-MAR-2000.

PF 24-AUG-1999; 99WO-US019351.

XX 24-AUG-1998; 98US-0097638P.

PR 24-AUG-1998; 98US-0097659P.

PR 09-SEP-1998; 98US-0099618P.

PR 28-SEP-1998; 98US-0102092P.

PR 25-NOV-1998; 98US-0109978P.

PR 23-DEC-1998; 98US-0113645P.

PR 23-DEC-1998; 98US-0113646P.

PR 23-AUG-1999; 99US-00379246.

XX (ALPH-) ALPHAGEN INC.

PA Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX WPI; 2000-224657/19.

XX New secreted or transmembrane proteins and polynucleotides encoding them,

PT useful for treating neurodegenerative disorders, autoimmune diseases and cancer.

PS Claim 73; Page 322-325; 357pp; English.

XX The invention relates to 40 human secreted proteins (AAY94981-Y95020),  
CC and cDNA sequences encoding them (AA23423-A23462). The secreted proteins  
of the invention include those that are thought to be only partially  
secreted, i.e., transmembrane proteins. The proteins of the invention may

Aab82350 Human NOG  
Aan47954 Human RTN  
Abg30937 Human NOG  
Abp68601 Human pan  
Adb81079 Human neu  
Adi63044 Human apo  
Adk67503 Human RTN  
Adp67235 Human NOG  
Adk67502 Human RTN  
Aan93484 Human pol  
Adl31138 Human pro  
Adk67504 Human RTN  
Aay35903 Extended  
Adp19211 Human sec  
Adt89537 Mus muscu  
Aay711385 Alternati  
Aay711310 Rat neuro  
Abb81074 Rat neuro  
Ado26399 Rat trunc

CC exhibit one or more activities selected from the following: cytokine  
 CC activity; cell proliferation; differentiation; immune modulation;  
 CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
 CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
 CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
 CC proteins may be administered to patients as vaccines, and the nucleotides  
 CC may be used as part of a gene therapy regime. Diseases or conditions that  
 CC may be treated using the proteins or nucleotides of the invention include  
 CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
 CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
 CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
 CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
 CC allergic reactions such as asthma and anaemia. They may also be used for  
 CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
 CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
 CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
 CC activity may additionally be useful as contraceptives. Nucleic acid  
 CC sequences of the invention may be used in chromosome mapping, and as a  
 CC source of diagnostic primers and probes. The present sequence represents  
 CC one of the 40 proteins of the invention  
 XX  
 SQ Sequence 893 AA;

Query Match 100.0%; Score 931; DB 3; Length 893;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 60  
 Db 705 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 764  
 QY 61 IQSDGEGHPFRAYLSEVAISEELVQKYSNSALGHVNCITKELRRLFLVDLVDLSLKFAV 120  
 Db 765 IQSDGEGHPFRAYLSEVAISEELVQKYSNSALGHVNCITKELRRLFLVDLVDLSLKFAV 824  
 QY 121 LMWVFTYVGCALFNGTLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAKIOAK 180  
 Db 825 LMWVFTYVGCALFNGTLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAKIOAK 884  
 QY 181 IPGLKRAE 189  
 Db 885 IPGLKRAE 893

RESULT 2  
 ABU11573  
 ID ABU11573 standard; protein; 983 AA.  
 AC ABU11573;  
 XX

DT 12-FEB-2003 (first entry)

XX Human MDDT polypeptide SEQ ID 520.

KW MDDT: human; disease detection and treatment molecule polypeptide;  
 KW anti-inflammatory; immunosuppressive; osteoparic; cytostatic; anti-HIV;  
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
 KW gene therapy; protein replacement therapy; cell proliferative disorder;  
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
 KW psoriasis; hepatitis.

XX Homo sapiens.

XX WO20027949-A2.

XX 10-OCT-2002.

XX 27-MAR-2002; 2002WO-US009944.

XX 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.  
 PR 16-MAY-2001; 2001US-0291280P.  
 PR 17-MAY-2001; 2001US-0291829P.  
 PR 17-MAY-2001; 2001US-0291849P.  
 PR 19-JUN-2001; 2001US-0299428P.  
 PR 20-JUN-2001; 2001US-0299776P.  
 PR 20-JUN-2001; 2001US-0300001P.

XX (INCY-) INCYTE GENOMICS INC.

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;  
 PI Daucherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX WPI; 2003-058431/05.  
 DR N-PSDB; ABX34563.

XX New purified disease detection and treatment molecule proteins and  
 PT polynucleotides, useful for diagnosing, treating or preventing cancers  
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
 PT or hepatitis.

XX Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule  
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
 CC osteoparic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
 CC and the polypeptides of the invention can be used for gene therapy,  
 CC protein replacement therapy and are useful for treating a variety of  
 CC diseases or conditions. These polypeptides or polynucleotides are  
 CC particularly useful for diagnosing, treating or preventing cell  
 CC proliferative disorders (e.g. cancers including adenocarcinoma,  
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), Goodpasture's  
 CC disease, acquired immunodeficiency syndrome (AIDS), Crohn's  
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded  
 CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 983 AA;

Query Match 100.0%; Score 931; DB 6; Length 983;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 60  
 Db 795 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 854

QY 61 IQSDGEGHPFRAYLSEVAISEELVQKYSNSALGHVNCITKELRRLFLVDLVDLSLKFAV 120  
 Db 855 IQSDGEGHPFRAYLSEVAISEELVQKYSNSALGHVNCITKELRRLFLVDLVDLSLKFAV 914

QY 121 LMWVFTYVGCALFNGTLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAKIOAK 180  
 Db 915 LMWVFTYVGCALFNGTLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAKIOAK 974

QY 181 IPGLKRAE 189

Db 975 IPGLKRAE 983

RESULT 3

AAAY71311

ID AAAY71311 standard; protein; 1178 AA.

XX AC AAAY71311;

XX

DT 02-NOV-2000 (first entry)  
DE Human neurite growth inhibitor Nogo.  
XX  
XX Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 187 /label= Unknown  
FT  
FT Misc-difference 188 /label= Unknown  
FT  
FT Misc-difference 189 /label= Unknown  
FT  
FT Misc-difference 190 /label= Unknown  
FT  
FT Misc-difference 221 /label= Unknown  
FT  
FT Misc-difference 328 /label= Unknown  
FT  
FT Misc-difference 477 /label= Unknown  
FT  
FT Region 977. .1012 /note= "Region specifically described in claim 16"  
FT  
FT Region 994. .1174 /note= "Region specifically described in claim 16"  
FT  
FT Region 1079. .1113 /note= "Region specifically described in claim 16"  
FT  
XX WO200031235-A2.  
PN  
XX  
XX 02-JUN-2000.  
PD  
XX  
XX 05-NOV-1999; 99WO-US026160.  
PF  
XX  
XX 06-NOV-1999; 98US-0107446P.  
PR  
XX  
XX (SCHW/) SCHWAB M E.  
PA  
XX (CHEN/) CHEN M S.  
PI  
XX Schwab ME, Chen MS;  
XX  
XX WPI; 2000-400052/34.  
XX  
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
XX Claim 11; Fig 13; 122pp; English.  
PS  
XX The present sequence is a human Nogo protein which is a potent neural  
CC cell growth inhibitor and is free of all central nervous system (CNS)  
CC myelin material with which it is natively associated. The human Nogo  
CC sequence was derived by aligning human expressed sequence tags (ESTs)  
CC e.g. AA158636, AA33267, AA081783, AA167765, AA092565, AA081525  
CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments  
CC displaying neurite growth inhibitory activity are used in the treatment  
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,  
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
CC activity can be used to treat or prevent hyperproliferative or benign  
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
CC production of Nogo protein to induce regeneration of neurons or to  
CC promote structural plasticity of the CNS in disorders where neurite

CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However the specification does not include sequences for  
XX these SEQ ID numbers  
SQ Sequence 1178 AA;  
Query Match 100.0%; Score 931; DB 3; Length 1178;  
Best Local Similarity 100.0%; Pred. No. 6.6e-92;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVPFSIVSVYAYIALALLSVTISFRIYKGVIOA 60  
DB 990 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVPFSIVSVYAYIALALLSVTISFRIYKGVIOA 1049  
QY 61 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 120  
DB 1050 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1109  
QY 121 LMWVFTYVGFNGLTLLILALISLFSVPVYIYERHQAQIDHYGLANKVNDAMAKIOAK 180  
DB 1110 LMWVFTYVGFNGLTLLILALISLFSVPVYIYERHQAQIDHYGLANKVNDAMAKIOAK 1169  
QY 181 IPGLKRAE 189  
DB 1170 IPGLKRAE 1178  
RESULT 4  
AAV56967  
ID AAV56967 standard; protein; 1192 AA.  
XX  
XX AAV56967;  
AC  
XX  
XX 25-APR-2000 (first entry)  
DT  
XX  
XX Human MAGI polypeptide.  
DE  
XX  
XX MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
KW psychiatric disorder; developmental disorder; inflammatory disorder;  
KW stroke; cytostatic; cerebroprotective; neuroprotective.  
XX  
OS Homo sapiens.  
XX  
XX WO200005364-A1.  
FN  
XX  
XX 03-FEB-2000.  
PD  
XX  
XX 21-JUL-1999; 99WO-GB002360.  
PF  
XX  
XX 22-JUL-1998; 98GB-00016024.  
PR  
XX 19-JUL-1999; 99GB-00016898.  
PR  
XX (SMK ) SMITHLINE BEECHAM PLC.  
PA  
XX Michalovich D, Prinjha RK;  
XX WPI; 2000-182693/16.  
XX N-PSDB; AAZ56886.  
XX Novel polypeptides related to neuroendocrine-specific proteins and  
PT polynucleotides useful for diagnosis of various diseases and for  
PT treatment of cancer and neurological disorders.  
XX  
XX Claim 2; Page 20-21; 35pp; English.  
XX The invention relates to human MAGI protein, which is similar to  
CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides

CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke, and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents the human MAGI protein

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 3; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
 QY 61 IQKSDGCHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 120  
 Db 1064 IQKSDGCHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 1123  
 QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIOAK 180  
 Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIOAK 1183

QY 181 IPGLKRAE 189

Db 1184 IPGLKRAE 1192

RESULT 5

AAB82349  
 ID AAB82349 standard; protein; 1192 AA.

AC AAB82349;

DT 23-JUL-2001 (first entry)

DE Human NOGO-A protein.

XX NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX Homo sapiens.

XX WO20013631-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-GB004345.

XX 15-NOV-1999; 99GB-00026995.

XX 24-JAN-2000; 2000GB-00001550.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha R;

XX WPI; 2001-343822/36.

XX N-PSDB; AAF90324.

XX New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.

XX Disclosure; Page 26-27; 25pp; English.

XX The present sequence is that of human NOGO-A. NOGO-A is a previously  
 CC known splice variant of the human NOGO gene on chromosome 2p21. The  
 CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It

CC provides NOGO-C polypeptides and polynucleotides, and methods for  
 CC producing such polypeptides by recombinant techniques. Also disclosed are  
 CC methods for utilizing NOGO-C polypeptides and polynucleotides in the  
 CC treatment of diseases including neuropathies, spinal injury, brain  
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease  
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders  
 CC and developmental disorders. Also provided are methods for identifying  
 CC agonists and agonists for use in treating conditions associated with NOGO  
 CC -C imbalance, and diagnostic assays for detecting diseases associated  
 CC with inappropriate NOGO-C activity or levels

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 4; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
 QY 61 IQKSDGCHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 120  
 Db 1064 IQKSDGCHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 1123  
 QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIOAK 180  
 Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
 QY 181 IPGLKRAE 189  
 Db 1184 IPGLKRAE 1192

RESULT 6

AU04591  
 ID AU04591 standard; protein; 1192 AA.

XX AC AU04591;

XX 26-SEP-2001 (first entry)

XX Human Nogo protein.

XX Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;  
 KW cranial trauma; cerebral trauma; spinal cord injury; stroke;  
 KW demyelinating disease; multiple sclerosis; monophasia demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;  
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;  
 KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;  
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;  
 KW Krabbe's disease.

XX Homo sapiens.

XX Key

XX Domain

XX /label= Lumenal extracellular domain

XX /note= "This sequence is specifically claimed"

XX Peptide

XX /label= Pep1

XX /note= "Receptor binding inhibitory peptide. This  
 sequence is specifically claimed"

XX Peptide

XX /label= Pep2

XX /note= "Receptor binding inhibitory peptide. This  
 sequence is specifically claimed"

XX Peptide

XX /label= Pep3

XX /note= "Receptor binding inhibitory peptide. This  
 sequence is specifically claimed"

XX Peptide

XX /label= Pep4



FT		/note= "Receptor binding inhibitory peptide. This
FT	Peptide	sequence is specifically claimed"
FT		1095. .1119
FT		/label= Pep5
FT		/note= "Receptor binding inhibitory peptide. This
FT		sequence is specifically claimed"
XX		
PN	WC200151520-A2.	
XX		
XX	19-JUL-2001.	
XX		
XX	12-JAN-2001; 2001WO-US001041.	
XX		
PR	12-JAN-2000; 2000US-0175707P.	
PR	26-MAY-2000; 2000US-0207366P.	
PR	29-SEP-2000; 2000US-0236378P.	
XX		
XX	(UYUA ) UNIV YALE.	
PA		
PI	Strittmatter SM;	
XX		
XX	WPI; 2001-442138/47.	
DR	N-PSDB; AAS09453.	
XX		
XX	Novel Nogo receptor protein useful for identifying modulator of Nogo	
PT	protein or Nogo receptor protein, which is useful for treating central	
PT	nervous system disorders.	
XX		
XX	Example 1; Page 101-104; 109pp; English.	
XX		
CC	The sequence is the human Nogo protein, a 250kDa myelin-associated axon	
CC	growth inhibitor. The invention relates to the use of the nogo receptor,	
CC	nogo protein, their nucleic acids, vectors expressing them and antibodies	
CC	against them, to isolate agents which block nogo receptor mediated axonal	
CC	growth. The agent is useful for treating a central nervous system	
CC	disorder which is a result of cranial or cerebral trauma, spinal cord	
CC	injury, stroke or a demyelinating disease selected from multiple	
CC	sclerosis, monophasis demyelination, encephalomyelitis, multifocal	
CC	leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,	
CC	contine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,	
CC	Spongy degeneration, Alexander's disease, Canavan's disease,	
CC	metachromatic leukodystrophy, viral infection and Krabbe's disease	
XX		
SQ	Sequence 1192 AA;	
	Query Match 100.0%; Score 931; DB 4; Length 1192;	
	Best Local Similarity 100.0%; Pred. No. 6.7e-92;	
	Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60	
Db	1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063	
QY	61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKPAV 120	
Db	1064 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKPAV 1123	
QY	121 LKWVFTVVGALFNGLTLLIALLSLFSVPVPIYERHQAOIDHYLGLANKNVKDKAMAKIOAK 180	
Db	1124 LKWVFTVVGALFNGLTLLIALLSLFSVPVPIYERHQAOIDHYLGLANKNVKDKAMAKIOAK 1183	
QY	181 IGPLKRAE 189	
Db	1184 IGPLKRAE 1192	
RESULT 7		
ABG30938		
ID	ABG30938 standard; protein; 1192 AA.	
XX		
AC	ABG30938;	
XX		
DT	21-OCT-2002 (first entry)	

Db 1124 LMWFTYVGALFNGLTLLILALISLPSVPVIYERHOAQIDHYLGLANKNVKDMAKIOAK 1183

QY 181 IPGLKRAE 189

Db 1184 IPGLKRAE 1192

# RESULT 8

ABP68600

ID ABP68600 standard; protein; 1192 AA.

XX

AC ABP68600;

XX 14-JAN-2003 (first entry)

DT Human pancreatic cancer expressed protein SEQ ID NO 71.

DE Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

KW Cytostatic; tumour.

XX Homo sapiens.

XX WO200260317-A2.

PN 08-AUG-2002.

XX 30-JAN-2002; 2002WO-US002781.

XX 30-JAN-2001; 2001US-0265305P.

PR 31-JAN-2001; 2001US-0265682P.

PR 09-FEB-2001; 2001US-0267568P.

PR 21-MAR-2001; 2001US-0278651P.

PR 28-APR-2001; 2001US-0287112P.

PR 16-MAY-2001; 2001US-0291631P.

PR 12-JUL-2001; 2001US-0305484P.

PR 20-AUG-2001; 2001US-0313999P.

PR 27-NOV-2001; 2001US-0333626P.

XX (CORI-) CORIXA CORP.

XX Benson DR, Kalos MD; Lodes MJ, Persing DH, Hepler WT, Jiang Y;

XX WPI; 2002-627435/67.

DR N-PSDB; ABV94680.

XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for

PT diagnosing, preventing and/or treating cancer, particularly pancreatic

PT cancer.

XX Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.

PS The invention relates to an isolated polynucleotide (I) comprising: (a)

XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)

CC complements of (a); (c) sequences consisting of at least 20 contiguous

CC residues of (a); (d) sequences that hybridize to (a), under moderately

CC stringent conditions; (e) sequences having at least 75% or 90% identity

CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-

CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer

CC in a patient and compositions comprising polypeptides, polynucleotides,

CC antibodies, fusion proteins, T cell populations and antigen presenting

CC cells expressing the polypeptide are useful in treating pancreatic cancer

CC and stimulating an immune response. The polynucleotides can be used as

CC probes or primers for nucleic acid hybridisation, in the design and

CC preparation of ribozyme molecules for inhibiting expression of the tumour

CC polypeptides and proteins in the tumour cells, in vaccines and for gene

CC therapy. Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at fcp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1192 AA;

SQ

Query Match 100.0%; Score 931; DB 5; Length 1192;

Best Local Similarity 100.0%; Pred. No. 6.7e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTFTVFSIVSVTAIALALLSVTISFRIYKGVIOA 60

Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTFTVFSIVSVTAIALALLSVTISFRIYKGVIOA 1063

QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 120

Db 1064 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 1123

QY 121 LMWFTYVGALFNGLTLLILALISLPSVPVIYERHOAQIDHYLGLANKNVKDMAKIOAK 180

Db 1124 LMWFTYVGALFNGLTLLILALISLPSVPVIYERHOAQIDHYLGLANKNVKDMAKIOAK 1183

QY 181 IPGLKRAE 189

Db 1184 IPGLKRAE 1192

## RESULT 9

ABB81078

ID ABB81078 standard; protein; 1192 AA.

XX

AC ABB81078;

XX 05-NOV-2002 (first entry)

DT Human neurotransmitter receptor protein Nogo-A.

XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

XX central nervous system; peripheral nervous system; tranquilizer; Nogo;

KW neurotrophic; neuroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW noloergic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

KW neurotransmitter receptor; human; receptor.

XX Homo sapiens.

XX US2002072493-A1.

XX 13-JUN-2002.

XX 28-JUN-2001; 2001US-00893348.

XX 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

PI Moalem G;

XX WPI; 2002-607255/65.

DR N-PSDB; ABN86601.

XX Promoting nerve regeneration and preventing neuronal degeneration in the

CC central/peripheral nervous system from injury/disease, comprises

CC administering nervous system-specific activated T cells/antigen, or

PT analogs/peptides.

XX Example; Page 53-56; 93pp; English.

PS The invention relates to promoting nerve regeneration or conferring

CC neuroprotection and preventing or inhibiting neuronal degeneration in the

CC central/peripheral nervous system (NS). The method involves administering

CC NS-specific activated T cells, NS-specific antigen, its analogue or its

CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or

CC combinations. The method is useful for promoting nerve regeneration and

CC preventing neuronal degeneration in central/peripheral nervous system

CC from injury/disease, where the injury is spinal cord injury, blunt

CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or

CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren-Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polynuropathies,  
 CC adrenomyeloneuropathy, giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the human  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 5; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOA 60  
 DB 1004 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOA 1063

QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDLVDLSLKFAV 120  
 DB 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDLVDLSLKFAV 1123

QY 121 LMWVFTYVYGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
 DB 1124 LMWVFTYVYGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183

QY 181 IPGLKRAE 189  
 DB 1184 IPGLKRAE 1192

RESULT 10

ABR59667  
 ID ABR59667 standard; protein; 1192 AA.

AC ABR59667;

XX 22-JUL-2003 (first entry)

XX Human NogoA protein.

XX Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

OS Homo sapiens.

XX WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US032007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYVA ) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.  
 DR N-PSDB; ACC81048.  
 XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 XX injury, e.g. spinal cord injury.  
 PS Disclosure; Page 131-135; 148pp; English.

XX The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (PI,  
 CC human Nogo receptor (NGR) NLRCT domain), or residues 27-309 of PI with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 CC axonal growth by a central nervous system (CNS) neuron. The Ngr  
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an Ngr protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 6; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOA 60  
 DB 1004 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOA 1063

QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDLVDLSLKFAV 120  
 DB 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDLVDLSLKFAV 1123

QY 121 LMWVFTYVYGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
 DB 1124 LMWVFTYVYGALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183

QY 181 IPGLKRAE 189  
 DB 1184 IPGLKRAE 1192

RESULT 11

ADO08103  
 ID ADO08103 standard; protein; 1192 AA.

XX ADO08103;

XX 01-JUL-2004 (first entry)

XX Human polypeptide #65.

XX Human; fat cell number; fat cell size; obesity; diabetes; anorectic;  
 KW antidiabetic.

XX Homo sapiens.

XX US2004071700-A1.

XX 15-APR-2004.

XX 09-OCT-2002; 2002US-00267502.

XX 09-OCT-2002; 2002US-00267502.  
XX (LIFE-) LIFE SCI DEV CORP.  
XX Kim J, Galant R;  
XX WPI; 2004-328526/30.  
XX N-PSDB; ADO07886.  
XX Identifying compounds that influence fat cell number or size for treating  
XX PT or preventing obesity or diabetes by exposing the cell to the agent and  
XX PT identifying fat cell number or size relative to cells not exposed to the  
XX PT agent.  
XX Claim 14; SEQ ID NO 429; 275pp; English.  
XX The invention relates to a method of identifying compounds that influence  
XX fat cell number or size comprising providing a cell that expresses a gene  
XX and an agent, exposing the cell to the agent and identifying fat cell  
XX number or size relative to cells not exposed to the agent. The method  
XX also comprises providing an expression vector and an agent, exposing the  
XX vector to the agent, detecting a change in expression of the gene  
XX relative to expression of the gene in an expression vector not exposed to  
XX the agent, treating a subject with the agent and identifying fat cell  
XX number or size in the subject. The agent comprises an antisense  
XX oligonucleotide. The subject comprises a mammal, preferably a human. The  
XX method also comprises providing a polypeptide and an agent, exposing the  
XX polypeptide to the agent, detecting binding of the agent to the  
XX polypeptide or a change in an activity of the polypeptide, treating a  
XX subject with the agent and identifying fat cell number or size in the  
XX subject. The agent comprises an antibody. A method of regulating fat cell  
XX number or size comprises providing a subject containing fat cells and an  
XX agent that changes the expression of a gene, and treating the subject  
XX with the agent under conditions so that fat cell size or number in the  
XX subject is altered. The method is useful for identifying compounds that  
XX influence fat cell number or size, for preparing a composition for  
XX treating or preventing obesity or diabetes. This sequence represents a  
XX human polypeptide used in the scope of the invention.  
XX Sequence 1192 AA;  
Query Match 100.0%; Score 931; DB 8; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 120  
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
QY 121 LMWFTYVYGALFNGLLTLLILALISLFSVPVIYERHOAQIDHYLGLANKNVKDMAKIOAK 180  
Db 1124 LMWFTYVYGALFNGLLTLLILALISLFSVPVIYERHOAQIDHYLGLANKNVKDMAKIOAK 1183  
QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192  
RESULT 12  
AD026400  
ID ADO26400 standard; protein; 1192 AA.  
XX ADO26400;  
XX 29-JUL-2004 (first entry)  
XX Human truncated Nogo-A protein.  
XX

XX rat; human; Nogo-A; truncated; affinity; membrane-bound protein.  
XX Homo sapiens.  
XX WO2004039836-A1.  
XX 13-MAY-2004.  
XX 31-OCT-2002; 2002WO-EP012210.  
XX 31-OCT-2002; 2002WO-EP012210.  
XX (PIER-) PIERIS PROTEOLAB AG.  
XX Skerra A, Fiedler M;  
XX WPI; 2004-376159/35.  
XX New isolated truncated Nogo-A polypeptide that corresponds to a truncated  
XX form of the Nogo-A protein, useful for identifying a compound having  
XX detectable affinity to a Nogo-A protein.  
XX Claim 1; Fig 6B; 80pp; English.  
XX The present invention relates to an isolated truncated Nogo-A polypeptide  
XX that corresponds to a truncated form of the Nogo-A protein from the rat  
XX and from the human. The truncated polypeptide is useful for identifying a  
XX compound having detectable affinity to a Nogo-A protein. The present  
XX sequence is a Nogo-A polypeptide of the invention.  
XX Sequence 1192 AA;  
Query Match 100.0%; Score 931; DB 8; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 120  
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
QY 121 LMWFTYVYGALFNGLLTLLILALISLFSVPVIYERHOAQIDHYLGLANKNVKDMAKIOAK 180  
Db 1124 LMWFTYVYGALFNGLLTLLILALISLFSVPVIYERHOAQIDHYLGLANKNVKDMAKIOAK 1183  
QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192  
RESULT 13  
ADP45551  
ID ADP45551 standard; protein; 1192 AA.  
XX AC ADP45551;  
XX 09-SEP-2004 (first entry)  
XX Human NogoA protein SEQ ID NO:5.  
XX binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;  
XX nerve repair; neuroprotective; gene therapy;  
XX central nervous system injury; CNS injury; neurodegenerative disorder.  
XX Homo sapiens.  
XX WO2004052932-A2.  
XX 24-JUN-2004.  
XX

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PF 09-DEC-2003; 2003WO-EP013960.
XX
XX
PR 10-DEC-2002; 2002GB-00028832.
XX
XX (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS PHARMA GMBH.
XX (UYZU-) UNIV ZUERICH.
XX
XX Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
PI Zurini M;
XX
XX WPI; 2004-468818/44.
DR N-PSDB; ADP45550.
XX
XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
PT D20 or NogoA623-640, useful in preparing a composition for treating CNS
PT injury or neurodegenerative disorders.
XX
XX Claim 1; SEQ ID NO 5; 121pp; English.
XX
XX The present invention describes a binding molecule which binds to human
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a
CC dissociation constant of less than 100nM. Also described: (1) a
CC polynucleotide encoding the binding molecule; (2) an expression vector or
CC system comprising the polynucleotide; (3) a host cell comprising the
CC expression system; (4) a pharmaceutical composition comprising the
CC binding molecule and a carrier or diluent; and (5) treating diseases
CC associated with nerve repair. The binding molecule has neuroprotective
CC activity, and can be used in gene therapy. The binding molecule is useful
CC in preparing a composition for treating central nervous system (CNS)
CC injury or neurodegenerative disorders. The present sequence represents
CC human NogoA, which is used in the exemplification of the present
XX invention.
XX
XX Sequence 1192 AA;
SQ
Query Match 100.0%; Score 931; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.7e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 120
Db 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 1123
Qy 121 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAK 180
Db 1124 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAK 1183
Qy 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192
RESULT 14
ADP67234
ID ADP67234 standard; protein; 1192 AA.
XX
XX ADP67234;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human Nogo-A protein.
DE
XX human; Nogo-A; neurite outgrowth inhibitor; Nogo;
XX contactin-associated protein-1; Caspr; neuroprotective; gene therapy;
KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.
XX
XX Homo sapiens.
OS
XX
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PN WO2004052389-A2.
XX
XX PD 24-JUN-2004.
XX
XX 05-DEC-2003; 2003WO-GB005329.
PF
XX 06-DEC-2002; 2002US-0431549P.
PR
XX 20-JUN-2003; 2003US-0480138P.
PR
XX (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FORR/) FORREST G R.
XX
XX Xiao Z;
PI
XX
XX WPI; 2004-468705/44.
DR
XX
XX New composition comprising Nogo and Caspr or a substance capable of
PT promoting interaction between Nogo and Caspr useful for treating injury
PT to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis,
PT epilepsy or stroke.
XX
XX Disclosure; Page 14; 202pp; English.
XX
XX The invention relates to a novel composition comprising neurite outgrowth
CC inhibitor (Nogo) and contactin-associated protein-1 (Caspr) or its
CC mimetics or a substance capable of promoting interaction between Nogo and
CC Caspr, in combination with a carrier. A composition of the invention has
CC neuroprotective activity, and may have a use in gene therapy. The
CC composition is useful for treating injury to or disease of the CNS, e.g.
CC spinal cord injury, multiple sclerosis, epilepsy or stroke. The present
CC sequence represents human Nogo-A.
XX
XX Sequence 1192 AA;
SQ
Query Match 100.0%; Score 931; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 6.7e-92;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 120
Db 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 1123
Qy 121 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAK 180
Db 1124 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAK 1183
Qy 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192
RESULT 15
ADP13966
ID ADP13966 standard; protein; 1192 AA.
XX
XX ADP13966;
AC
XX
XX 23-SEP-2004 (first entry)
DT
XX
XX Human Nogo-A.
DE
XX
XX human; myelin-associated glycoprotein; MAG; neural growth;
KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW multiple sclerosis; Creutzfeldt-Jacob disease; kuru;
KW multiple system atrophy; Lou Gehrig's disease;
KW progressive supranuclear palsy.
XX
XX Homo sapiens.
OS
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XX	US2004121341-A1.
PN	XX
XX	XX
PD	24-JUN-2004.
XX	XX
PF	20-DEC-2002; 2002US-00327213.
XX	XX
PR	20-DEC-2002; 2002US-00327213.
PA	(FILB/) FILBIN M T.
XX	(DOME/) DOMENICONI M.
PA	(CAOZ/) CAO Z.
XX	XX
PI	Filbin MT, Domeniconi M, Cao Z;
XX	XX
WPI:	2004-479666/45.
DR	N-PSDB; ADR13965.
XX	XX
PT	New myelin-associated glycoprotein (MAG) derivative comprises a mutation in or flanking MAG Ig-like domain 5 (Igds), excluding the MAG derivative (dl-3)-Fc, where the mutation reduces or eliminates the ability of the derivative to regulate neurite outgrowth as compared to endogenous or soluble MAG without eliminating binding to neuronal surfaces. The inhibitors of MAG are useful for promoting neural growth and regeneration. They are also useful for treating neural degeneration associated with injuries, disorders, or diseases. The disorder, disease, or condition is associated with apoptosis or results from a demyelinating disease and includes amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease, kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou Gehrig's disease), or progressive supranuclear palsy. The present sequence represents the amino acid sequence of human NOGO-A.
XX	XX
PS	Disclosure; SEQ ID NO 9; 81pp; English.
XX	XX
CC	The invention relates to a myelin-associated glycoprotein (MAG) derivative comprising a mutation in or flanking MAG Ig-like domain 5 (Igds), excluding the MAG derivative (dl-3)-Fc, where the mutation reduces or eliminates the ability of the derivative to regulate neurite outgrowth as compared to endogenous or soluble MAG without eliminating binding to neuronal surfaces. The inhibitors of MAG are useful for promoting neural growth and regeneration. They are also useful for treating neural degeneration associated with injuries, disorders, or diseases. The disorder, disease, or condition is associated with apoptosis or results from a demyelinating disease and includes amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease, kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou Gehrig's disease), or progressive supranuclear palsy. The present sequence represents the amino acid sequence of human NOGO-A.
CC	sequence represents the amino acid sequence of human NOGO-A.
XX	XX
SQ	Sequence 1192 AA;
	Query Match . 100.0%; Score 931; DB 8; Length 1192;
	Best Local Similarity 100.0%; Pred. No. 6.7e-92;
	Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFVSIVSVTAYIALALLSVTSIFRIYKGVIQA 60
Db	1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFVSIVSVTAYIALALLSVTSIFRIYKGVIQA 1063
QY	61 IQSDSGHPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 120
Db	1064 IQSDSGHPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123
QY	121 LMWFFTVGALFNGFLTLLILLALLSLFSVPVPIYERHQAQIDHYGLANKNVKDAMAKIQAK 180
Db	1124 LMWFFTVGALFNGFLTLLILLALLSLFSVPVPIYERHQAQIDHYGLANKNVKDAMAKIQAK 1183
QY	181 IGPLKKRAE 189
Db	1184 IGPLKKRAE 1192

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 7.13706 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SWDLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	927	99.6	199	2	US-08-700-607-1
2	927	99.6	201	4	US-09-949-016-9124
3	682	73.3	208	2	US-08-700-607-7
4	682	73.3	356	2	US-08-700-607-6
5	682	73.3	439	4	US-09-949-016-9180
6	682	73.3	776	2	US-08-700-607-5
7	682	73.3	776	4	US-09-949-016-6998
8	665	71.4	267	2	US-08-700-607-8
9	627.5	67.4	192	4	US-09-949-016-8859
10	541.5	58.2	168	4	US-09-149-476-563
11	518	55.6	219	4	US-09-270-767-45132
12	512	55.0	241	2	US-08-700-607-3
13	473.5	50.9	588	4	US-09-949-016-7290
14	285	30.6	92	4	US-09-149-476-411
15	246	26.4	114	4	US-09-513-999C-7861
16	144	15.5	374	4	US-09-248-796A-16008
17	100	10.7	468	3	US-08-905-223-411
18	89	9.6	468	4	US-08-487-536-8
19	89	9.6	468	4	US-08-660-451A-8
20	88.5	9.5	1278	4	US-09-462-136-2
21	88.5	9.5	1318	4	US-09-949-016-10152
22	88	9.5	382	4	US-09-949-016-11596
23	87.5	9.4	592	4	US-09-134-000C-5477
24	87.5	9.4	1051	3	US-09-134-001C-5005
25	85	9.1	414	4	US-08-956-171E-5246
26	85	9.1	414	4	US-08-781-986A-5246
27	83	8.9	744	4	US-09-785-381-1

28	83	8.9	744	4	US-09-785-381-3
29	82.5	8.8	554	4	US-09-252-991A-27968
30	81.5	8.8	598	2	US-08-853-659A-53
31	81	8.7	970	4	US-09-795-927-7
32	80.5	8.6	280	4	US-09-543-681A-6175
33	80.5	8.6	593	4	US-09-328-352-4866
34	79.5	8.5	252	4	US-09-583-110-4880
35	79.5	8.5	257	4	US-09-107-433-4818
36	79	8.5	459	4	US-09-602-787A-302
37	79	8.5	844	4	US-09-949-016-9438
38	79	8.5	993	4	US-08-836-687B-30
39	78.5	8.4	446	4	US-09-543-681A-6579
40	78	8.4	292	4	US-09-489-039A-12212
41	78	8.4	349	4	US-09-198-452A-973
42	78	8.4	358	4	US-09-438-185A-902
43	77.5	8.3	383	4	US-09-248-796A-14833
44	77	8.3	154	1	US-08-366-783-5
45	77	8.3	424	4	US-09-543-681A-7510

ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
US-08-700-607-1

Query Match 99.6%; Score 927; DB 2; Length 199;  
Best Local Similarity 100.0%; Pred. No. 7.9e-93;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 VVDLYWRDIKKTGVVFGASIFLLLSLTVPFSIVSVAYIALALLSVTISFRIYKGVQAI 61

Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71  
QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 121  
Db 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 131  
QY 122 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 181  
Db 132 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 191  
QY 182 PGLKRAE 189  
Db 192 PGLKRAE 199

## RESULT 2

US-09-949-016-9124  
; Sequence 9124, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9124  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9124

Query Match 99.6%; Score 927; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 8e-93; Indels 0; Gaps 0;  
Matches 188; Conservative 0; Mismatches 0

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 14 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 73  
QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 121  
Db 74 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 133  
QY 122 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 181  
Db 134 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 193  
QY 182 PGLKRAE 189  
Db 194 PGLKRAE 201

## RESULT 3

US-08-700-607-7  
; Sequence 7, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 208 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307311  
US-08-700-607-7

Query Match 73.3%; Score 682; DB 2; Length 208;  
Best Local Similarity 68.4%; Pred. No. 3.8e-66;  
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQ 62  
Db 22 IDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVVAYLALAALSATISFRIYKSVLQAVQ 81  
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYLM 122  
Db 82 KTDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYLM 141  
QY 123 WYFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKIP 182  
Db 142 WLLTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKIP 201  
QY 183 GLKRAE 189  
Db 202 GAKRAE 208

## RESULT 4

US-08-700-607-6  
; Sequence 6, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304



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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307309
US-08-700-607-6

Query Match 73.3%; Score 682; DB 2; Length 356;
Best Local Similarity 68.4%; Pred. No. 8e-66;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIAIQ 62
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Db 170 IDLLYWRDIKQTGIVFGSFLLLSFTQFSVVVAYLALAALSATISFRIYKSVLQAVQ 229

QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITKELRRFLVDLVDLSLKFVLM 122
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 230 KTDEGHPFKAYLELITLSQEQIQYDCLQFYVNSTLKELRRFLVDLVDLSLKFVLM 289

QY 123 WVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIQAKIP 182
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 290 WLLTYVGALFNGLTLLMAVSMFTLPVVYVKHQAQIDQYLGVLVTRTHINAVVAKIQAKIP 349

QY 183 GLKRAE 189
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Db 350 GAKRAE 356

RESULT 5
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180
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Query Match 73.3%; Score 682; DB 4; Length 439;
Best Local Similarity 68.4%; Pred. No. 1.1e-65;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIAIQ 62
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Db 253 IDLLYWRDIKQTGIVFGSFLLLSFTQFSVVVAYLALAALSATISFRIYKSVLQAVQ 312

QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITKELRRFLVDLVDLSLKFVLM 122
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 313 KTDEGHPFKAYLELITLSQEQIQYDCLQFYVNSTLKELRRFLVDLVDLSLKFVLM 372

QY 123 WVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIQAKIP 182
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 373 WLLTYVGALFNGLTLLMAVSMFTLPVVYVKHQAQIDQYLGVLVTRTHINAVVAKIQAKIP 432

QY 183 GLKRAE 189
|||
Db 433 GAKRAE 439

RESULT 6
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 1.5
; CURRENT APPLICATION DATA: US/08/700,607
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

Query Match 73.3%; Score 682; DB 2; Length 776;
Best Local Similarity 68.4%; Pred. No. 2.4e-65;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIAIQ 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 590 IDLLYWRDIKQTGIVFGSFLLLSFTQFSVVVAYLALAALSATISFRIYKSVLQAVQ 649
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; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match      67.4%; Score 627.5; DB 4; Length 192;
Best Local Similarity 61.1%; Pred. No. 2.9e-60;
Matches 116; Conservative 38; Mismatches 35; Indels 1; Gaps 1;

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Db 3 SVHDLIFWRDVKKTGFVGTTLIMLLSLAAPSIVSWSYLLALSVTIRIYKSVIOA 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 IOKSDEGHPPFRAYLSEVAISELVQKYSNAGLHVNCTIKELRFLVDDLVSLKFAV 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VQSEEGHPPFRAYLDVDTLSEAFHNTYNAWVHINRAKLIIRFLVEDLVSLKLA 122
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 LMWVTYVYGVALFNGTLLILALISLFSVPVYERHQAIIDHYGLANKVNDMAKIOAK 180
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 FWMIMTYVGVAVFNGITLLILAEILFSPVIVVEKYKTQIDHYVGIARDQTKSIVEKIOAK 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 IPGL-KRKA 189
   :|||:|||||
Db 183 LPGIACKKAE 192
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RESULT 10
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
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; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
```



APPLICANT: Goli, Surya K.  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: THPINOB01  
CLONE: 31870  
US-08-700-607-3

Query Match 55.0%; Score 512; DB 2; Length 241;  
Best Local Similarity 52.4%; Pred. No. 1.4e-47;  
Matches 98; Conservative 35; Mismatches 34; Indels 20; Gaps 1;  
QY 1 SVVDLLYWRDIKKTGVFCASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 60  
DB 47 AVHDLIXWRDVKTGFVGTLLMLLSAASFVISVSVLLIALLSVTISFRIYKSVIOA 106  
QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCITKELRRLFLVDDLVDSLKPAV 120  
DB 107 VQKSEGHPPKAYLDVDTLSSEAFHYNMAAMVHNRAKLIIRLFLVEDLVDSLKLV 166  
QY 121 LMWVTTYGALFNGTLTLLIALLISLFSVPVIYERHOAQIDHYGLANKNVKDMAKIOAK 180  
DB 167 FNLMTYTGAVFNGTLLIALLISLFSVPVIYXKY-----KVPESK 206  
QY 181 IPLKRX 187  
DB 207 TPWRQK 213

RESULT 13  
US-09-949-016-7290  
Sequence 7290, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7290  
LENGTH: 588  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7290  
Query Match 50.9%; Score 473.5; DB 4; Length 588;  
Best Local Similarity 47.3%; Pred. No. 7.8e-43;  
Matches 95; Conservative 37; Mismatches 56; Indels 13; Gaps 1;  
QY 2 VVDLLYWRDIKKTGVFCASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 61  
DB 388 VADLLYWKDTRTSGVFTGLMVSLCLLHFSIVSVAHALLLCCGTISLRYRKVLOAV 447  
QY 62 QKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCITKELRRLFLVDDLVDSLKFAVL 121  
DB 448 HRGDGANFPQAYLDVDTLTREQTERLSHOITSRVVSATQLRHFFVEDLVDSLKALL 507  
QY 122 MWVTTYGALFNGTLTLLIALLISLFSVPVIYERHOAQIDHYGLANKNVKDMAKIOAK 181  
DB 508 FVILTFVGAIENGLTLLIILGVLGTLFTLLYRQHQAOIDQVVGVLVTNQLSHIKAKIRAKI 567  
QY 182 PGL-----KKAE 189  
DB 568 PGTGALASAAAAVSGSKAE 588  
RESULT 14  
US-09-149-476-411  
Sequence 411, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: PZ002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618

[illegible]

EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 30.6%; Score 285; DB 4; Length 92;  
Best Local Similarity 57.1%; Pred. No. 1.9e-23;  
Matches 52; Conservative 20; Mismatches 19; Indels 0; Gaps 0;  
Oy 90 NSALGHVNCITKELRRLFLVDDLVDLSLKFVFLMWVFTYVVGALFNGLTLLILALISLPSVP 149  
Db 2 NAAMVHNRALKLIIRLFLVEDVDSLKLAVFMWMTYVGAVFNGITLLILAEELLIFSVP 61  
Oy 150 VIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
Db 62 IVEYKYQTIDHYVGIARDQTKSIVEKIPSK 92

RESULT 15  
US-09-513-999C-7861  
Sequence 7861, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO. 7861  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -48...-1  
OTHER INFORMATION: score 4.6  
OTHER INFORMATION: seq VFGSFLLLFSLT/QF  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 22  
OTHER INFORMATION: Xaa=Phe or Leu  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 41  
OTHER INFORMATION: Xaa= \* or Gly or Arg  
US-09-513-999C-7861

Query Match 26.4%; Score 246; DB 4; Length 114;  
Best Local Similarity 69.6%; Pred. No. 4.4e-19;  
Matches 48; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Oy 3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQ 62  
Db 22 IDLLYWRDIKQTGVVFGSFLLLFSLTQFSVVSVVAYIALAALSATISXRIYKSVLQAVQ 81

Oy 63 KSDEGHPR 71  
Db 82 ITDEGHRXR 90  
Search completed: June 16, 2005, 12:33:40  
Job time : 8.13706 secs,

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 5.68322 Seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SWVDLLYWRDIKKTGWFGA.....VKDAMAKIQAKIPGLKRAE 189.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	682	73.3	208	2 I60904	neuroendocrine-spe
2	682	73.3	776	2 A46583	neuroendocrine-spe
3	665	71.4	267	2 A60021	tropomyosin-relate
4	335	36.0	2484	2 T26216	hypothetical prote
5	335	36.0	2607	2 T26215	hypothetical prote
6	334	35.9	222	2 T26213	hypothetical prote
7	191	20.5	255	2 E84899	hypothetical prote
8	182	19.5	271	2 T13013	hypothetical prote
9	163	17.5	275	2 T05595	hypothetical prote
10	147	15.8	393	2 S67763	probable membrane
11	144.5	15.5	242	2 B85016	hypothetical prote
12	131	14.1	183	2 A84527	hypothetical prote
13	127.5	13.7	295	2 S59439	probable membrane
14	124	13.3	206	2 T01153	probable seed matu
15	109.5	11.8	264	2 T47948	hypothetical prote
16	104.5	11.2	203	2 T47571	hypothetical prote
17	95	10.2	288	2 B90043	conserved hypothet
18	94.5	10.2	458	2 A72258	hypothetical prote
19	93	10.0	160	2 C84422	hypothetical prote
20	92.5	9.9	527	2 A84645	probable cytochrom
21	86.5	9.5	405	2 H71692	hypothetical prote
22	88	9.5	224	2 D71915	hydrogenase, cytoc
23	87.5	9.4	296	2 S46018	probable membrane
24	85.5	9.2	442	2 C75057	hypothetical prote
25	85.5	9.2	823	2 H83724	hypothetical prote
26	85.5	9.2	1065	2 E69795	acriflavin resista
27	85	9.1	224	1 A64599	hydrogenase (EC 1.
28	85	9.1	459	2 G86264	F3F19 hypothetical
29	85	9.1	468	2 A38223	nicotinic acetylch

30	85	9.1	1055	2 H90023	hypothetical prote
31	84.5	9.1	151	2 G96705	unknown protein, 7
32	84.5	9.1	457	2 H85095	hypothetical prote
33	84.5	9.1	464	2 C70414	NADH2 dehydrogenas
34	84.5	9.1	677	2 F95232	immunity protein,
35	84.5	9.1	680	2 H98096	conserved hypothet
36	84	9.0	299	2 B69155	hypothetical prote
37	82.5	8.9	570	2 S52765	secD protein - Str
38	82.5	8.9	955	2 T33040	hypothetical prote
39	82	8.8	589	2 F64201	transport ATP-bind
40	81.5	8.8	324	2 A81700	phospho-N-acetylm
41	81.5	8.8	369	2 H90587	hypothetical prote
42	81.5	8.8	598	2 T14886	leukotoxin expres
43	81.5	8.8	822	2 T41622	probable ABC trans
44	81.5	8.8	937	2 T41400	probable peroxisom
45	81	8.7	537	2 G82873	conserved hypothet

#### ALIGNMENTS

##### RESULT 1

I60904

neuroendocrine-specific protein C - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: I60904

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.;

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-sp-

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: I60904

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-208 <RES>

A:Cross-references: UNIPROT:Q16799; GB:L10335; NID:G307310; PID:AA59952.1; PID:G307311

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 73.3%; Score 682; DB 2; Length 208;  
Best Local Similarity 68.4%; Pred. No. 2.8e-55;  
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

Qy	3	VDLLYWRDIKKTGVVFGASLRLLSLTVFSTVSTAYTALALLSVTISFRIYKGVIOAQ	62
Db	22	IDLLYWRDIKQTGIVFGSFLRLLSLTQFSVVSVVAYLALAAALSATISFRIYKSVLQAVQ	81
Qy	63	KSDEGHPFRAYLGESEVAISELVQKYSNSALGHVNCTIKELRRFLVDLVDLSKFAVLV	122
Db	82	KTDEGHPFKAYLELEITLSQEQIKYTDCLQFYVNSTLKELRRFLVQDLVDLSKFAVLV	141
Qy	123	WVTVYVGFALFNGLTLLILALISLFSVPVIYERHQADHYGLGNKVKDAMAKIQAKIP	182
Db	142	WLLTVYVGFALFNGLTLLMAVSMFTLPVVYVKHQADIDQYLGLVTRHINAVVAKIQAKIP	201
Qy	183	GLKRAE 189	
Db	202	GAKRAE 208	

##### RESULT 2

A46583

neuroendocrine-specific protein, splice form A - human

N:Contains: neuroendocrine-specific protein, splice form B

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.;

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: A4583  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-776 <ROE1>  
A:Cross-references: UNIPROT:Q16799; GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307  
A:Accession: I60903  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 421-776 <ROE2>  
A:Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309  
C:Genetics:  
A:Gene: GDB:RTN1; NSP  
A:Cross-references: GDB:203968; OMIM:600865  
A:Map position: 14q21-14q22

Query Match 73.3%; Score 682; DB 2; Length 776;  
Best Local Similarity 68.4%; Pred. No. 1.3e-54;  
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;  
QY 3 VDLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62  
DB 590 IDLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 649  
QY 63 KSDEGHPPFRAYLESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLM 122  
DB 650 KTDGEHPFRAYLESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLM 709  
QY 123 WFTYVYGVLFNGTLTLLILSLFSPVVIYERHQAOIDHYGLANKNVKDMAKIOAKIP 182  
DB 710 WLLTYVGVLFNGTLTLLILSLFSPVVIYERHQAOIDHYGLANKNVKDMAKIOAKIP 769  
QY 183 GLKRAE 189  
DB 770 GAKRAE 776

RESULT 3  
A60021  
tropomyosin-related protein; neuronal - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 05-Nov-1999  
C:Accession: A60021  
R:Wiczorek, D.F.; Hughes, S.R.  
Brain Res. Mol. Brain Res. 10, 33-41, 1991  
A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.  
A:Reference number: A60021; MUID:91278684; PMID:1647480  
A:Accession: A60021  
A:Molecule type: mRNA  
A:Residues: 1-267 <WIE>  
A:Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550  
C:Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Query Match 71.4%; Score 665; DB 2; Length 267;  
Best Local Similarity 67.2%; Pred. No. 1.4e-53;  
Matches 123; Conservative 33; Mismatches 27; Indels 0; Gaps 0;  
QY 3 VDLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62  
DB 13 IDLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 72  
QY 63 KSDEGHPPFRAYLESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLM 122  
DB 73 KTDGEHPFRAYLESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVLM 132  
QY 123 WFTYVYGVLFNGTLTLLILSLFSPVVIYERHQAOIDHYGLANKNVKDMAKIOAKIP 182  
DB 133 WLLTYVGVLFNGTLTLLILSLFSPVVIYERHQAOIDHYGLANKNVKDMAKIOAKIP 192  
QY 183 GLK 185  
DB 193 GAR 195

RESULT 4  
T26216  
hypothetical protein W06A7.3c - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26216  
R:Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z20173  
A:Accession: T26216  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2484 <WIL>  
A:Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CBSP:W06A7  
A:Experimental source: clone W06A7  
C:Genetics:  
A:Gene: CBSP:W06A7.3c  
A:Map position: 5  
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 36.0%; Score 335; DB 2; Length 2484;  
Best Local Similarity 33.7%; Pred. No. 3.6e-22;  
Matches 62; Conservative 46; Mismatches 76; Indels 0; Gaps 0;  
QY 2 VDLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 61  
DB 2289 VLDVYWRDAKSAIVLSLALVLFVLAQYPLTVVTVYSLLLALGAAAGFRVFKVQAI 2348  
QY 62 OKSDEGHPPFRAYLESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVL 121  
DB 2349 KKTDEHPFSEILAQDLTPQEKVHAQADVFEHATCIANKLKVVFVSPLESIKFGLV 2408  
QY 122 MVVFTYVGVLFNGTLTLLILSLFSPVVIYERHQAOIDHYGLANKNVKDMAKIOAKI 181  
DB 2409 LWSLTIVIASWFGFTLAILGLGVSPVKVYESNQEAIDPHLATISGHKLVNQNIIDEKL 2468  
QY 182 PGLK 185  
DB 2469 PFLR 2472

RESULT 5  
T26215  
hypothetical protein W06A7.3a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26215  
R:Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z20173  
A:Accession: T26215  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2607 <WIL>  
A:Cross-references: UNIPROT:Q23187; EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CBSP:W06A7  
A:Experimental source: clone W06A7  
C:Genetics:  
A:Gene: CBSP:W06A7.3a  
A:Map position: 5  
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match 36.0%; Score 335; DB 2; Length 2607;  
Best Local Similarity 33.7%; Pred. No. 3.8e-22;  
Matches 62; Conservative 46; Mismatches 76; Indels 0; Gaps 0;  
QY 2 VDLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 61  
DB 2412 VLDVYWRDAKSAIVLSLALVLFVLAQYPLTVVTVYSLLLALGAAAGFRVFKVQAI 2471  
QY 62 OKSDEGHPPFRAYLESEVAISELVOKYSNSALGHVNCITIKELRLFLVDDLVSLKFAVL 121  
DB 2472 KKTDEHPFSEILAQDLTPQEKVHAQADVFEHATCIANKLKVVFVSPLESIKFGLV 2531

RESULT 7  
E84899 hypotheical protein At2g46170 [imported] - Arabidopsis thaliana  
C.Species: Arabidopsis thaliana (mouse-ear cress)  
C.Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C.Accession: E84899  
R.Ribin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
L.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Heuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter,  
J.  
Nature 402, 761-768, 1999  
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A.Reference number: A84420; PMID:20083487; PMID:10617197  
A.Accession: E84899  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-255 <STO>  
A.Cross-references: UNIPROT:O82352; GB:AE002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN  
C.Genetics:  
A.Gene: At2g46170  
A.Map position: 2  
  
Query Match 20.5%; Score 191; DB 2; Length 255;  
Best Local Similarity 27.9%; Pred. No. 4.3e-10;

A/Map position: 4  
A/Introns: 89/1; 149/2; 196/3; 220/1  
A/Note: F9D16.100



C:Accession: S59439  
R:Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S59423  
A:Accession: S59439  
A:Molecule type: DNA  
A:Residues: 1-295 <MUR>  
A:Cross-references: UNIPROT:Q04947; EMBL:Z48612; PID:g728671; PID:g728688; GSPDB:GN00004  
F:40-56/Domain: transmembrane #status predicted <TM1>  
F:146-162/Domain: transmembrane #status predicted <TM2>

Query Match 13.7%; Score 127.5; DB 2; Length 295;  
Best Local Similarity 21.6%; Pred. No. 0.00034;  
Matches 45; Conservative 43; Mismatches 69; Indels 51; Gaps 5;  
QY 4 DLLYWRDIKKTGVFGASLFLSLTFSIVSVTAYIALALLSVTISFRIYKGVIAQK 63  
DB 22 DLLWRNPVQTKYFGSLLALLLKKVNLITFFLKVAYTILFT-----GSIEFV-- 72  
QY 64 SDEGHPPFRAYLESEVAISEELVQKY-----SNSALGHVNCITIKEL-----RRLFL 108  
DB 73 -----SKLFLOGLITKYGKPCNFIAGFIKPHIDEALKQLPVQAHIRKTVF 120  
QY 109 VDDLVDLSLKFAVLMMVFTYVGVGALFNGLTLLILALISLFSVPVYERHQAQID----- 160  
DB 121 AQVPHKTEKTAVALPFLHKKFSWFSITWTFVADIFTTLPVYHSYKHEIDATVAQGV 180  
QY 161 -----HYLGLANKVNDAMAKIOAKI 181  
DB 181 ISKQKTQBSQACEKTPYLDKVESKL 208

RESULT 14  
T01153  
probable seed maturation protein [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F27L4.17  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text\_change 09-Jul-2004  
A:Accession: T01153; T02426; C84627  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, June 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.  
A:Reference number: Z14198  
A:Accession: T01153  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-206 <ROU>  
A:Cross-references: EMBL:AC004482; NID:g3152602; PID:g3152617  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: C84627  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-206 <STO>  
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C:Genetics:  
A:Gene: At2g23640; F26B6.29; F27L4.17  
A:Map position: 2  
A:Introns: 14/1; 76/2; 147/1  
C:Superfamily: Arabidopsis thaliana hypothetical protein F27L4.17

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Best Local Similarity 24.4%; Pred. No. 0.00048;  
Matches 48; Conservative 44; Mismatches 75; Indels 30; Gaps 8;  
QY 2 VDDLWRDIKKTGVFGASLFLSLTFSIVSVTAYIALALLSVTISFRIYKGVIAQK 59  
DB 16 VEDIYLRKRLAPSTLLVSTSTWLLSYFGFTTIVSWIGIAVSMIF---LWGSLLR 72  
QY 60 AIQKSDGHPFRAYLESEVA---ISEELVQKYSNLSALGHVNCI---KELRRLFLVDDLV 113  
DB 73 LLSK-----VEPELSGLEVSEEFVETVRS-----CRMMEEMVVRMFRVGAES 116  
QY 114 DSLKFA--VL--MWFTYVGVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKV 170  
DB 117 EWFVARTVLGFWILSRIGNLLDFTCLFGLVGLTVPKLWEYGDQIQKHLGSLKDKS 176  
QY 171 KDMAKIOAKIPGLKRRK 187  
DB 177 KGAYNTTKEILEMKNK 193

RESULT 15  
T47948  
hypothetical protein F2A19.160 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T47948  
R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Que  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z24480  
A:Accession: T47948  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <DEH>  
A:Cross-references: UNIPROT:Q9M312; EMBL:AL132962  
A:Experimental source: cultivar Columbia; BAC clone F2A19  
C:Genetics:  
A:Map position: 3  
A:Introns: 68/1; 128/2; 164/1; 210/1  
A:Note: F2A19.160

Query Match 11.8%; Score 109.5; DB 2; Length 264;  
Best Local Similarity 25.2%; Pred. No. 0.014;  
Matches 55; Conservative 37; Mismatches 69; Indels 57; Gaps 14;  
QY 4 DLLYWRDIKKTGVFG--ASLFLSLTFSIVSVTAYI-----ALALLSVTISFRIYK 55  
DB 70 DVFLWRDKLSASVLGVATAIWLVELVEHFLSLVCHILIFALAAFLLSNAHAF--MVK 128  
QY 56 GVIO-----AIQKSDG-----HPFRAYLESEVAISEELVQK--YSN--SALGHVNCI 102  
DB 129 GTFPPYDCFTKRAEPGLCYFKHCKLRKGLBE---ISHELIQSTYETFSINGFVTRT--- 182  
QY 103 LRRFLVLDLVDLSLKFAVL--MWFTYVGVGALFNG--LTLILALISLFSVPVYERHQAQ 158  
DB 183 -----SIYIGSGFWADVNLGC---GKLVQLDSCFVLHVTVMLEYKHEDK 227  
QY 159 IDHYLGLANKVNDAM-----AKIOAKIPGLKRRKAE 189  
DB 228 VD---PVAEKTLLKELKHHVMVDFDEKVLKSLPVSASLAK 262

Search completed: June 16, 2005, 13:32:01  
Job time : 6.68322 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 25.6406 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SVVDLLYWRDIIKKTGVVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	931	100.0	986	2 Q81UA4	Q81ua4 homo sapien
2	931	100.0	1192	1 RTN4 HUMAN	Q9nqc3 homo sapien
3	928	99.7	392	2 Q96B16	Q96b16 homo sapien
4	927	99.6	199	2 Q7YRW9	Q7yrw9 bos taurus
5	927	99.6	343	2 Q6IPN0	Q6ipn0 homo sapien
6	923	99.1	199	2 Q6IM70	Q6im70 sus scrofa
7	919	98.7	187	2 Q6IG15	Q6ig15 sus scrofa
8	918	98.6	199	2 Q7PCJ7	Q7pcj7 macaca fasc
9	915	98.3	578	2 Q8OW95	Q8ow95 mus musculus
10	915	98.3	639	2 Q8K290	Q8k290 mus musculus
11	915	98.3	1046	2 Q8BGK7	Q8bgk7 mus musculus
12	915	98.3	1162	2 Q8BGM9	Q8bgm9 mus musculus
13	912	98.0	375	2 Q8BHf5	Q8bhf5 mus musculus
14	911	97.9	199	1 RTN4 MOUSE	Q99p72 mus musculus
15	911	97.9	356	2 Q8BH78	Q8bh78 mus musculus
16	908	97.5	1163	1 RTN4 RAT	Q9jk11 rattus norv
17	904.5	97.2	1163	2 Q8K3G8	Q8k3g8 mus musculus
18	900.5	96.7	357	2 Q8K3G7	Q8k3g7 mus musculus
19	889	95.5	658	2 Q8RS58	Q8rs58 gallus gall
20	882	94.7	199	2 Q7T224	Q7t224 gallus gall
21	867	93.1	179	2 Q9GM33	Q9gm33 macaca fasc
22	790	84.9	193	2 Q61FY5	Q61fy5 xenopus tro
23	789	84.7	315	2 Q61FY4	Q61fy4 xenopus tro
24	781	83.9	1024	2 Q6JRV2	Q6jrv2 xenopus lae
25	781	83.9	1043	2 Q6JRV0	Q6jrv0 xenopus lae
26	781	83.9	1055	2 Q6JRV1	Q6jrv1 xenopus lae
27	778	83.6	193	2 Q6JRV6	Q6jrv6 xenopus lae
28	778	83.6	330	2 Q6JRV4	Q6jrv4 xenopus lae
29	777	83.5	199	2 Q6PB23	Q6pb23 xenopus lae
30	777	83.5	311	2 Q6JRV3	Q6jrv3 xenopus lae
31	752	80.8	1013	2 Q6JRV9	Q6jrv9 xenopus lae

32	752	80.8	1032	2 Q6JRV7	Q6jrv7 xenopus lae
33	752	80.8	1044	2 Q6JRV8	Q6jrv8 xenopus lae
34	750	80.6	214	2 Q7T222	Q7t222 carassius a
35	749	80.5	193	2 Q6JRW4	Q6jrw4 xenopus lae
36	749	80.5	323	2 Q6JRW1	Q6jrw1 xenopus lae
37	748	80.3	199	2 Q6JRW3	Q6jrw3 xenopus lae
38	748	80.3	304	2 Q6JRW0	Q6jrw0 xenopus lae
39	748	80.3	316	2 Q6JRW2	Q6jrw2 xenopus lae
40	729	78.3	196	2 Q61E16	Q61e16 cyprinus ca
41	725	76.8	193	2 Q61EJ4	Q61ej4 fugu rubrip
42	710	76.3	197	2 Q66H23	Q66h23 brachydania
43	696.5	74.8	209	2 Q61EJ1	Q61ej1 oncorhynch
44	682	73.3	199	2 Q9BQ59	Q9bq59 homo sapien
45	682	73.3	776	1 RTN1_HUMAN	Q16799 homo sapien

ALIGNMENTS

RESULT 1  
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ID Q81UA4 PRELIMINARY; PRT; 986 AA.  
AC Q81UA4; TREMBLrel. 23, Created  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE RTN4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform F) (RTN4 isoform G) (RTN4 isoform Aa).  
DE F) (RTN4 isoform G) (RTN4 isoform Aa).  
GN Name=RTN4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Van der Putten H.;  
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RP Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RC TISSUE=Testis;  
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RA Oertle T., Schwab M.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; AY123523; AAM64527.1; -  
DR EMBL; AY123524; AAM64528.1; -  
DR EMBL; AY123525; AAM64529.1; -  
DR EMBL; AY123526; AAM64530.1; -  
DR EMBL; AY123527; AAM64531.1; -  
DR EMBL; AY123528; AAM64532.1; -  
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DR EMBL; AY123531; AAM6453

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121 LKMFVTVGALFNGLLTLLIALISLSPVIVYERHQAQIDHYLGLANKVNDAMAKIOAK 180  
918 LKMFVTVGALFNGLLTLLIALISLSPVIVYERHQAQIDHYLGLANKVNDAMAKIOAK 977  
181 IPGLKRAE 189  
978 IPGLKRAE 986  
RESULT 2  
RTN4\_HUMAN  
ID RTN4\_HUMAN STANDARD; PRT; 1192 AA.  
AC Q9NQC3; Q94962; Q9BXG5; Q9H212; Q9H313; Q9UQ42; Q9V293; Q9V2V7;  
AC Q9V5U6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Focoten)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
DE protein C homolog) (RTN-X) (Reticulon 5) (My043 protein).  
GN Name=RTN4; Synonyms=ASV, KIAA0886, NOGO;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Printha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
RA Michalovich D., Simmons D.L., Walsh F.S.;  
RT "Inhibitor of neurite outgrowth in humans.";  
RL Nature 403:383-384(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Brain;  
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";  
RT Oncogene 19:5736-5746(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
RT 2p14-->2p13 by radiation hybrid mapping.";  
RT Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RA Jin W.-L., Ju G.;  
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";  
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human.";  
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";  
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Placenta;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
RA Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Nature 403:439-444(2000).  
RL [15]

RL [15]  
RN [15]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;  
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
RT "Identification of the Nogo inhibitor of axon regeneration as a  
RT reticulon protein.";  
RL Nature 403:439-444(2000).  
RN [15]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
RX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 5:355-364(1998).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
RA Bosak S.A., McGowan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Umbilical cord blood;  
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells.";  
RL Genome Res. 10:1546-1560(2000).  
RN [12]  
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
RC TISSUE=Brain;  
RA Mao Y.M., Xie Y., Zheng Z.H.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RA Sha J.H., Zhou Z.M., Li J.M.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP TOPOLOGY.  
RC TISSUE=Brain;  
RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;  
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
RT "Identification of the Nogo inhibitor of axon regeneration as a  
RT reticulon protein.";  
RL Nature 403:439-444(2000).  
RN [15]

Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.





DR GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro: IPR003388; Reticulon.  
 DR Pfam: PF02453; Reticulon; 1.  
 DR PROSITE: PS0845; RETICULON; 1.  
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 Best Local Similarity 99.5%; Pred. No. 5.5e-71;  
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QY 121 LMWFTYVGLFNGLTLLILALISLFSVPVYERHOAQIDHYLGLANKNVKDMAKIOAK 180  
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QY 181 IFGLKRAE 189  
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 Db 384 IFGLKRAE 392  
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RESULT 4  
 QY7RW9 PRELIMINARY; PRT; 199 AA.  
 AC Q7YRW9;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE RTN4-C.  
 GN Name=RTN4;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22715887; PubMed=12832288;  
 RA Oertle T.; Klinger M.; Stuermer C.A.; Schwab M.E.;  
 RT "A reticular thapsody: phylogenetic evolution and nomenclature of the  
 RT RTN/Nogo gene family";  
 RL FASEB J. 17:1238-1247(2003).  
 DR EMBL; AV164744; AAP47319.2; -.  
 DR GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro: IPR003388; Reticulon.  
 DR Pfam: PF02453; Reticulon; 1.  
 DR PROSITE: PS0845; RETICULON; 1.  
 SQ SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;

Query Match 99.6%; Score 927; DB 2; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-71;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71  
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QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 121  
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 Db 72 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 131  
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QY 122 MVVFTYVGLFNGLTLLILALISLFSVPVYERHOAQIDHYLGLANKNVKDMAKIOAKI 181  
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QY 182 PGLKRAE 189  
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Db 192 PGLKRAE 199  
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RESULT 5  
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 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RTN4 protein.  
 GN Name=RTN4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.B.; Feingold E.A.; Grouse L.H.; Derge J.G.;  
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;  
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;  
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;  
 RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;  
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;  
 RA Brownstein M.J.; Udgin T.B.; Ioshizuka S.; Carninci P.; Prange C.;  
 RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;  
 RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;  
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;  
 RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;  
 RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;  
 RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;  
 RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;  
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;  
 RA Krzywinski M.I.; Skalska U.; Smailus D.E.; Scherch A.; Schein J.E.;  
 RA Jones S.J.; Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; BC071848; AAH71848.1; -.  
 DR GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro: IPR003388; Reticulon.  
 DR Pfam: PF02453; Reticulon; 1.  
 DR PROSITE: PS0845; RETICULON; 1.  
 SQ SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;

Query Match 99.6%; Score 927; DB 2; Length 343;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-71;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
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 Db 156 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 215  
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 Db 216 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 275  
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QY 122 MVVFTYVGLFNGLTLLILALISLFSVPVYERHOAQIDHYLGLANKNVKDMAKIOAKI 181  
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 Db 276 MVVFTYVGLFNGLTLLILALISLFSVPVYERHOAQIDHYLGLANKNVKDMAKIOAKI 335  
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QY 182 PGLKRAE 189  
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 Db 336 PGLKRAE 343  
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RESULT 6
Q6IM70
ID Q6IM70 PRELIMINARY; PRT; 199 AA.
AC Q6IM70;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
RTN4-C.
DE RTN4-C.
GN Sus scrofa (Pig).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family."
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ third party annotation (TPA) entry.
DR EMBL; BK001795; DAA01967.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22425 MW; C61D11DF3FB34D80 CRC64;

Query Match 99.1%; Score 923; DB 2; Length 199;
Best Local Similarity 99.5%; Pred. No. 7.4e-71;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDILLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 12 VDILLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

Qy 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 121
Db 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 131

Qy 122 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 181
Db 132 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 191

Qy 182 PGLKRAE 189
Db 192 PGLKRAE 199

RESULT 7
Q6IG15
ID Q6IG15 PRELIMINARY; PRT; 187 AA.
AC Q6IG15;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
RTN4-Aw (Fragment).
DE RTN4-Aw (Fragment).
GN Sus scrofa (Pig).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family."
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ third party annotation (TPA) entry.
DR EMBL; BK003966; DAA01973.1; -.

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DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 187 AA; 20967 MW; A17D87A143C4607C CRC64;

Query Match 98.7%; Score 919; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 1.5e-70;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VDILLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 62
Db 1 VDILLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 60

Qy 63 KSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 122
Db 61 KSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 120

Qy 123 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 182
Db 121 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 180

Qy 183 GLKRAE 189
Db 181 GLKRAE 187

RESULT 8
Q7PCJ7
ID Q7PCJ7 PRELIMINARY; PRT; 199 AA.
AC Q7PCJ7;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
RTN4-C.
DE RTN4-C.
GN Name=RTN4;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family."
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ third party annotation (TPA) entry.
DR EMBL; BK001695; DAA01940.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22469 MW; 761A5FDB6C1DEC3C CRC64;

Query Match 98.6%; Score 918; DB 2; Length 199;
Best Local Similarity 98.4%; Pred. No. 2e-70;
Matches 185; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDILLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 12 VDILLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

Qy 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 121
Db 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 131

Qy 122 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 181
Db 132 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 191

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QY 182 PGLKRAE 189
Db 192 PGLKRAE 199

RESULT 9
Q80W95 PRELIMINARY; PRT; 578 AA.
ID Q80W95
AC Q80W95;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN Names=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 98.3%; Score 915; DB 2; Length 578;
Best Local Similarity 98.4%; Pred. No. 1e-69;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 390 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 449
QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLVDSLKPAV 120
Db 450 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLVDSLKPAV 509
QY 121 LMWFTYVYVGFALFNGLLTLLILALISLFSVPVYERHQAQIDHYGLANKVNDAMAKIOAK 180
Db 510 LMWFTYVYVGFALFNGLLTLLILALISLFSVPVYERHQAQIDHYGLANKVNDAMAKIOAK 569
QY 181 IPLKRAE 189
Db 570 IPLKRAE 578

RESULT 10
Q8K290 PRELIMINARY; PRT; 639 AA.
ID Q8K290
AC Q8K290;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-WAR-2004 (TREMBlrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032192; AAH32192.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 98.3%; Score 915; DB 2; Length 639;
Best Local Similarity 98.4%; Pred. No. 1.2e-69;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 451 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 510
QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLVDSLKPAV 120
Db 511 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLVDSLKPAV 570
QY 121 LMWFTYVYVGFALFNGLLTLLILALISLFSVPVYERHQAQIDHYGLANKVNDAMAKIOAK 180
Db 571 LMWFTYVYVGFALFNGLLTLLILALISLFSVPVYERHQAQIDHYGLANKVNDAMAKIOAK 630
QY 181 IPLKRAE 189
Db 631 IPLKRAE 639

RESULT 11
Q8BGK7 PRELIMINARY; PRT; 1046 AA.
ID Q8BGK7
AC Q8BGK7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Rtn4.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SvcJ7, and 129SvCJ7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [2]
RP SEQUENCE FROM N.A.
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RC STRAIN=129/SvcJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102280; AAM73502.1; -.  
DR EMBL; AY102286; AAM73507.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E238ED51222 CRC64;  
  
Query Match 98.3%; Score 915; DB 2; Length 1046;  
Best Local Similarity 98.4%; Pred. No. 1.9e-69;  
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 858 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 917  
  
Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRFLVDDLVSLKFAV 120  
Db 918 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRFLVDDLVSLKFAV 977  
  
Qy 121 LMWFTYVYVGFALFNGTLTLLILALISLFSVPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 180  
Db 978 LMWFTYVYVGFALFNGTLTLLILALISLFSVPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 1037  
  
Qy 181 IPGLKRKAE 189  
Db 1038 IPGLKRKAE 1046  
  
RESULT 12  
Q8BGM9 PRELIMINARY; PRT; 1162 AA.  
AC Q8BGM9;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE RTN4.  
GN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SVCJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102284; AAM73506.1; -.  
DR PROSITE; PS50845; RETICULON; 1.

DR EMBL; AY102286; AAM73511.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1162 AA; 126612 MW; 855697PBEE11781F CRC64;  
  
Query Match 98.3%; Score 915; DB 2; Length 1162;  
Best Local Similarity 98.4%; Pred. No. 2.1e-69;  
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 974 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1033  
  
Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRFLVDDLVSLKFAV 120  
Db 1034 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRFLVDDLVSLKFAV 1093  
  
Qy 121 LMWFTYVYVGFALFNGTLTLLILALISLFSVPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 180  
Db 1094 LMWFTYVYVGFALFNGTLTLLILALISLFSVPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 1153  
  
Qy 181 IPGLKRKAE 189  
Db 1154 IPGLKRKAE 1162  
  
RESULT 13  
Q8BHF5 PRELIMINARY; PRT; 375 AA.  
AC Q8BHF5;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE RTN4.  
GN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SVCJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102282; AAM73504.1; -.  
DR EMBL; AY102286; AAM73509.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.



DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	RTN4.
DE	GN
OS	Name=Rtn4;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	STRAIN=129/SvcJ7, and 129SVScJ7;
RX	MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2936(02)01179-8;
RA	Certle T., Huber C., van der Putten H., Schwab M.E.;
RT	"Genomic structure and functional characterisation of the promoters of
RT	human and mouse nogo/rtn4.";
RL	J. Mol. Biol. 325:299-323(2003).
RL	[2]
RP	SEQUENCE FROM N.A.
RP	STRAIN=129/SvcJ7;
RC	Van der Putten H.;
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL	[3]
RP	SEQUENCE FROM N.A.
RP	STRAIN=129SVScJ7;
RC	Van der Putten H., Mir A.;
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY102281; AAM73503.1; -;
DR	EMBL; AY102286; AAM73508.1; -;
DR	MGD; MGI:1915835; Rtn4.
DR	GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR	GO; GO:0005515; F:protein binding; IPI.
DR	GO; GO:0001525; P:angiogenesis; IMP.
DR	GO; GO:0007399; P:neurogenesis; IDA.
DR	InterPro; IPR003388; Reticulon.
DR	Pfam; PF02453; Reticulon; 1.
DR	PROSITE; PS50845; RETICULON; 1.
DR	SEQUENCE 356 AA, 38403 MW, 4366C03BA9630B56 CRC64;

Query Match	97.9%;	Score 911;	DB 2;	Length 356;
Best Local Similarity	98.4%;	Pred. No. 1.4e-69;		
Matches 185;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;
QY	2	VDLLYWRDIIKKTGVVFGASLFLLLSLTVFSIYSVTAYIALALLSVTISFRIYKGVIOAI	61	
Db	169	VDLLYWRDIIKKTGVVFGASLFLLLSLTVFSIYSVTAYIALALLSVTISFRIYKGVIOAI	228	
QY	62	QKSDGHPFPFRAYILESEVAISEELVQKYSNSALGHVNCTIIKELRRLFLVDDLVDSLKPFAVL	121	
Db	229	QKSDGHPFPFRAYILESEVAISEELVQKYSNSALGHVNSTIIKELRRLFLVDDLVDSLKPFAVL	288	
QY	122	MMVFTTVGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAKI	181	
Db	289	MMVFTTVGALFNGLTLLILALISLFSIPVIYERHQAOIDHYLGLANKSVKDMAKIOAKI	348	
QY	182	PGLKRXAE	189	
Db	349	PGLKRXAE	356	

Search completed: June 16, 2005, 13:17:43  
Job time : 26.6406 secs

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